SEQ	Predicted	Predicted end	Amino agid a
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
3	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
J	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	"	\=possible nucleotide insertion)
			ISDYFERRYEQPLYGLDGSAAKEATEEQSALPTLMSVMLAKPRL
1	Ì		DTEQLAQRGAGLCFTFVSAQQNSPSSTGSGNTEHSCSSQKQISI
1	J	Í	QHRQT\QSDLTIEKISALENSKNSDLEKKEGRIDDLLRANCDLR
l			RQI\DEQQKMLEKYK\ERLNRCFDNEFRNFLIEKSKQEKMACRD
			KSMQDRLRLGHFTTVRHGASFTEQWTDGYAFQNLIKQQERINSQ
1	Į.		REEIERORKMLAKRKPPAMGQAPPATNEQKORKSKTNGAENETL
	1		TLAEYHEQEEIFKLRLGHLKKEEAEIQAELERLERVRNLHIREL
			KRIHNEDNSQFKDHPTLNDRYLLLHLLGRGGFSEVYKAFDLTEQ
			RYVAVKIHQLNKNWRDEKKENYHKHACREYRIHKELDHPRIVKL
1	1		YDYFSLDTDSFCTVLEYCEGNDLDFYLKQHKLMSEKEARSIIMQ
1			IVNALKYLNEIKPPIIHYDLKPGNILLVNGTACGEIKITDFGLS
1			KIMDDDSYNSVDGMELTSOCACTYMYLDDBCDSTACHDD
1			KIMDDDSYNSVDGMELTSQGAGTYWYLPPECFVVGKEPPKISNK VDVWSVGVIFYQCLYGRKPFGHNQSQQDILQENTILKATEVQFP
			PKPVVTPEAKAFIRRCLAYRKEDRIDVQQLACDPYLLPHIRKSV
	[STSSPAGAAIASTSGASNNSSSN
5996	1612	981	DQQACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
	ł		LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
1			AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
			FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
			FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP
5997	1612	981	DQQACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
	· .		LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
	1		AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
]	1		FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
	<u></u>		FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP
5998	1612	981	DQQACLLGLMLTLEFGILEFDPSWIGSWIQR/SWVSWRSRPGCE
i i	ŀ		LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
1			AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
1 1	1		FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
L			FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP
5999	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP
1 1	ļ	ļ	GDGHDSHTLPEEWKYLPFLALPDGAHNYOEDTVFFHT.DDBNGNG
1 1	i		ATVFGISCYR\QIEAKALKVROADITRETVOKSVCVI,SKI,DI,VC
1	į.		LLQAKLQLITHAYFEEKDFSOISILKELYEHMNSSI.GGASI.EGS
1 1	1	7	QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVI,FYTSDUNKT,UG
l i	ŀ		ALMIVLSLFPGMIEHGLSDCSOYRPRKSMSEDGGIOESNPCADD
1. !			FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFOVEDSS
] [i	j	KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVI,EDPNI,KFPF
Į [}	İ	QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE
	j	i	EDQYGMPLAIFTKGYLCLPYMALOOHHLLSDVTVRGFVAGATNI
		[LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADI. PFADVI.
1			VRHVTENRUDVFLDGTGWEGGDEWIRAOFAVYTHAT.I.AATLOT.V
		İ	LFRIVNVAKKIGNVMVTT\SRNVVOTGK\AVGOSVCCAFS\SAK
6000	101	156	TA\MSSWLSTFTTSTSOSLTEPPDEKP
	101	1561	TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL
! !	ì		DDFEDKVFYRTEFONREFKATMCNLLAYLKHI.KGONEALECT.B
ŀ	ļ		KAEELIQQEHADQAEIRSLVTWGNYAWVYYHMGRLSDVQIYVDK
ļ	İ	J.	VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNONERAKUCFFK
J	į	J.	ALEKKPKNPEFTSGLAIASYRLDNWPPSONATDPLPOATDLWDD 1
1	ſ	1	NQYLKVLLALKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV
1		1.	LRSAA\KFYRGKDEPDKAIELLKKALEYIP\NNAYLHCOTGCCV
}		.	RAKVFQVMNLRBNGMYGKRKLLELIGHAVAHLKKADEANDNI.FP
1		1	VCSILASLHALADQYEDAEYYFQKEFSKELTPVAKOLLHLRYGN
1		1	FQLYQMKCEDKAIHHFIEGVKINQKSREKEKMKDKLOKTAKMRI.
1		1 :	SKNGADSEALHVLAFLQELNEKMQQADEDSERGLESGSLIPSAS
6001	176	1	SWNGE]
		1038	AFAHSPSRGHRHTHIHTPRHTPRCTMAESHLQSSLITASQFFEI
	ļ		WLHFDADGSGYLEGKELONLIOELOOARKKAGLELSPEMKTEVD
		1.9	QYGQRDDGKIGIVELAHVLPTEENFLLLFRCQQLKSCE\EFMKT
			WRKYDTDHSGFIETEELKNFLKDLLEKANKTVDDTKLAEYTDLM
			• • • • • • • • • • • • • • • • • • • •

SEQ	Predicted	Predicted end	Amino acid segment
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
]	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S-Serine, T-Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			LKLFDSNNDGKLELTEMARLLPVQENFLLKFQGIKMCGKEFNKA
		,	FELYDQDGNGYIDENELDALLKDLCEKNKQDLDINNITTYKKNI
]		MALSDGGKLYRTDLALILCAGDN
6002	977	81	LAPPGGGLHIPPRTPLSHSRPPPSHHAPHPSPLPLPPADLHPHS
	j		SMAQRSDLLELDCQLTRDRVVVVSHDENLCRQSGLNRDVGSLDF
			EDLPLYKEKLEVYFSPGHFAHGSDRRMVRLEDLFQRFPRTPMSV
	1	1	EIKGKNEELIREQ/VLVRRYDRNEITIWASEKSSVMKKCKAANP
			EMPLSFTISRGFWVLLSYYLGLLPFIPIPEKFFFCFLPNIINRT
		i	YPPFSCSCLNQLLAVVSKWLIMRKSLIRHLEERGVQVVFWCLNE
	1		ESDFEAAFSVGATGVITDYPTALRHYLDNHGPAARTS
6003	140	4098	GKLPAFPCMBDI TOVDI CONVO
	1		GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRPSSAASAFKVP
			APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA
			PTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR
i			SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA
			HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII
			RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLQEWQTHSLE
			RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY
	!		NSLEPSYQKSLQTYLKSSGSVASLPQSDRSSSSSQESLNRPFSS
i			KWSTANPSTVAGRVSAGSSKASSLPGSLQRSRSDIDVNAAAGAK
			AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV
1			RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQPGSRSGSPGRVLT
1		•	TTALSTVSSGVQRVLVNSASAQKRSKIPRSQGCSREASPSRLSV
-	1		ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFQPLASRHHSRS
i			TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLNTGSDVEEA
- 1	ļ		VADALLLGDIRTKKKPARRYESYGMHSDDDANSDASSACSERS
	}		YSSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGLLGLQN
	1		LLKNORTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI
1			QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES
	İ		FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD
ľ		İ	FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFELNTPE
}	,	j	FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSMGSPLTRPTP
1			RSPANWSSPLTSPTNTSQNTLSPSAFDYDTENMNSEDIYSSLRG
1			VTEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPRA
1	1		GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPYNYSDSIS
	•		PFNKSALKEAMFDDDADQFPDDLSLDHSDLVAELLKELSNHNER
1	1	i	VEERKIALYELMKLTQEESFSVWDEHFKTILLLLETLGDKE>T
1	l	Į	IRALALKVLREILRHOPARFKNYAELTVMKTLEAHKDPHKEVVR
	{		SABEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQT
1			KVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKACVFCLVAV
		1	HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS GOS
6004	140	4098	GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRPSSAASAFKVP
ł			APKTSGNDDNSAPKDGSAGGDKKGAGGGGNGSAASAFKVP
ļ	1	ł	APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA FTDVPSIQIYSSRELBETLNKIREILSDDKHDWDQRANALKKIR
- 1	i	ł	SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA
1		-	HISTVICANCEDUCAEA THEME DIVINION TO THE STATE OF THE STAT
	Į.] ;	HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII
		;	RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLQEWQTHSLE
1		1;	RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY
i	j		NSLEPSYQKSLQTYLKSSGSVASLPQSDRSSSSSQESLNRPFSS
- 1	1	1 ;	KWSTANPSTVAGRVSAGSSKASSLPGSLQRSRSDIDVNAAAGAK
1		1;	AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV
İ		1.5	RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQPGSRSGSPGRVLT
ļ		1;	TTALSTVSSGVQRVLVNSASAQKRSKIPRSQGCSREASPSRLSV
- 1	1	[*	ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFQPLASRHHSRS
ļ	İ	13	GALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLNTGSDVERA
- 1	ł	1.	/ADALLIGDIRTKKKPARRYESYGMHSDDDANSDASSACSERS
	I	j Y	SSRNGSIPTYMRQT\EDV\ABVLNRCASSNWSERKEGI.GT.ON
		I	LKNQRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI
	i	F 1	THE PERSON OF TH
		9	VHKDDLQDWLFVLLTQLLKKMGADLLGSVOAKVOKALDVTBEC
		F	VHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES PNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD 'INSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFELNTPE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ĺ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ľ	sequence	bequence	\=possible nucleotide insertion)
	bequence	 	FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSMGSPLTRPTP
		1	
-			RSPANWSSPLTSPTNTSQNTLSPSAFDYDTENMNSEDIYSSLRG
1		}	VTEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPRA
			GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPYNYSDSIS
j	į		PFNKSALKEAMFDDDADQFPDDLSLDHSDLVAELLKELSNHNER
1	1	f	VEERKIALYELMKLTQEESFSVWDEHFKTILLLLLETLGDKEPT
i	Ì		IRALALKVLREILRHQPARFKNYAELTVMKT_EAHKDPHKEVVR
			SAEEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQT
1	1		KVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKACVFCLVAV
1			HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS
5005			GQS
6005	133	5955	RSSGRRQEQLGQFPGRERKGMASGLGSPSPCSAGSEEEDMDALL
1	1		MNSLPPPHPENEEDPEEDLSETETPKLKKKKPKKPRDPKIPKS
1			KRQKKERMLLCRQLGDSSGEGPEFVEEBEEVALRSDSEGSDYTP
			GKKKKKLGPKKEKKSKSKRKEEEEEDDDDDDDSKEPKSSAQLL
ĺ	İ		BDWGMEDIDHVFSEEDYRTLTNYKAFSQFVRPLIAAKNPKIAVS
Į.			KMMMVLGAKWREFSTNNPFKGSSGASVAAAAAAAVAVVESMVTA
			TEVAPPPPPVEVPIRKAKTKEGKGPNARRKPKGSPRVPDAKKPK
į.	1		PKKVAPLKIKLGGFGSKRKRSSSEDDDLDVESDFDDASINSYSV
1			SDGSTSRSSRSRKKLRTTKKKKKGEEEVTAVDGYETDHQDYCEV
			CQQGGEIILCDTCPRAYHMVCLDPDMEKAPEGKWSCPHCEKEGI
1	1		QWEAKEDNSEGEEILBEVGGDLEEEDDHHMEFCRVCKDGGELLC
			CDTCPSSYHIHCLNPPLPEIPNGEWLCPRCTCPALKGKVQKILI
1	ľ		WKWGQPPSPTPVPRPPDADPNTPSPKPLEGRPERQFFVKWQGMS
1			YWHCSWVSELQLELHC\QVMFRNYQRKNDMDEPPSGDFGGDEEK
			S\RKRKNKDPKFAEMEERFYRYGIKPEW\MMIHRILNHSVDKKG
]			HVHYLIKWRDLPYDQASWESEDVEIQDYDLFKQSYWNHRELMRG
			EEGRPGKKLKKVKLRKLERPPETPTVDPTVKYERQPEYLDATGG
1			TLHPYQMEGLNWLRFSWAQGTDTILADEMGLGKTVQTAVFLYSL
			YKEGHSKGPFLVSAPLSTIIN\WEREFEMWAPDMYV\VTYVGDK
1			DSRAIIRENEFS\FEDNAIRGGKKASRMKKEASVKFHVLLTSYE
1	į		LITIDMAILGSIDWACLIVDEAHRLKNNQSKFFRVLNGYSLQHK
			LLLTGTPLQNNLEELFHLLNFLTPERFHNLEGFLEEFADIAKED
i			QIKKLHDMLG\PHMLRRLKADVFKNMPSKTBLIV\RVELSPM\Q
		i	KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNHPY
			LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEGGH
	1		RVLIFSQMTKMLDLLEDFLEHEGYKYERIDGGITGNMRQEAIDR
1 1			FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQ
			AFSRAHRIGONKKVMIYRFVTRASVEERITOVAKKKMMLTHLVV RPGLGSKTGSMSKQELDDILKFGTEELFKDEATDGGGDNKEGED
1			SSVIHYDDKAIERLLDRNODETEDTELOGMNEYLSSFKVAOYVV
j	[REEEMGEEEEVEREIIKQEESVDPDYWEKLLRHHYEQOOEDLAR
j i			NIGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEGDE
] !			DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFNAR
, !	!		QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVSLF
	1		MRHLCEPGADGAETFADGVPREGLSROHVLTRIGVMSLIRKKVO
1	1		EFEHVNGRWSMPELAEVERNKKMSOPGSPSPKTPTPSTPGDTOP
1	İ		NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIECT
] i	ļ		OAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKGKG
1	İ		AADVEKVEEKSAIDLTPIVVEDKEEKKEEEEKKEVMLQNGETPK
1	İ		DLNDEKQKKNIKQRFMFNIADGGFTBLHSLWONEERAATVTKKT
j		ł	YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKGEM
		1	NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDPSH
	(ŀ	PSMALNTRFAEVECLAESHOHLSKESMAGNKPANAVLHKVLKOL
1 1			EELLSDMKADVTRLPATIARIPPVAVRLOMSERNILSRLANRAP
(1		İ	EPTPQQVAQQQ
6006	1	965	DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC
''''	-	703	GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAAVS
, [1		ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKVGV
}	}	1	CRVDPRGKPCETVFORLSYNGOSSVVRCRPLTGRTHOIRVHLOF
[]			LGHPILNDPIYNSVAWGPSRGRGGYIPKTNEELLRDLVAEHQAK
———— <u> </u>			

SEO	Predicted	Predicted end	Drive said coment containing at the said
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
J	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
· F	residue of		S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}		sequence	Codon, /=possible nucleotide deletion,
	aedneuce		\=possible nucleotide insertion)
ļ	i		QSLDVLDLCEGDLSPGLTDSTAPSSELGKDDLEELAAAA\QKME
	1		EVAEAAPQELDTIALASEKAVETDVMNQ\RQT\TLCRVPAGATG
			SLAPRPCDVPTCPTL
6007	3	2351	HELGQVEYVFTDKTGTLTENEMQFRECSINGMKYQEINGRLVPE
	ļ		GPTPDSSEGNLSYLSSLSHLNNLSHLTTSSSFRTSPRNETELIK
			EHDLFFKAVSLCHTVQINNVQTDCTGDGPWQSNLAPSQLEYYAS
			SPDEKALVEAAARIGIVFIGNSEETMEVKTLGKLERYKLLHILE
1			FDSDRRRMSVIVQAPSGEKLLFAKGAESSILPKCIGGEIEKTRI
	[HVDEFALKGLRTLCIAYRKFTSKEYEEIDKRIFEARTALQQR\E
	1		EKLAAVFQFIEKDLILLGATAVEDRLQDKVRETIEALRMAGIKV
1	1		WVLTGDKHETAVSVSLSCGHFHRTMNILELINQKSDSECAEQLR
	1		QLARRITEDHVIQHGLVVDGTSLSLALREHEKLFMEVCRNCSAV
Į.	1		LCCRMAPLQKAKVIRLIKISPEKPITLAVGDGANDVSMIQEAHV
1	1		GIGIMGKEGRQAARNSDYAIARFKFLSKLLFVHGHFYYIRIATL
1	ł		VQYFFYKNVCFITPOFLYQFYCLFSQOTLYDSVYLTLY\NICFT
1			SLPILIYSLLEQHVDPHVLQNKPTLYRDISKNRLLSIKTFLYWT
Ĭ			ILGFSHAFIFFGSYLLIGKDTSLLGNGQMFGNWTFGTLVFTVM
			VITVTVXMALETHFWTWINHLVTWGSIIFYFVFSLFYGGILWPF
1			
Í	ļ		LGSQNMYFVFIQLLSSGSAWFAIILMVVTCLFLDIIKKVFDRHL
1	i		HPTSTEKAQLTETNAGIKCLDSMCCFPEGEAACASVGRMLERVI GRCSPTHISRSWSASDPFYTNDRSILTLSTMDSSTC
6008	4554	1000	
0000	4354	1089	AGVRRAGARRGPGRALPAGATAVPPPSARRRRCPAPEHAGPAR
			ASRPSQETMFQLPVNNLGSLRKARKTVKKILSDIGLEYCKEHIE DFKOFEPNDFYLKNTTWEDVGLWDPSLTKNODYRTKPFCCSACP
	j i		
1			FSSKFFSAYKSHFRNVHSEDFENRILLNCPYCTFNADKKTLETH
1			IKIFHAPNASAPSSSLSTFKDKNKNDGLKPKQADSVEQAVYYCK
			KCTYRDPLYEIVRKHIYREHFQHVAAPYIAKAGEKSLNGAVPLG
	1		SNAREESSIHCKRCLFMPKSYEALVQHVIEDHERIGYQVTAMIG
ľ	İ		HTNVVVPRSKPLMLIAPKPQDKKSMGLPPRIGSLASGNV\RSLP
Į i			SQQMVNRLSIPKPNLNSTGVNMMSSVHLQQNNYGVKSVGQGYSV
[1		GQSMRLGLGGNAPVSIPQQSQSVKQLLPSGNGRSYGLGSEQRSQ
) .	ł i		APARYSLQSANASSLSSGQLKSPSLSQSQASRVLGQSSSKPAAA
	l		ATGPPPGNTSSTQKWKICTICNELFPENVYSVHFEKEHKAEKVP
			AVANYIMKIHNFTSKCLYCNRYLPTDTLLNHMLIHGLSCPYCRS
	l		TFNDVEKMAAHMRMVHIDEEMGPKTDSTLSFDLTLQQGSHTNIH
ł I			LLVTTYNLRDAPAESVAYHAQNNPPVPPKPQPKVQEKADIPVKS
]			SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ
			TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN
!!!			GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP
1			SFFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP
			TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL
(1			LGFNMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN
j l			LGKEDDSSSDSFENLEEESNESGSPFDPVFEVEPKISNDNPEEH
i I			VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS
ļ			EVDQDDVVEWKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDE
1 1			SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD
			QSQW:XNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP
L 1			MHGSLAGVKLSSQQA
6009	4272	1534	CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC
]			HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW
1			EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG
1			RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL
[]		NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG
			NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA
1	ſ		VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL
i 1	l		FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP
	ļ		I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN
ŀ	j		AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG
ļ j			DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP
1	ł		RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT
-	İ	į	RDLLRGGDRGHVVVIVLCRLGSLVGGLGTDELLWFGGR*LIIIG
			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	1		1 · · · · · · · · · · · · · · · · · · ·
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		į.	Codon, /=possible nucleotide deletion,
İ	amino acid	sequence	
ſ	sequence		\=possible nucleotide insertion
			I**RGRLSGEWGCGLGRGELFQVSIGIGVSIVHIGQGDHEVLGG
			AGLVERGALHATGOGVEALVQQLLDVGPAGALGLCDGAALFQGP
1	,	Į.	GRVGQLPAEGLQVCITLVAQWRMHDGRELGGAEWPWQALHGAAI
l .	l	1	
ŀ	1		CGVGGAILLKALSQYFLKGG*RLWCARGQ*PVKKRQRRWRG*TR
1	1	į.	R*NGLTIHCFN*LI*GAVCCRLVILRWCGLLEVHGVYGT*IHCL
1		1	GSFPGRLWP*PFISQERPNGHCQWEFRLAVPSWKCRWSRWRVRG
l	ľ	Į.	TWRYGNPLLNLL*GAWLGGAACGGQQGGPLSTWQACTGPGQAAF
[ŀ		1
1	1		LPPFQGACRPRTQRCRTWVCPIAWRQLLAYTRD
6010	1	3533	IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM
i .	ł	I.	AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD
	1	1	PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA
1		i	
1		[TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL
1	1	1	VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS
ĺ		í	IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP
		l .	PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC
	1	l	
1	1	1	IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP
1		I	IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM
Į.			TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK
l .			EAVDDIMVTI:NEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG
l	1		TFVDYOTTVVKYSKAIAVTAOEMMTKSVTNPBELGGLASOMTSD
İ	Į.	1	
	l .		YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\
ł	}	1	ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI
	1	ł	TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA
	İ		KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA
1		1	
į.	1		SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM
!	i	Ì	YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ
1	į.		ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE
	1		DVIATANLSRKAVSDMLTACKQASFHPDVSDEVRTRALRFGTEC
		1	TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA
	i	!	
1	1	i	EAMKGTEWVDPEDPTVIAETELLGAAASIEAAAKKLEQLKPRAK
1	İ		PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGK
			VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVQGHA
ļ	Į.		SEEKLISSAKOVAASTAOLLVACKVKADODSEAMRRLQAAGNAV
1		i	
i			KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM
	ł		LKKERELEEARKKLAQIRQQQYKFLPTELREDEG
6011	446	1835	LLQPAMRKSPGLSDCLWAWILLLSTLTGRSYGQPSLQDELKDNT
1	-		TVFTRILDRLLDGYDNRLRPGLGERVTEVKTDIFVTSFGPVSDH
1	1	Ì	DMEYTIDVFFRQSWKDERLKFKGPMTVLRLNNLMASKIWTPDTF
1	1		
1			FHNGKKSVAHNMTMPNKLLRITEDGTLLYTMRLTVR\AECPMAF
ŀ	ļ	1	GRDFPM\D\AHACPLKFGSYAYTRAEVVYEWTREPARSVVVAED
1	1]	GSRLNQYDLLGQTVDSGIVQSSTGEYVVMTTHFHLKRKIGYFVI
1	1	1	QTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTTLSIS
1	1]	ARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGYA
[}	1	
			WDGKSVVPEKPKKVKDPLIKKNNTYAPTATSYTPNLARGDPGLA
ł		ĺ	TIAKSATIEPKEVKPETKPPEPKKTFNSVSKIDRLSRIAFPLLF
Ī	1	!	GIFNLVYWATYLNREPQLKAPTPHQ
6012	351	5013	PAELFOSFAIWHKELYDWRLGPWNQCQPVISKSLEKPLECIKGE
0012	1 331	2013	1
[1	l	EGIQVREIACIQKDKDIPAEDIICEYFEPKPLLEQACLIPCQQD
1		1	CIVSEFSAWSECSKTCGSGLQHRTRHVVAPPQFGGSGCPNLTEF
1	1		QVCQSSPCEAEELRYSLHVGPWSTCSMPHSRQVRQARRRGKNKE
ł	1	Ì	REKDRSKGVKDPEARELIKKKRNRNRONROENKYWDIOIGYOTR
i	1	l	1
1		I	EVMCINKTGKAADLSFCQQEKLPMTFQSCVITKECQVSEWSEWS
1	İ		PCSKTCHDMVSPAGTRVRTRTIRQFPIGSEKECPEFEEKEPCLS
1	1		QGDGVVPCATYGWRTTEWTECRVDPLLSQQDKRRGNQTALCGGG
1	Į.		IOTREVYCVQANENLLSQLSTHKNKEASKPMDLKLCTGPIPNTT
i	1		_ =
ŀ	I		QLCHIPCPTECEVSPWSAWGPCTYENCNDQQGKKGFKLRKRRIT
I	1		NEPTGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGK
l	1		ECGPGTQVQEVVCINSDGEEVDRQLCRDAIFPIPVACDAPCPKD
l	1		CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP
J	1		[· · · · ·
l	1	Ī	NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTW
l	<u> </u>	L	NGEASCSVGMQTRKVICVRVNVGQVGPKKCPESLRPETVRPCLL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
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	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence		\=possible nucleotide insertion)
			PCKKDCIVTPYSDWTSCPS\SCKEGDSSIRKQSRHRVIIQLPAN
1		į	GGRDCTDPLYEEKACEAPQACQSYRW\KTHKW\HRCQ\LVP\WS
ſ	İ	ĺ	VQQDSP\GAQEGCGPGRQARAITCRKQDGGQAGIHECLQYAGPV
i	Į.		PALTQACQIPCQDDCQLTSWSKFSSCNGDCGAVRTRKRTLVGKS
1	ĺ		KKKEKCKNSHLYPLIETQYCPCDKYNAQPVGNWSDCILPEGKVE
1			VLLGMKVQGDIKECGQGYRYQAMACYDQNGRLVETSRCNSHGYI
1	ł		EEACIIPCPSDCKLSEWSNWSRCSKSCGSGVKVRSKWLREKPYN
1	1		GGRPCPKLDHVNQAQVYEVVPCHSDCNQYLWVTEPWSICKVTFV
i			NMRENCGEGVQTRKVRCMQNTADGPSEHVEDYLCDPEEMPLGSR
1	1		VCKLPCPEDCVISEWGPWTQCVLPCNQSSFRQRSADPIRQPADE
1 .	1		GRSCPNAVEKEPCNLNKNCYHYDYNVTDWSTCQLSEKAVCGNGI
1			KTRMLDCVRSDGKSVDLKYCEALGLEKNWQMNTSCMVECPVNCQ
	1		LSDWSPWSECSQTCGLTGKMIRRRTVTQPFQGDGRPCPSLMDQS
1	1		KPCPVKPCYRWQYGQWSPCQVQEAQCGEGTRTRNISCVVSDGSA
			DDFSKVVDREFCADIBLIIDGNKNMVLEESCSQPCPGDCYLKDW
1	1		SSWSLCQLTCVNGEDLGFGGIQVRSRPVIIQELENQHLCPEQML
1	1		ETKSCYDGQCYEYKWMASAWKGSSRTVWCQRSDGINVTGGCLVM
1]		SQPDADRSCNPPCSQPHSYCSETKTCHCEEGYTEVMSSNSTLEQ
			CTLIPVVVLPTMEDKRGDVKTSRAVHPTQPSSNPAGRGRTWFLQ
			PFGPDGRLKTWYYGVAAGAFVLLIFIVSMIYLACKKPKKPQRRQ NNRLKPLTLAYDGDADM
6013	1161	710	GAFIAGVFVOPVLIRYPNSLDTTSWAWRGPGVLKVLWLTASOPC
0013	1 -101	/10	SIVDVEFLPVYHPSPEESRDPTLYANNVQRVMAQALGIPATECE
1			FVGSLPVIVVGRLKVALEPQL/WGTGKSASEGWAVRWLCGRWGR
	·		ARPESNDOPGRYCOAATAL
6014	2857	613	EAVAGGMEKSRMNLPKGPDTLCFDKDEFMKEDFDVDHFVSDCRK
3011	2037	013	RVQLEELRDDLELYYKLLKTAMVELINKDYADF\VNLSTNLVGM
1			DKALNOLSVPLGQLREEVLSLRSSVSEGIRAVDERMSKQEDIRK
1			KKMCVLRLIQVIRSVEKIEKILNSQSSKETSALEASSPLLTGQI
i			LERIATEFNQLQFHACQSK\GMPLLDKVRPRIAGITAMLQQSLE
			GLLLEGLQTSDVDIIRHCLRTYATIDKTRDAEALVGQVLVKPYI
ł			DEVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS
	ŀ		EKGNTVPGYDFLVNSVWPQIVQGLEEKLPSLFNPGNPDAFHEKY
1	į		TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI
[RFREIAGSLEAALTDVLEDAPAESPYCLLASHRTWSSLRRCWSD
			EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE
i			IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV
			ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALEDSQSSFS
1			ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS
1			SYVDSALKPLFQLQSGHKDKLKQAIIQQWLEGTLSESTHKYYET
			VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL
Į.			QLALDVEYLGEQIQKLGLQASDIKSFSALAELVAAAKDQATAEQ
			P
6015	13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC
1			VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN
1			RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
	j		GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT
			HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR
1			EGIBEEDQEEDKNIVVDDITEQKPBPQDDGKSTESDVKADGDSK GSEEVDSHCKKALSHKELYERARELLVSYEEEQFTVLEKFRYLP
			KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT
			PEOLAALQIEYEENVDLNDVLVPKPFSQFWQPLLRGLHSQNFTQ
			ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF
			SAGOWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPQLLRII
[F\KAMGQGLQDE\EQEKLLRICSIYTQSGENSLVQEGSEASPIG
			KSPYTLDSLYWSVKPASSSFGSEAKAQQQEEQGSVNDVKEEEKE
			EKEVLPDOVEEEEENDDQEEEEEDEDDEDDEEEDRMEVGPFSTG
	Ì		QESPTAENARLLAQKRGALQGSAWQVSSEDVRWDTFP\LGRMPR
			SRPRTPAELMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL
,			\SCGVGS\GNCSNSSSSNFRGAFLLEARGSLH\GL\KTGLQLF
			AEGCAERRGTEPVVELSMSWESGAGPGLGSOGMDLVWSAWYGKC
6016.	13	2237	I AEGCAERRGIEPVVELSMSWESGAGPGLGSOGNDLDVWSAWIGRU I

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
L	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion) VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN
			RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
l]		GMALVREVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT
į.	Ì		HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR
ļ			EGIEEEDQEEDKNIVVDDITEQKPEPQDDGKSTESDVKADGDSK
	1		GSEEVDSHCKKALSHKELYBRARELLVSYEEEQFTVLEKFRYLP
l	İ		KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT
]		FEQLAALQIEYEENVDLNDVLVPKPFSQFWQPLLRGLHSQNFTQ
}			ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF
		ļ	SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPQLLRII
Į	ļ		F\KAMGQGLQDE\EQEKLLRICSIYTQSGENSLVQEGSEASPIG
			KSPYTLDSLYWSVKPASSSFGSEAKAQQQEEQGSVNDVKEEEKE
	1		RKEVLPDQVEEEERNDDQEEEEEDEDDEDDEEEDRMEVGPFSTG
			QESPTAENARLLAQKRGALQGSAWQVSSEDVRWDTFP\LGRMPR
	1		SRPRTPAELMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL \SCGVGS\GNCSNSSSSNFRGAFLLEARGSLH\GL\KTGLOLF
6017	203	3469	SHOEIEONSAMAPRKRGGRGISFIFCCFRNNDHPEITYRLRNDS
001,	243	2.02	NFALOTMEPALPMPPVEELDVMFSELVDELDLTDKHREAMFALP
	i .		AEKKWOIYCSKKKDOEENKGATSWPEFYIDQLNSMAARKSLLAL
1		İ	EKEEEERSKTIESLKTALRTKPMRFVTRFIDLDGLSCILNFLK
			TMDYETSESRIHTSLIGCIKALMNNSQGRAHVLAHSESINVIAQ
İ			SLSTENIKTKVAVLEILGAVCLVPGGHKKVLQAMLHYQKYASER
1	•		TRFQTLINDLDXSTGRYRDEVSLXTAIMSFINAVLSQGAGVESL
			DFRLHLRYE\FLMLGIHPVMDKLRKHENSTLDRHLDFFEMLRNE
1	i		DELEFAKRFELVHIDTKSATOMFELTRKRLTHSEAYPHFMSILH
	i		HCLQMPYKRSGNTVQYWLLLDRIIQQIVIQNDKGQDPDSTPLEN FNIKNVVRMLVNENEVKOWKEQAEKMRKEHNELQQKLEKKEREC
	(DAKTQEKEEMMQTLNKMKEKLEKETTEHKQVKQQVADLTAQLHE
ł			LSRRAVCASIPGGPSPGAPGGPFPSSVPGSLLPPPPPPPPLPGGM
			LPPPPPPLPPGGPPPPPGPPPLGAIMPPPGAPMGLALKKKSIPQ
1	<u> </u>		PTNALKSFNWSKLPENKLEGTVWTEIDDTKVFKILDLEDLERTF
			SAYQRQQDFFVNSNSKQKEADAIDDTLSSKLKVKELSVIDGRRA
			QNCNILLSRLKLSNDEIKRAILTMDEQEDLPKDMLEQLLKFVPE
1			KSDIDLLEEHKHELDRMAKADRFLFEMSRINHYQQRLQSLYFKK
l			KFAERVAEVKPKVEAIRSGSEEVFRSGALKQLLEVVLAFGNYMN
	1		KGQRGNAYGFKISSLNKIADTKSSIDKNITLLHYLITIVENKYP SVLNLNEELRDIPQAAKVNMTELDKEISTLRSGLKAVETELEYQ
1	ļ		KSQPPQPGDKFVSVVSQFITVASFSFSDVEDLLAEAKDLFTKAV
			KHFGEEAGKIQPDEFFGIFDQFLQAVSEAKQENENMRKKKEEEE
			RRARMEAQLKEQRERERKMRKAKENSEESGEFDDLVSALRSGEV
			FDKDLSKLKRNRKRITNOMTDSSRERPITKLNF
6018	13	2510	TISQSGGIRRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY
	!		ALSSSYSSDALDFETEHKLDPVFDSPRMSRRSLRLATTACTLGD
	1	}	GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV
			TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD
ł			GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT
			AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIW
			ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYOFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG
1			LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ
			PLOGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK
	1		LOARVDOMEGGAAGPSASVRDAVGOPPRETDFMAFHQEHEVRMS
	ļ		HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL
)		ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED
			QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV
			TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG
			MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR
			VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL
			SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF
6019		1000	QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK TPNDREPPPQRPPSSRRASHLAQEITSAASLGDQTQILGSLTTA
10013	2	1066	TENDURELEGUES DE LEGUES DE

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	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ì	to first	amino acid	P-Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	
ĺ			S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			PVITSAIRSMPGISSQILTNAQGQVIGTLPWVVNSASVAAPAPA
1		f	QSLQVQAVTPQLLLNAQGQVIATLASSPLPPPVAVRK\PSTPES
İ	j	1	LLKSEVQPIKPTPTVPQPAVVIASPAPAAKPSASAPIPITCSET
1	1	ł	PTVSQLVSKPHTPSLDEDGINLEEIREFAKNFKIRRLSLGLTQT
1	1	ł	QVGOALTATEGPAYSQSAICRFEKLDITPKSAQKLKPVLEKWLN
1			EAELRNOEGOONLMEFVGGEPSKKRKRRTSFTPOAIEALNAYFE
1	ì		KNPLPTGQBITEIAKELNYDREVVRVWFCNRRQTLKNTSKLNVF
ļ	1	i	OIP
	L		
6020	4953	549	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
Ī	1		AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI
1	1		QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
			RKLRSRSLSQIHEAAVRMRSBATDVKSTLAEIEDWLDKLMQLTE
	1		EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
1	1		GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
	ĺ		GTFTVFAEMYENOALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
	1		FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP
]	1	i	GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
J			AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
1			LTQTASSTAGAMEELQDQEGWEYASLIGWKFHNKQRSSDTFRRR
}			RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA
ì			TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
1			YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ
1 :			NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
}			HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP
i .]		QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVBCGGERV
1			ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ
(FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR
	i		DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEERIV
		İ	DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVABFEGLT
1			
1			DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVPAPP
			ROFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
1	1 .		KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
İ			TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
1			RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
			FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP
1			NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
1			NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW
]			SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI
			HFLOKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGNW
]		PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP
	ĺ		KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL
1			LFVAVLLYSLPNYLSMKIVKPNV
6021	4953	549	EAIOFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
5521	7.503	343	AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI
1 1	İ		· · · · · · · · · · · · · · · · · · ·
			QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
[RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE
			EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
[GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
1 1			GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
}			FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP
1 1			GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
1			AVDEKGWEYGITIPPDHKPKSWVAABKMYHTHRRRRLVRKRKKD
[LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTFRRR
			,
, 1			RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA
			TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
[[YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ
1			NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
i l			HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP
1	İ		QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV
]			ESVVIKNLKKTPNFPSSVLFMKVFLPKEBLYMPPLVIKVIDHRQ
]			FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ļ	location	corresponding	Glutamic Acid, F=Phenylalamine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
]	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine
	residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown + 2500
İ	sequence	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV
	i		DWWSKFYASSGEHEKCGOYIOKGYSKLKIYNCELENVAFFECLT
			DESDTEKLYRGKSDENEDPSVVGEFKGSFRIVDI.PDDDSVDADD
		İ	ROFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
			KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
			TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
			PEANKILHOHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP
	1		WIS/RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
			NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW
	1		SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI
			HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASI,FEOKSMKGWW
			PCYAEROGARVMAGKVEMTLEILNEKEADERDAGKGDDEDNIMND
			KLDLPNRPBTSFLWFTNPCKTMKFIVWRRFKWVITGLT.FLT.T.
6022	4953	F48	LEVAVLLYSLPNYLSMKIVKPNV
	.,,,,	549	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
			AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI
			QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
	1		RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE EPONSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
]		GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
			GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
]		FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP
			GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSVDIND
			AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRIJVPKPKZD
		}	LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKORSSDTEDDD
			RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKOKHGA
			TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
	1		YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ
			NPPKVIMELFONDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
1		İ	HPVMNGDKACGDVLVTABLILRGKDGSNLPILPPQRAPNLYMVP QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV
		1	ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ
1		i	FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR
			DIVIEWEDTKPLLASKCLSSMSTALSKMASPATUHLTEKERETU
	į	1	DWWSKFYASSGEHEKCGOYIOKGYSKI.KIYNCELENWARERGI.T
1		i i	DFSDTFKLYRGKSDENEDPSVVGEPKGSFRIYDI, DDDSVDA DD
	1		ROFRELPDSVPQECTVRIYIVRGLELOPODNNGLCDPVTKITLG
- 1	ĺ	į	KKVIE \DRDHYIPNTLNPVFGRMYELSCYLPOEKDI.KISVVDVD
- 1			TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
		ŀ	RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
		1	FEANKILHOHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
		•	NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW
.			SIDQTEFRIPPR\LIIOIW\DNDKFS\LDDYLGEPPTLTCPUTT
j		1.	HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASI.FEOKSMKGWW
1	}	1.	PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDERNMND
1		1.	KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLTI.
6023	102		LFVAVLLYSLPNYLSMKIVKPNV
	102	916	SQELGMFVELNNLLNTTPDRAEQGKLTLLCDAKTDGSFLVHHPL
		1.5	FYLKANCKVCFVALIOSFSHYSTVGOKTGVST.TMAPERGOTATE
1		4	LEGL/IVCSGR\VFOAOKEPHPLOPLREANAGNIKDI.FFF10F7
1		; 1	LKPVDSGEARWTYPVLLVDDLSVLLSLGMGAVAVIDFTHYCDAT
		1,	/CWELKGNMVVLVHDSGDAEDEENDILLNGLSHQSHLILRAEGL
	_	, f	ATGFCRDVHGQLRILWRRPSQPAVHRDQSFTYQYKIQDKSVSFF
5024	3		LSFLCYPRFRCLFCLQFAIPASRMEQLNELELLMEKSFWEEAB
	١ د	3200 I R	
	·		PAELFOKKVVASEPPTVI STOMMENT IN THE TOTAL
	,	Ī	PAELFQKKVVASFPRTVLSTGMDNRYLVLAVNTVONKEGNCEV
	3	L	PAPLIFOKKVVASFPRTVLSTGMDNRYLVLAVNTVQNKEGNCEK LVITASQSLENKELCILKNDWCSVPVEPGDIIHLEGDCTSDTW IDKDFGYLILYPDMLISGTSIASSIRCMRRAVLSETFRSSDPA

SEQ	Predicted	Predicted end	1 Amino - / 3
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Ston
- 1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence	<u>i. </u>	(\=possible nucleotide insertion)
1			YRLNLSQDEIKQEVEDYLPSFCKWAGDFMHKNTSTDFPOMOLST
			PSDNSKDNSTCNIEVVKPMDIEESIWSPRFGLKGKIDVTVGVKI
İ	· ·	}	HRGYKTKYKIMPLELKTGKESNSIEHRSOVVLYTLLSOERRADD
			EAGLLLYLKTGQMYPVPANHLDKRELLKLRNOMAFSLFHRISKS
1			ATROKTQLASLPQIIEEEKTCKYCSOIGNCALYSRAVROOMDCG
1	į		SVPIVMLPKIEEETQHLKQTHLEYFSLWCLMLTLESOSKDNKKN
J		ł	HQNIWLMPASEMEKSGSCIGNLIRMEHVKIVCDGOYLHNFOCKH
l l	ĺ		GAIPVTNLMAGDRVIVSGEERSLFALSRGYVKEINMTTVTCLLD
ł			RNLSVLPESTLFRLDQEEKNCDIDTPLGNLSKLMENTFVSKKLR
			DLIIDFREPQFISYLSSVLPHDAKDTVACILKGLNKPQRQAMKK
1	1		VLLSKDYTLIVGMPGTGKTTTICTLVRILYACGFSVLLTSYTHS
ĺ	1		AVDNILLKLAKFKIGFLRSR\QIQKVHPAIQQFTEHEICRSKSI
	}		KS\LALLEELYTSQLIDATTCMGINHPIFSRKIFDFCIVDEASQ
1			ISQPICLGPLFFSRRFVLVGDHQQLPPLVLNREARALGMSESLF
ŀ	1		KRLEQNKSAVVQLTVQYRMNSKIMSLSNKLTYEGKLECGSDKVA NAVINLRHFKDVKLELEFYADYSDNPWLMGVFEPNNPVCFLNTD
1			KVPAPEQVEKGGVSNVTEAKLIVFLTSIFVKAGCSPSDIGIIAP
1 .			YRQQLKIINDLLARSIGMVEVNTVDKYQD\RDKSIVLVSFVRSN
j	·		KDGTVGELLKDWRRINVAITRAKHKLILLGCVPSLNCYPPI.EKI.
6025			LNHLNSEKLIIDLPSREHESLCHILGDFORE
0023	3977	89	GGFPAQSDHLPPVFPLRSDLLITMSTLYVSPHPDAFPSLRALIA
			ARYGEAGEGPGWGGAHPRICLQPPPTSRTSFPPPRLPALEQGPG
ı			GLWVWGATAVAQLLWPAGLGGPGGSRAAVLVQQWVSYADTELIP
1			AACGATLPALGLRSSAQDPQAVIGALGRALSPLEEWLRLHTYLA GEAPTLADLAAVTALLLPFRYVLDPPARRIWNNVTRWFVTCVRQ
1		1	PEFRAVLGEVVLYSGARPLSHQPGPEAPALPKTAAQLKKEAKKR
			EKLEKFQQKQKIQQQQPPPGEKKPKPEKREKRDPGVITYDLPTP
			PGEKKDVSGPMPDSYSPRYVEAAWYPWWEQQGFFKPEYGRPNVS
İ			AANPRGVFMMCIPPPNVTGSLHLGHALTNAIODSLTRWHRMPGE
	1		TILWNPGCDHAGIATQVVVEKKLWREOGLSRHOLGREAFLOEUW
	1		KWKEEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTRAFVP
1]	i	LHEEGIIYRSTRLVNWSCTLNSAISDIEVDKKELTGRTLLSVPG
	1		YKEKVEFGVLVSFAYKVQGSDSDEEVVVATTRIETMLGDVAVAV
1	1	1	HPKDTRYQHLKGKNVIHPFLSRSLPIVFDEFVDMDFGTGAVKIT PAHDQNDYEVGQRHGLEAISIMDSRGALINVPPPFLGLPRFEAR
ļ	1 1		KAVLVALKERGLFRGIEDNPMVVPLCNRSKDVVEPLLRPQWYVR
1	1	l	CGEMAQAASAAVTRGDLRILPERHQRTWHAWMDNIRE\WCMFPG
]		KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGRYWVSGRNRARARE
			KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSILGWPNOSED
		ļ	LSVFYPGTLLETGHDILFFWVARMVMLGLKLTGRLPFREVYLHA
i	1		IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS
i i			EVEKAKEGQKADFPAGIPECGTDALRFGLCAYMSQGRDINLDVN
1		j	RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR
1			WIRSRLTEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC LKPVLNGVDQVAABCARQTLYTCLDVGLRLLSPFMPFVTEELFQ
1		İ	RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA
1 1		į ·	VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG
		Į ·	QAQVVVAVAEPWGLPAP\OGCAVALASDRCST\HLOLOG\LLDP
i i		1.	ARELG\KLQ\AKRVEAQ\ROAO\RLR\ERRA\ASGNPVKVPT.\F
6026	2632		VQEADEAKLQQTEAELRKVDEAIALFQKML
1 0020	2674	514	GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC
]			TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ
	i		TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV
	[YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN
}	ļ	1;	LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH
		1	VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL
	i	1 3	ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESIML
		1	NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN
		3	IRFMEPDSLFCVDPPEFOGONVROVHFRDMMEICLPLIAPESFD
			ENLNVEAGSYVSFHCRATA\EPQPEIYWITPSGQKLLPNT\LTD

SEQ	Predicted	Predicted end	I Design
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	In-nighting, C=CVSTPING D_Nessuri = n = 1 n
	location		Glucamic Acid, F=Phenvlalanine G-Glucine
1	corresponding	corresponding	n=nistidine, I=Isoleucine K-Tareine
	to first	to first	L=Leucine, M=Methionine, N=Asparagine
- 1	amino acid	amino acid	P=Proine, Q=Glutamine, R=Arginine
ł		residue of	S=Serine, T=Threonine, V=Valine
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine Y=Unknown + 0+
J	amino acid	sequence	[Codon, /=possible nucleotide deletion
	sequence	_i	\=Fossible nucleotide insertion)
			KFYVHSEGTLDINGVTPKEGGLYTCIATNLVGADLKSVMIKVDG
- 1			SFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFVK
1			TENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNR
1		1	KKCVNVTTKGLHPDQKEYEKNNTTTLMACLGGLLGIIGVICLIS
	1	ł	CLSPRMMCDCCUCYUDAYY OYDDAYY GALLOCALGIGVICLIS
L			CLSPEMNCDGGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKS TSLKVKATVIGLPTNMS
6027	5254	4148	
I	· F	12.0	GGRRAPGRPGRSIKDEEEETVFREVVSFSPDPLPVRYYDKDTTK
1	1		PISFYLSSLEELLAWKPRLEDGFNVALEPLACROPPLSSQRPRT
ŀ	1		LLCHDMMGGYLDDRFIQGSVVQTPYAFYHWQCIDVFVYFSHHTV
ļ	ľ	1	TIPPVGWTNTAHRHGVCVLGTFITEWNEGGRLCEAFLAGDERSY
ļ	1		QAVADRLVQIT\RFFRFDGWLINIENSLSLAAVGNMPPFLRYLT
1	i		TQUHRQVPGGLVLWYDSVVOSGOLKWODELNOHNDVFEDGCDCE
		1	FININGREEHLERMLGOAGERRADUVUGUDUFARGNINGGREDE
1			DKVGGGFRPRASGPVPPLGPHFLMDI,PFPSAPOPNDSCCSCOCC
6028	120		DPVALRNRCPAPAKLCPH
	120	3432	NCLLLQAKGFHGEIEDLQQWLTDTERHLLASKPLGGLPETAKEQ
]	1		I WANTER CAAFEAKEETYKSLMOKGOOMI A DCDYGA PTNITDODT
i	· ·		MNLKEKWESVETKLNER\KT\KLREALNIA\MEFHNSI\ODBIN
			WLTQAEQTLNVASRPSLILDTVLFOTDRHKVFANEUNGUDBOTT
	f .		ELDKIGTHLKYFSQKQDVVLIKNLLITSVOSRWEKUVORLIEBOR
1	j i		SLUDARKKAKQFHEAWSKLMEWLRESEKSIDSET.FTANDDDVIV
	[[TQLAQHKEFQKSLGAKHSVYDTTNRTGRSI,KEKTSI,ADDM VID
	,	I	DMLSSLRDKWDTICGKSVERONKLEEA\T.LESCOFTDALOALID
1	j		WLIKVEPQLAEDQPVHGDIDLVMNT,IDNHKAFOKELGKBTCCVD
			ALKKSAKELIEGSRDDSSWVKVOMOELSTRWETUCALSISVOMD
1	1		LEAALRQAEEFHSVVHALLEWLAEAEQTLRFHGVLPDDEDALRT
1	1		LIDOHKEFMKKLEEKRAELNKATTMGDTVLAICHPDSITTIKHW
i	[]	İ	ITIIRARFEEVLAWAKQHQQRLASALAGLIAKQELLEALLAWLQ
1	1		WAETTLIDKDKEVIPQEIEEVKALIAEHQTFMEEMTRKQPDVDK
1]]	VTKTYKRRAADPSSLQSHIPVLDKGRAGRKRFPASSLYPSGSQT
]	i I	i	QIETKNPRVNLLVSKWQQVWLLALERRRKLNDALDRLEELREFA
1	i	i	NFDFDIWRKKYMRWMNHKKSRVMDFFRRIDKDQDGKITRQEFID
1 .		,	GILSSKFPTSRLEMSAVADIFDRDGDGYIDYYEFVAALHPNKDA
			YKPITDADKIEDEVTRQVAKCKCAKRFQVEQIGDNKYRFFLGNQ
j i	Í	ŀ	FGDSQQLRLVRILRSTVMVRVGGGWMALDEFLVKNDPCRAKGRT
1 1		f.	NMBLREKFILADGASQGMAAFRPRGRRSRPSSRGASPNRSTSVS
}	1	1	SQAAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA
]		1	ECSDFPVPSAEGTPIQGSKLRLPGYLSGKGFHSGEDSGLITTAA
1 1	j		ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE
1 1	i	1	IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK
		1	LDKSSKR
6029	1	3533	IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM
1	ſ	1.	AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD
! [PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA
	ļ] -	TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL
1 1	1	1,	VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS
l i		1 :	IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP
1	1] ;	PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC
1 1	}	1 ;	PRIFOASIANISOSI AMBRITISTROKAPGORECDYSIDGINRC
		1 :	RDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP
			ATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM
		[]	TVLDQTKTLABSALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK
}		1.5	AVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG
ŀ		1.3	PVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD
			GHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\
1		l A	LQVCPTDSYTKRELIECARAVTEKVSLVI.SAIOAGNKGTOAGT
1		{ 1	AATAVSGIIADLDTTIMFATAGTLNARNSETFADHDENTLYTA
- 1		Į K	ALVEDTKLLVSGAASTPDKLAOAAOSSAATTTOLAEVVYLCAA
ļ	1	Į S	LGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPUDDDOM
ľ		Į ¥	QLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALRATIECIKO
J	!	l R	LTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNGODOR
		D	VIATANLSRKAVSDMLTACKQASFHPDVSDEVRTRALRFGTEC
			- GIBC

Deginning nucleotide location corresponding corresponding corresponding cofiret amino acid residue of amino acid residue of amino acid sequence sequ	SEO	Predicted	Predicted end	I mino paid coment contribution
No: nucleotide location corresponding to first saino acid saino acid raidue of raidue	. ~		ľ	Amino acid segment containing signal peptide
corresponding to first sain acid to first sain acid residue of amino acid sequence s			1	Glutamia Acid E-Dhomalalanina G clari
Lefeucine, Membilonine, Nappingine, to first amino acid residue of amino acid residue of amino acid sequence Paproline, Qeolutamine, Rahgining, Nappining, on the sequence Paproline, Qeolutamine, Rahgining, Nappining, on the sequence Paproline, Qeolutamine, Rahgining, Nappining, on the sequence Paproline, Veryosine, Xubintonom, *stop Codon, /spossible mucleotide delection, Veryosine, Xubintonom, *stop Codon, /spossible mucleotide delection, Veryosine, Xubintonom, *stop Codon, /spossible mucleotide delection, Veryosine, Xubintonom, *stop Codon, /spossible mucleotide delection, Veryosine, Xubintonom, *stop Codon, /spossible mucleotide delection, Veryosine, Xubintonom, Veryosine, Xubin		3		U-Wietiding T T-1-1
to first maino acid mesidue of serine, Teffreonine, Vevaline, maino acid maino acid sequence	İ	1		n=mistidine, i=isoleucine, K=Lysine,
maino acid residue of amino acid sequence solvent proposals, N-Pyposing, N-Stop Codon, /-possible nucleotide deletion, **Stop Codon, /-possible nucleotide deletion, **Stop Codon, /-possible nucleotide deletion, **Stop Stop Stop Stop Stop Stop Stop Stop				b=Leucine, M=Methionine, N=Asparagine,
xesidue of amino acid sequence	İ	•		P=Proline, Q=Glutamine, R=Arginine,
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### TIGNIDLISHVIVILGKETELKOQIAAFSKRAVGAVTELIGAR ### EMMKOTEMVDEDTVILGTELIGAASSIRAANGANSLOCHRAK PQADETLIPSEQILEAAKSIAAATSALVKSASAQORSLUGARK PQADETLIPSEQILEAAKSIAAATSALVKSASAQORSLUGARK VOSIFANRAADGOGKSGGIISAAKVAAATSSLUKSASAQORSLUGAK KASADNIVRAAQOGKSGGIISAAKVAAATSSLUKSASAQORSLUGAK KASADNIVRAAQOGKSGGIISAAKVAADTSALVKSASAQORSLUGAK KASADNIVRAAQOVUTUTUTUAGUATATA LKKSRELEEAAKUAQIKQQVKFLPTELREBSS LKKSRELEEAAKUAQIKQQVKFLPTELREBSS LKKSRELEEAAKUAQIKQQVKFLPTELREBSS **********************************		sequence		\=possible nucleotide insertion)
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DSSSPQNVQRPHSSPPRFYTVEELLETARGVTNNALAHEIVVNN DPQIKPVELPENSLKRRVKEIVHKAFWDCLSVGLSEDPPAYDHA IKLVGEIKFILLSFLLDGHTRIQTIEVLDLDLKGBENGAL DISKLAFFIIGMMGTLCAPARDEEVKKLKDIKEIVPLFREIFSV LDLMKVDMANFAISSIRPHLMQQSVEYERKFGEILERQNSLD FVTOWLEEASEDLAMTOKYKHALPVGGMAAGSGOMPRISPVAVON YAYLKLLKUPHLORPFPETVLMDQSFPFERVKGGILERQNSLD LLVYFSMAAPGISSQADPAEKKMIVKILLTDMHLPSFHLKDVL TTIGEKVCLEVSSCLSLCGSSPFTTDKETVLKGQIQAVASPDDP IRRIMESRILTFIETYLASGHQKPLPTVPGGLSPVQRELEVAI KFARLVMYNKMVCPYYDAILSKULVRS SCDRIKEEFOPLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS GUTMAELMAIGQQQLQAQHLSHGGGLPVPLTPHPSGLQPPATP PIGSSAGLLALSSALGQSHLPLKEKKHDHNDHQRDRDSIKSS VSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGEDKTRLLKKOAPISP ASIASSSSTPSSKELSLINKSSTPVSKNNTTPFRTDAPTPGS NSTEGLPPVGKPPGVPDVBLASSLRTPMAVPCPYPTPFGIVPHAG MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAANSPSVOFD PHHMRVPAIPPNLTGIGGGRAVSFHVSADGGMQVPPPPPDAL IGPGIPHARQINTINHGEVVCAVTISNPTRHVYTGGKGVVKW DISHPGNKSPVSQLDCLNRDNYISCRLPPGTTLVGGEASTL SIMDLAAPTFRIKAELTSSAPACYALAISPDSKVCPSCCSDGNI AVMDLHNQTLVRQFGHTDGASCIDISNDGTKLWTGGLDNTYRS W\DLREGRGLQOMD/FFTSPVFGYCP\TEEMLAGMENSN\V EVLHVYKPDKYQLHHHSCVLSLKFAHCGKWP\VSTGKDNLLNA W\RTPYG\ASIF\QSKESSS\VJSCDI\SVDOKYIVTGS\GDK\ PATVYKVIY AARLCRAQPTKSAMWIRDLSKMYPQTRHPAPHQPAQPFKFTISE SCDRIKGEFOPLQAQYHSLKLECKLKABEKTEMQRHYVMYYEMS GUTMBELMAIIGOOOLOAGHLSHGHGLFVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGGSHLFI KDEKKHHDDNORDDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEKEIAARYDSDGEK SDDNLVVDVNENEDSSSPRSSFAHSPRENGLDKTRLLKKDAPISG SVSPSASFRGAEKHRNSADYSSESKKQKTEKEIAARYDSDGEK SDDNLVVDVNENEDSSSPRSSFAHSPRENGLDKTRLLKKDAPISG				
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DPQIKPVELPENSIKKRVKEIVHIKAPDCLEVQLSEDPPAYDEA IKLVGEIKETLLSFLIEGHTKIRNQITEVIDLDLIKQBAENGAL DISKLAEFIIGMMGTLCAPARDEEVKKLKDIKEIVPLFREIFSV LDLMKVUMANFAISSIRPHLMQQSVETERKKFQEILERQPNSLGI FVTOWLEBASEDLMTOKYKHALPVGGMAAGSGMPRISPVAVQN YAYLKLLKWDHLQRPFETTLMQGSRHEIQLQ\REQLTILGAV LLVTFSMAAPGISSQADFAEKLKMIVKILLTDMHLPSFHLKDVL LLVTFSMAAPGISSQADFAEKLKMIVKILLTDMHLPSFHLKDVL TTIGEKVCLEVSSCLSLCGSSPFTTDKETVLKGQIQAVASPDDP IRRIMERRILTFLETYLASGHQKPLPTVPGGLSPVQRELEEVAI KFARLVMYNKMVKPCPYYDAIKILVES SCDRIKEERQFLGAQVIFSKIKLURS ARRICRAQPTKSAMMIRDLSKMYPQTRHPAPHQPAQPFKFTTSE SCDRIKEERQFLGAQVIFSKLKLECEKLASEKTEMQRHVVMYYEMS YGILNIEMHKQASIVTKILNAICAQVIPFLSGEHQQQVVQAVERAK QVTMAELMAITGQQCLQAGHLSKGHCLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGGSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSESKKQKTEEKEIAARYDSDGEK SDDNLVVUVSNEDPSSFRGSPAISRENGLDKTRLLKKDAPISP ASIASSSTTPSSKSKSLSLINESTTYPSKSNTPTFRTDAPTDGS NSTFGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG MNGELTSPGAAYAGHNISFQMSAAAAAAAAAAGNGRSPVVGFD PHHHMRVPAIPPDNLTCIFGGKPAYSFNVSADGOMQPVVPPPDAL IGPGIPHARQINTLNHGEVVCAVTISNTTRHVYTGGKGCVKVW DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGKSCVKVW DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGKSCVKVW DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGKSCVKVW NDLHNQTLVRQFGGHTDGASCIDISNDGTKLWTGGKDTVTRS W\DLERGRGLQOHD/PTTSPVSGYCYP\TEMIAVGMENSN\V EVLHVYKPDKYQLHLHESCVLSLKPAHCGKWP\VSTGKDNLINA W\RTPYG\ASIP\QSKESS\VLSCDILSVDDKYIVTGS\GDK\ PATVYBVIY ARRICRAQPTKSAMMIRDLSKMYPQTRHPAPHQPGPAQPFKFTISE SCDRIKEEFQFIQAQYHSLKLECKLASEKTEMQRHYVMYYEMS YGLNIEMHKQASIVKRLMAICAQVIPFLSGEHQCOVVQAVERAK QVTMAELMAICQOQLOAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGGSHLPIKDEKHANDHORDRDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK SUDNLVVUVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSSTPSSKSELSLINEKTTTPVSKSNTPTPTTADAPTPGS				DSSSPORVORPHSSPPRFVTVEELLETARGVTNMALAHETUUNG
IKLVGEIKETLLSELLEGHTTLENNQITEVLDLDLIKQBAENGAL DISKLAEFI IGMMGTLCAPARDEVKKKLDIKEIVPLFREIFSV LDLMKVDMANFAISSIRPHLMQQSVETERKKFQEILERQPNSLD FVTOWLEBASEDLMTOKYKHALPVGGGMAAGSGMPRELSPVAVQN VAYLKLKUPLORPFETVLMQGSRPHELGQLQNEQLTILGAV LLVTFSMAAPGISSQADFAEKLKMIVKILLTDMHLPSFHLKOVL TTIGEKVCLEVSSCLSICGSSPFTIDKETVLKQQIQAVASPDDP IRRIMESRILIFLETYLASGHQKPLFTVPGGLBPVQRELHEVAI KFARLVAYNKNVFCPYYDAILSKILVES AARLCRAQPTKSAMMIRDLSKMYPQTRHPPAHQPAQFFKFTISE SCDRIKEEFOFLQAQVHSLKLECEKLASEKTEMQRHYVMYYEMS YGLMIEMHKQAETVKRIMAICAQVIPPLSQEHQQQVVQAVERAK QVTMAELMAIIQQQLQAQHLSHGLGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGGSHLFIKDEKKHHDNDHQRDRISISS SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK SDDNLVVDVSNEDPSSPROSJSPRENGLDKTRLLKKDAPISP ASIASSSTPSSKKELSLNEKSTTPVSKSNTFTRTDAPTFGS NSTFGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG MNGELTSPGAAVAGLHNISPGMAAAAAAAAAAAAVGSPVOGPD PHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPPPDDAL IGPGIPRHARQINTLNHGEVVCAVTISBPTRHVYTGGKGCVVKW DISHPGNKSFVSQLDCLNENDYIRGSRLDFRTLIVGGLDNTVRS W\DLRBGRGLQQHD/FTTSPVTSLGYCP\TEBWLAVGMEDSN\V EVLHVYKPDKYQLHLHESCVLSLKFAHCGKWV\VSTGKDNLINA W\RPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\ AAVLCHAQPTKSAMMIRDLSKMYPQTRHPAPHQPAQPFKFTISE SCDRIKEEFOFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLNIEMHKQAEIVKRNAICAQVIPFLSQEHQQVVQAVERAK QVTMAELMAIIGQQOLQAQHLSHGGLLPVPITPHPSGLQPPAIP PIGSSAGLLALSSALGGGSHPLFIKEKETTPVSKSNTTPTFTDAPTPGS SCDRIKEEFOFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLNIEMHKQAEIVKRNAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELMAIIGQQOLQAQHLSHGGGLPVPITPHPSGLQPPAIP PIGSSAGLLALSSALSGGGSHPLFIKEKSTTPVSKSNTTPTFTTDAPTPGS ASIASSSSTPSSKSEELSLNEKSTTPVSKSNTTPTFTTDAPTPGS				DFOIKPVELPENSLKKRVKETVHKAFWDOLGVOLGEDDBAVDUA
DISKLAEFIIGMMGTLCAPARDEBYKKLKDIKEIVPLFREIFSV LDLMKVDMANPAISSIRPHLMGOOSVEYERKKPGEILERQPNSLD FVTQWLEEASEDLMTQKYKHALPVGGMAAGSGDMRRLSPVAVQN YAYLKLLKWDHLQRFFBETVLMDGSRFHELGLQ\REQUITLGAV LLVTFSMAAPGISSQADFRLKMTVYKLLTDMHDFSFHLKDUL TTIGEKVCLEVSSCLSLGGSSFTTDKETVLKGQIQAVASPDDP IRRIMESRILTFLETYLASGHQKPLPTVPGGGSPVQRELBEVAI KFARLVAYNKHVFCPYYDAILSKLLVRS ARRLCRAOPTKSAMWIRDLSKMYPGTRHPAPHOPAQPFKPTISE SCDRIKEEFGPLQAQVHSLLECEKLASEKTEMQRHYVMYYEMS YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELMAIIGQQQLQAQHLSHCHGLSVPDTPHBSGLQFPAIP PIGSSAGLLALBSALGGGALBHSHCHGLSVPDTPHBSGLQFPAIP PIGSSAGLLALBSALGGGSLBFKKSKTFFYKRDAFTGS NSTFGLRSVPGCKPPGVDPLASSLRTPMAVPCPYPPFGIVPHAG MNGELTSFGAAYAGLHNISPQMSAAAAAAAAAAAAGRSPVVGFD PHHMRVPAIPPHLTGIFGCKPAYSFHVSAGGQMQPVFFPPDAL IGGGIRHARQINTLNHGSVCAVTISNPTHHVTGGGGCVKVW DISHPGMKSPVSQLDCLINRNYIRSCRLLDPGRTLIVGGBASTL SIMDLAAPTFRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI AVMDLHNQTLVRGFGGHTDGASCIDISNDGTKLMTGGLDNTVRS W\DLREGRQQOHD/FFTSVFSIGYCP\TEBWLAVGMENSN\V EVLHVTKPDKYQLHLHSCVLSLKFAHCGKMP\VSTGKDNLLNA W\RTPYG\ASIF\QSKESSS\VLSCKTTPTSCDKNNLINA W\RTPYG\ASIF\QSKESSS\VLSCKTTPTSCDKNLINA W\RTPYG\ASIF\QSKESSS\VLSCKTTPTSCDKNPYYTYSS\GDK\ TANVYBVIY AARLCRAOPTKSAMMIRDLSKMYFQTTHPAAPHQBAQPFKFTISE SCDRIKESFOPLOAQVYASLLECEKLASEKTEMQRHYVMYYEMS YGLNIEMHKQAEIVRAINAICAQVIFFLSGEHQAQVVQAVERAK QVTMABLNAIIGQOQLOACHLSRGLIPVLTPHPSGLQPPAIP PIGSSAGLLALSSALGGSHLPIKDBCHRONDHQRDRDGIKSS SVSPSASFRGREKHRNSADVSSESKKQKTEEKSIAARYDSDGEK SDDNLVVUDVSNEDDSSPRGSPAHSPRENGLDKTRLKKOAPIGF ASIASSSSTPSSKSKELSLEKSTTPVSKSNTTPFRTADAPTPGS ASIASSSSTPSSKSKELSLEKSTTTPVXRSNTTPRTADAPTPGS	1	l		
LDLMKVDMANFAISSIRPHLMQGSVEYERKKFQEILERQPNSLD FVTQWLEEASEDLMTQKYKHALPVGGMAAGSGDMPRLSPVAVQN YAYLKLLKWDHLQRFPETVLMDGSRFHELGLQ\REQLTILGAV LLVTFSMAAPGISSQADFAEKLKMVKILLTIMHLPSFHLKDVL TTIGEKVCLEVSSCLSLGSSFFTTDKETVLKGQIQAVASPDDP IRRIMESRILTFLETYLASGHQKPLPTVPGGISPVQRELBEVAI KFARLVMYNKWVFCPYYDAILSKILVRS ARRICRAQPTKSAWMIRDKNYPQTRHPAPHQPAQPFKFTISE SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLMIEHHKQAEIVKRLMAICAQVIPFISGEHQQQVVQAVERAK QVTMAELMAITGQQQLQAHSHGHGLPVPLTPHSGELQPPAIP PIGSSAGLLALSSALGGGSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGAEKHRNSADVSSEKKQXTEEKEILARXDSDGEK SDDNLVVDVSNEDPSSPRGSPSHSPRENGLDKTRILKKADPISP ASIASSSTFSSKSKELSLNEKSTTPVSKSNTPTFTTDAPTPGS NSTPGLRPVPGKPPGVDPLASSLRTPWAVPCPYPTPFGIVPHAG MNGELTSPGAAYAGLHNISQMSAAAAAAAAAAAAARAYGSPVVGFD PHHHMRVPAIPPNITGIPGGKPAVSFHVSADGQMQPVPPPPDAL IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW DISHPGNKSPVSQLDCLMRNNYIRSCRLLPDGRTLIVGGERSTI SIMDLAAPTERIKRELTSSAPACYALAISPDSKVCFSCCSDGNI AVMDLNNGTLVTQFQGGHTDASCIDISNDGTKLWTGGLDTVTRS W\DLREGRQLQQHD/FFTSPVFSLGYCF\TEEWLAVGMENSN\V EVLHVYKPDKYQLHLHSCVLSLKFAHCGKMP\VSTGKDNLINA W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\ PATVYEVIY ARELGRAPTKSAMMIRDLSKMYPQTRHPAPHQPAQPFKFTISE SCDRIKEFGFLQAQPTKSLKLECEKLASEKTEMQRHVYMYYEMS YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQVVQAVERAK QVTMAELMAIIGQOQLOACHLSHGLIPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGOSHLPIKDEKKHNDNDQRORDGSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDGNGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSSTPSSKSKELSLEKKSTTPVSKSNTPTPRTDAPTPGS	1			DISKLAFFITCHMCTI.CADADDERUKK.KDIKETIDI EDAKUGAL
FYTONLEERSEDLMTCKYKHALPVGCMAAGSGDMRRLSPVAVQN YAYLKKLKWDHLQRPFETVVMDQSRPHELQLQ\REQLITIGAV LLVTFSMAAPGISSQADPAEKLMIVKILLITDMILPSPHLKDVL TTIGEKVCLEVSSCLSLGGSPFTTDKETVLKGQIQAVASPDDP IRRIMESRILTFLETYLASGHQKPLPTVPGGLSPVQRELBEVAI KPARLVNYNKMVFCPYYDAILSKILVRS 6032 39 2415 ARRLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLMIEMHKQAEIVKRLMAICAQVIPFLSGEHQQQVVQAVERAK QVTMAELMAITGQQLQAQHLSHGHGLDVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGQQSHLPIKDEKKHDNDHQRDDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS NSTTGLRPVPGKPPGVDPLASSLRTTMAVVPCPYPTPFGIVPHAG MNGELTSFGAAYAGHNISPQMSAAAAAAAAAAAAAAYGRSPVVGFD PHHMRVPAIPPNLTGIPGKPAYSFHVSADGQMQPVPFPPDAL IGBGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW DISHPGMKSPVSGLDCLMRDNYIRSCRLLPDGRFLIVGGRASTL SIMDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI AVMDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEMLAVGMENSN\V EVLHVTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLMA W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDKXIVTGS\GDK\ RATVYEVIY ARRLCRAQPTKSAMMIRDLSKMYPQTRHPAPHQFAQFFKFTISE SCDRIKSEFGFLQAQYHSLKLECEKLASEKTEMQRHVVMYYEMS YGLNIEMHKQAEIVKRLMAICAQVIPFLSGEHQQQVVQAVERAK QVTMAELMAIIGQOQLQAQHLSHEHGLPVPLTPHPSGLGPPAIP PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEBKEIAARYDSDGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSSTPSSKSKELSLMEKSTTPVSKSNTPTFRTDAPFPGS	1			
TAYLKILKWDHLQRPPETVLMQSRPHELQLQ\REQLITIGAV LLVTFSMAAPGISSQADFAEKLKMIVKILLIDMHLPSPHLKDVL TTIGEKVCLEVSSCLSCSSPTTTDRETVLKGQTQAVASPDDP IRRIMESRILTFLETYLASGHQKPLPTVPGGLSPVQRELEEVAI KFARLVNYNKMVFCPYYDAILSKILVRS ARRUCRAQPTKSAWNIRDLSKMYPQTRHPAPHQPAQPPKFTISE SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLNIEMHKQABIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELMAITGQQQLQAHLSHGHGLDVPLTPHSGEHQQVVQAVERAK QVTMAELMAITGQQQLQAHLSHGHGLDVPLTPHSGEGLQPPAIP PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEBKETAARYDSDGEK SDDNLVVDVSNEDPSSPSSPAHSPRENGLDKTRLLKKDAPISP ASIASSSTPSSKSKELSLNEKSTTPVSKSNTFIPRTDAPTPGS NSTFGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG MNGELTSFGAAYAGHNISPQMSAAAAAAAAAYGRSPVVGFD PHHMMRVPAIPPNITGIBGGKPAYSFHVSADGGMQPVPFPPDAL IGPGIPRHAQINTINHGEVCAVTISNPPRHVYTGGKGCVKVW DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGKBASTL SIMDLAAPTFRIKAELTSSAPACYALAISPDSKVCPSCCSDGNI AVMDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEBKLAVGMENSN\V EVLHVTKPDFYQLLHLHSCVLSLKFRHCGKWP\VSTGKDRLINA W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\ RATVYBVIY ARRUCRAOPTKSAWNIRDLSKMYPQTRHPAPHQPAQFFKFTISE SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHVVMYYEMS YGLNIEMHKQAETUKRLNAICAQVIPFLSQEHGQQVVQAVERAK QVTMAELNAIIGQOQLOAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEKEIAARYDSDGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSSTPSSKSKELSLMEKSTTPVSKSNTPTTRTDAPTPGS		١.		
LLVTFSMAAPGISSQADFAEKLKMIVKILLITDMILPSFHLKDVL TTIGEKVCLEVSSCLSLCGSSPFTTDKETVLKGQIQAVASPDDD IRRIMESRILTFLETYLASGHQKPLPTVPGGLSPVQRELBEVAI KFARLVNYNKWVFCPYYDAILSKILVRS 39 2415 AARLCRAQPTKSAWMIRDLSKMYPQTRHFAPHQFAQPFKFTISE SCDRIKEEFQFLQAQVHSLKLECEKLASEKTEMQRHYVMYYEMS YGLANIEMHKQAEIVKRLMAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELNAIIGQQQLQAQHLSHGHGLBVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGSHLPIKDBKKHHHDNHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSSTPSSKKSLSLMEKSTTPVSKSNTPTPRTDAPTPGS NSTFGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG MNGELTSFGAAYAGLHNISPQMSAAAAAAAAAAYGRSPVVGFD PHHHMRVPAIPPHLTGGKKPAVSFHVSADGGMPVPPPPDAL IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLLVGGERSTL SIMDLAAPTPRIKABLTSSAPACVALAISPDSKVCPSCCSDGNI AVMDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEBHLAVGMENSN\V EVLHVTRDKYQLHHESCVLSLKFAHCGKWF\VSTGKDNLLNA W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYTVTGS\GDK\ RATVYBVIY AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQFAQPFKFTISE SCDRIKEEFQPLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLNIBMHKQAEIVRRLNAICAQVIPPLSQEHQQQUVQAVERAK QVTMAELNAIIGQQQLOAGHLSHKGHGLLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGSSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSESSKKQKTEEKEIAARYDSDGRK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSTTSSKSKELSLNENSTTTVSKSNTPTFRTDAPTPGS				
TTIGEKVCLEVSSCLSLCGSSPFTTDKETVLKGGIQAVASPDDP IRRIMESRILTFLETYLASGHQKPLPTVPGGLSPVQRELBEVAI KFARLVNYNKMVFCPYYDAILSKLVRS ARRLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE SCDRIKEFFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLNIEMIKQASIVKRLMAICAQVIPFLSQEHQQVVQAVERAK QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGGSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEEKELARAYDSDGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSTPSSKSKELSLNEKSTTPVSKSNTFTPRTDAPTPGS NSTFGLRPVPGKPPGVDFANAVPCPYPTPFGIVPHAG MNGELTSFGAAYAGHNISPQMSAAAAAAAAAAAAAYGRSPVVGFD PHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW DISHPGKNSPVSQLDCLNRDNYIRSCRLLPDGRTLLVGGEASTL SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI AVWDLHNQTLURQFGGHTDGASCIDISNDGTKLWTGGLDNTVRS W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V EVLHVTKPDKYQLHLHESCVLSLKFAHGGKWF\VSTGKDNLLNA W\RTPYG\ASIT\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\ RATVYEVIY ARRLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQFAQPFKFTISE SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLNIEMHKQAEIVERLNAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELINAIIGQOQLOAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGGSHLPIKDEKKHHDNDHGRDRDSIKSS SVSPSASFRGAEKHRNSADYSESSKKQKTEKEIAARYDSDGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSTTSSKSKELSLNEKSTTVVSKSNTPTFRTDAPTPGS				
IRRIMESRILTFLETYLASGHOKPLPTVPGGLSPVQRELBEVAI KFARLVNYNKMVFCPYYDAILSKILVRS ARRICRAQPTKSAMMIRDLSKMYPQTRHPAPHQPAQPFKFTISE SCDRIKEEFOPLOAQYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLNIEMHKQAEIVKRLNAICAQVIPPLSQEHQQQVQAVBRAK QVTMAELMAIIGQQQLQAQHLSHGHGLPVPLTPHPBGLQPPAIP PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK SDDNLVVDVSNBDPSSPRGSPAISPERNGLDKTRLIKKDAPISP ASIASSSSTPSSKSKELSLNEKSTTPVSKSNTPTRTDAPTPGS NSTEGLRFVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG MNGELISFSGAAYAGLHNISPQMSAAAAAAAAAAYGRSPVVGFD PHHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL IGFGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL SIMDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI AVMDLHNGTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V EVLHVTKPDKYQLHLHESCVLSLKFPHCGKWP\VSTGKNDLINA W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\ RATVYBUY FGLNIEMHKQAEIVRLNAICAQVIPFLSGEHQQQVVQAVERAK QVTMAELNAIIGQQOLQAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEKESITAARYDSDGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSSTPSSKSKELSLNEKSTTPVSKSNTTPTRTDAPTPGS				LLVTFSMAAPGISSQADFAEKLKMIVKILLTDMHLPSFHLKDVL
6032 39 2415 AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE SCDRIKEFOPLOAQYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLNIEMHKQAEIVKRLNAICAQVIPPLSQEHQQVVQAVERAK QVTMAELMAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGQSHLPIKDEKKHDNDHQRDRDSIKSS SVSPSASFRGAEKHNSADYSSESKKQKTEKELAARYDSDGEK SDDNLVVDVSNBDPSSPRSPAHSPRENGLDKTRLLKKDAPISP ASIASSSTPSSKSKELLSLEKSTTPYSKSNTPTFRTDAPTPGS NSTTGLRSVPGKPPGVVPPDHPSIVPHAG MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAYGRSPVVGFD PHHHMRVDAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL IGPGIPRHARQINTLNGEVVCAVTISNPTRHVYTGGKGVKVW DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL SIMDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI AVWDLHNQTLVRQFQGHTDGASCIDISNDTKKMTGGLDNTVRS W\DLREGRQLQQPHO/FFTSPVFSLGYCP\TEBWLAVGMENSN\V EVLHVTKPDKYQLHLHESCVLSLKPAHCGKWF\VSTGKDNLLNA W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\ RATVYEVIY AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLNIEMHKQAEIVRRLNARCAQVIPFLSQEHQQQVVQAVERAK QVTMAELMAITGOOLOACHLSHGGGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGQSHLPIKDEKKHDNDHQRDDRDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEKESIAARYDSDGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP AGIASSSSTPSSKSKELSLNEKSTTPVSKSNTFTPRTDAPTPGS	1			TTIGEKVCLEVSSCLSLCGSSPFTTDKETVLKGQIQAVASPDDP
ARRLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE SCDRIKEEFGFLQAQYYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEEKELARAYDSDGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS NSTFGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG MNGELTSPGAAYAGLHNISPQMGAAAAAAAAAAAAAAYGRSPVVGFD PHHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL IGPGIPRHARQINTLNHGEVVCAVTISMPTRHVYTGGKGCVKVW DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL SIWDLAAPTFRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI AVNDLHNQTLVROFQGHTDGASCIDISNDGTKLWTGGLDNTVRS W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V EVLHVTRPDKYQLHLHSSCVLSLKFAHCGKWP\VSTGKDNLLMA W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\ RATVYBVIY AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQFAQPFKFTISE SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYYMYYEMS YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSSTPSSKKSELSLNEKSTTTVSKSNTPTPRTDAPTTGS	1 1	1		IRRIMESRILTFLETYLASGHQKPLPTVPGGLSPVQRELBEVAI
SCDRIKEFFOPLOAQYHSLKIECEKLASEKTEMQRHYVMYYEMS YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELANAIGQQQLQAGHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGAEKRRNSADYSSESKKQKTEEKEIAARYDSDGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG MNGELTSPGARYAGLHNISPQMSAAAAAAAAAAAARARSPVVGFD PHHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL SIMDLAAPTPRIKRELTSSAPACYALAISPDSKVCFSCCSDGNI AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V EVLHVVTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLMA W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\ RATVYEVIY 6033 39 2415 AARLCRAQPTKSAMMIRDLSKMYPQTRHPAPHQFAQPFKFTISE SCDRIKEEFQFLQAQYHAIKLECEKLASEKTEMQRHYYMYYEMS YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELNAIIGOQOLQAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGGSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGAEKKHRNSADYSSESKKQKTEEKSIARRYDSDCEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSSTPSSKSKELSLNEKSTTTVSKSNTPTPRTDAPPTGS				
SCDRIKEFGYLOAQYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELNATIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRCAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSTPSSKSKELSLMEKSTTPVSKSNTPTPRTDAPPTGS NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAYGRSPVVGFD PHHHMRVPAIPPNLTGIPGGKPAYSPHVSADGQMQPVPFPPDAL IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL SIWDLAAPTFRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI AVWDLHNQTLVQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V EVLHVTKPDKYQLHLHESCVLSLKFAHCGKWP\VSTGKDNLLNA W\RTPYG\ASIF\QSKESS\VLSCDI\SVDDKYIVTGS\GDK\ RATVYBVIY SCDRIKEFFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELNAIIGQQQLQAQHLSHGGGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSSTPSSKKELSLNEKSTTPVSKSNTPTPRTDAPTPGS	6032	39	2415	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHOPAOPFKFTISE
YGLNIEMHKQAEIVRKINAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGQSHLPIKDEKKHHDDHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSSTPSSKSKELSLNEKSTTPVSKSNTFTPRTDAPTPGS NSTPGLRPVPGKVPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAAGYGRSPVVGFD PHHHMRVPAIPPNLTGIPGGKPAYSPHVSADGQMQPVPFPPDAL IGPGIPRHARQINTINHGEVVCAVTISNPTRHVYTGGKGCVKVW DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEBWLAVGMENSN\V EVLHVTKPDKYQLHLHESCVLLSLKFAHCGKWP\VSTGKDNLLNA W\RTPYG\ASIF\QSKESS\VLSCDI\SVDDKYIVTGS\GDK\ RATVYEVIY 6033 39 2415 AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE SCDRIKEFFQFLQAQVYQAVERAK QVTMAELNAIIGQOOLQAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSCGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS	1			SCDRIKEEFOFLOAOYHSLKLECEKLASEKTEMORHYUMYYEMS
QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGABKHRNSADYSSESKKQKTEKELARYDSDGEK SDDNLVVDVSNEDPSSPRGSPATSPRENGLDKTRLLKKDAPISP ASIASSSSTPSSKSKELSLNEKSTTPVSKSNTPTRTDAPTPGS NSTGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAAACAGRSPVVGFD PHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL SIWDLAAPTFRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V EVLHVTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\ RATVYBVIY AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE SCDRIKEFFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLNIEMHKQAEIVRLNAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEEKSIAARYDSDGEK SDDNLVVDVSNEDPSSPRGSFAHSPRENGLDKTRLLKKDAPISP ASIASSSSTPSSKSKELSLNEKSTTPVSKSNTTPRTDAPTPGS	1 1	j		YGLNIEMHKOAEIVKRLNAICAOVIPFISOEHOOOVVOAVERAK
PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEEKELAARYDSDGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSSTPSSKSKELSLNEKSTTPVSKSNTFTPRTDAPTPGS NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAGRSPVVGFD PHHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V EVLHVTKPDKYQLHLHESCVLSLKFFAHCGKWF\VSTGKDNLLNA W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\ RATVYBVIY AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLNIEMHQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDGGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS	1 1	1		OVTMAELNATIGOOOLOAOHI,SHGHGI,DVDI,TDVDGGI,ODDATD
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SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
No:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ı	corresponding	to first	H=Histidinc, I=Isoleucine, K=Lysine,
}	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- 1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence		Codon, /=possible nucleotide deletion,
		 	\=possible nucleotide insertion)
- 1	1	1	MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAYGRSPVVGFD
ł			PHHIMRVPAIPPNLTGIPGGKPAYSFHVSADGOMOPVPFPPDAL
		İ	IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
-	i		DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL
	İ		SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI
1			AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS
	1		W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V EVLHUTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA
1		1	W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDXYIVTGS\GDK\
Ĺ	1	!	RATVYRVIY
6034	2683	714	ESGRRRLKRRSPCPGTAGGPGETNPGPGACPRGPREEAAAAM
}	İ		EIAPQEAPPVPGADGDIEEAPAEAGSPSPASPPADGRLKAAAKR
			VTFPSDEDIVSGAVEPKDPWRHAQNVTVDEVIGAYKQACQKLNC
	ĺ		RQIPKLLRQLQEFTDLGHRLDCLDLKGEKLDYKTCEALEEVFKR
1			LQFKVVDLEQTNLDEDGASALFDMIEYYESATHLNISFNKHIGT
			RGWQAAAHMMRKTSCLQYL\DARNTPLLDHSAPFVARALRIRSS
ŀ	ľ		LAVLHLENASLSGRPLMLLATALKMNMNLRELYL\ADNKLNGLQ
j			DSAQLGNLLKFNCSLQILDLRNNHVLDSGLAYICEGLKEQRKGL
l l			VTL\VLWNNQLTHTGMAFLGMTLPHTQSLETLNLGHNPIGNEGV
1]		RHLKNGLISNRSVLRLGLASTKLTCEGAVAVAEFIAESPRLLRL
			DLRENEIKTGGLMALSLALKVNHSLLRLDLDREPKKEAVKSFIE
1			TOKALLAEIONGCKRNLVLAREREEKEOPPOLSASMPETTATEP
1	į l		QPDDEPAAGVQNGAPSPAPSPDSDSDSDSDGEEEEEEGERDET
1			PSGAIDTRDTGSSEPQPPPEPPRSGPPLPNGLKPEFALALPPEP
6035			PPGPEVKGGSCGLEHELSCSKNEKELEELLLEASOESCOPTI
6035	19	404	SVTYLGIILHKNTGALPADPVOLISOTPTPSTKOOLLSELGMYG
	.]		IFILWIPGFAILTKPLCKLTKENLADAIDPKSFSHSSFPSI.kra
6036	1745		LENASTLALPDSSQPF\SLHTAEVOGCVVEILTOGLGDLDV
1 0030	1/45	356	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRRRKLOPN
l i	1	i	SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVDITGW
1			VDRAALDSGAFQSVWVSTDHDEIENVAKOFGAOVHRESSEVSKD
1 1			SSTSLDAIIEFLNYHNEVDIVGNIOATSPCLHPTDLOKVARMIR
} [ì		EEGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD
j l			WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV
1 1		j	DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS
i 1	i		GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK
!!		1	LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK
!!		ĺ	RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK
6037	2936	1919	WTSWWMSSVITTI I BELOONING THE
l	1		WTSWWMSSVLTILLFSLOGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR
1	ł		SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG
		Į.	DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI
	[HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL
ļ			DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA
· · · · · · · · · · · · · · · · · · ·		!	PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS
		1	SSSSHSGSDSPTLDNSRRLPIFSRLSISDD
6038	1450	426	SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH
1		ļ	YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS
1	1	ļ.	SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG
1	Ì	1 :	NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASOLEAHYSGTEHE
f	['	TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTGLONKTFHCR TOD
	į	١,	VHVNSETQLKQHISSRRHKDRAAGKPPKPKYSPYNKLQKTAHPL
	1	1	GVKLVFSKEPSKPLAPRILPNPLAAAAAAAAVAVSSPFSLRTAP
(03.5			AATLFQTSALPPALLRPAPGPIRTAHTPVLFAPV
6039	4073	1000	LDEYEARLTLANLDDFEEDNEDDDENRVNOERKAAKTTELTNEL
ſ		1 1	NFLDEAEKDLATVNSNPFDDPDAAELNPFGDPDSEEPITETASP
J		1 1	RKTEDSFYNNSYNPFKEVOTPOYLNPFDEPEAFVTIKDSPROST
İ		} 4	KKKNIRPVDMSKYLYADSSKTEEEELDESNPFYEPKSTDDDNNI.
			VNPVQELETERRVKRKAPAPPVLSPKTGVLNENTVSAGKDLSTS

	SEQ	Predicted	Predicted end	
	ID	beginning	nucleotide	actu bequent containing biggs
	NO:	nucleotide	location	(A=Alanine, C=Cvateine, D=Aenavtic Acid n
		location	1	Giucamic Acid, F=Phenylalanine G-Glycano
		corresponding	corresponding	n=H1StlQine, I=Isoleucine K-Lycine
		to first	to first	L=Leucine, M=Methionine, N=Asparagine
	1	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
	}	residue of	residue of	S=Serine, T=Threonine, V=Valine
	1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, Y=Unknown +-C+
	1		sequence	Codon, /=possible nucleotide deletion
	<u> </u>	sequence		\=possible nucleotide insertion
	1			PKPSPIPSPVLGRKPNASQSLLVWCKEVTKNYRGVKIINFTTSW
		1	1	RNGLSFCAILHHFRPDLIDYKSLNPQDIKENNKKAYDGFASIGI
	1	į.	1	SRLLEPSDMVLLAIPDKLTVMTYLYQIRAHFSGQELNVVQIEEN
	l		1	SSKSTYKVGNYETDTNSSVDQEKFYAELSDLKREPELQQPISGA
	l			VDFLSQDDSVFVNDSGVGESESEHQTPDDHLSPSTASPYCRRTK
	1	1	ł	SDTEPQKSQQSSGRTSGSDDPGICSNTDSTQAQVLLGKKRLLKA
	i	1	i	ETLELSDLYVSDKKKDMSPPFICEETDEQKLQTLDIGSNLEKEK
		1		LENSRSLECRSDPESPIKKTSLSPTSKLGYSYSRDLDLAKKKHA
	-	ì		SLRQTESDPDADRTTLNHADHSSKIVQHRLLSRQEELKERARVL
	}		}	LECARROLL CONVENTENTS & DECURE OF CONTROL OF
		1	1	LBQARRDAALKAGNKHNTNTAAPFCNRQLSDQQDEERRRQLRER
			1	ARQLIAEARSGGKMSELPSYGERAAEKLKERSKASGDENDNIEI
				DTNEEIPEGFVVGGGDELTNLENDLDTPEQNSKLVDLKLKKLLE
			İ	VOPOVANSPSSAAQKAVTESSEQDMKSGTEDLRTERLQKTTERF
			1	RNPVVFSKDSTVRKTQLQSFSQYIENRPEMKRQRSIQEDTKKGN
		1		EEKAAITETQRKPSEDEVLNKGFKDS\SQYVVGELAALENEQKQ
		1	i	IDTRAALVEKRLRYLMDTGRNTEEEEAMMQEWFMLVNKKNALIR
ļ		1	ļ	RMNQLSLLEKEHDLERRYELLNRELRAMLAIEDWQKTEAQKRRE
١		1		QLLLDE_VALVNKRDALVRDI.DAQEKQAEEEDEHLERTLEQNKG KMAKKEEKCVLQ
Ī	6040	475	1052	DTAL MTA DCCA DRIVE DRIV
- [1		PTALMTAPSCAFPVQFRQPSVSGLSQITKSLYISNGVAANNKLM
		ļ	1	LSSNQITMVINVSVEVVNTLYEDIQYMQVPVADSPNSRLCDFFD
1		İ		PIADHIHSVEMKQGR\TLLHCAAGVSRSAALCLAYLMKYHAMSL
ļ				LDAHTWTKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPV GMIPDIYEKEVRLMIPL
Ī	6041	2	3886	
1]	TEKDEKTAHNLENVLIHFWERLSEICVAKISEPEADVESVLGVS
1		1		NLLCVLQKPKGSLKSSKKKNGKVRFADEILESNKENEKCVSSEG
1				EKIECWELTTEPSLTHNSSGLLSPLRKKPLEDLVCKLADISINY
1		1		VNERKSEQHLRFLSTLLDSFSSSRVFKMLLGDEKQSIVQAKPLE
1		1		IAKLVQKNPAVQFLYQKLIGWLNEDQRKDFGFLVDILYSALRCC
1				DNDMERKKVLDDLTKVDLKWNSLLKIIEKACPSSDKHALVTPWL
L		j l		KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ
ı		Į į		HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEAESSDSSVSFIC
1		[]		DVAYNYFSSAKGCLLMPSSEDLLLTLFQLCAQSKEKTHLPDFLI
				CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL
L				DINSLOVLLSAVDDLLNTLLESEDSYLMCVYIGSVMPNDSEWEK
L				MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIXTLPSHLCT
L				SALLSKMVLIALRKETVLENNELEKIIAELLYSLQWCEELDNPP
ı				IFLIGFCEILQKMNITYDNLRVLGNMSGLLQLLFNRSREHGTLW
l		ł		SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP
1	. }	'		FLSKEEKKEFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ
		1		TKSIDDGELLHGILKIIISWKKEHEDIFLFSCNLSEASPEVLGV
1		i		NIEIIRFLSLFLKYCSSPLAESEWDFIMCSMLAWLETTSENQAL
i	- 1	ļ		YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK
	ŀ	i		EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCETLTY
		[ISKEQLLSHKLPARLVADQKTNLPEYLQTLLNTLAPLLLFRARP
	1		1	VQIAVYHMLYKLMPELPQYDQDNLKSYGDEEEEPALSPPAALMS
	ĺ		ľ	LISIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI
	- 1			LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAB
	1			TAVEVPNKDPKTFFTEELQLSIRETTMLPYHIPHLACSVYHMTL
		1	1	KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT
	- 1	1	ł	STQLFNGMTVKARATTREVMATYTIEDIVIELIIQLPSNYPLGS
	1]	IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN
	1	İ	ŧ	VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY
	6042	1306	253	KWFTSSNKSTCSLCRETFF
	1	·		MAELAPASPSDIKASVSNGDTTLLCSRRQSCGMNEVRQVSLTYP
	ĺ	I		GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY
	l		1	GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE
	- 1	i		LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV
		1	1	QYCODTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTQDRFS
	- 1	j	ĺ	PDLLGLQASSALAWLTLEVLAILLSLYLVTVNTDLTTIDLVAFL
				GYKYVGMIGGVLMGLLFGKIGYYLVLGWCCVAIFVFMIRTLRLK

SEQ	Predicted	Predicted end	Amino acid segment control
αz	beginning	nucleotide	Amino acid segment containing signal peptide (A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
Į	location	corresponding	H=HISTIGINE, I=Isoleucipe K-Tareine
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, O=Glutamine, R=Arginine
	amino acid	residue of	S=Serine, T=Threonine, V=Valine
	residue of	amino acid	W=Tryptophan, Y=Tyrosine Y=Noknown *-Shor
- }	amino acid	sequence	[Codon, /=possible nucleotide deletion
-	sequence		(\=possible nucleotide insertion)
6043			ILADAAAEGVPVRGARNOLRMYI,TMAVAAAODMI,MVWI,TEUI VD
6043	403	599	LCLFFPFPCATPVLPLPSLISAL/CLSHLSVSSWFCPCODDLDC
1000			PDPPLONKTAKGSLSTEOSERG
6044	793	412	KLEMWNFTLISKVKISREVTMIASKFGIGQQVRHSLLGYLGVVV
1	1		DIDPVYSLSEPSPDELAVNDELRAAPWYHVVMEDDNGI.DVMTVT.
6045	1.5-		AEAQLSSELQDEHP\EQPSMDELAOTIRKOLOAPRIRN
1 0043	155	2299	SPLPQVAAMNYLRRRLSDSNFMANLPNGYMTDI.ORPOPPDDDC
	ļ		AHSPGATPGPGTATAERSSGVAPAASPAAPSPGSSGGGGFFSGT.
			SNAVKQTTAAAAATFSEQVGGGSGGAGRGGAASRVIJVIDEDUT
Í		ł	DWAKYFKGKKIHGEIDIKVEOAEFSDLNLVAHANGGFSVDMPVI.
1			RNGVKVVRSLKPDFVLIROHAFSMARNGDYRSLVIGLOVAGIDS
	1		VNSLHSVYNFCDKPWVFAOMVRLHKKLGTEEFPI.TDOTEVPNUK
1	1	1	EMLSS \TTYPVVVKMGHGTLWGWGKVKVDNOHDFODTA SIZZALT
	1		KTYATAEPFIDAKYDVRVOKIGONYKAYMRTSVSGNWKTNTGSA
İ	1	Į	MLEQIAMSDRYKLWVDTCSEIFGGLDICAVEALHGKDGRDHTTF
1	1		VVGSSMPLIGDHQDEDKQLIVELVVNKMAQALPRQRQRDASPGR
-	1		GSHGQTPSPGALPLGRQTSQQPAGPPAQQRPPPQGGPPQPGPGP
ļ	1		QRQGPPLQQRPPPQGQQHLSGLGPPAGSPLPQRLPSPTSAPQQP
1			ASQAAPPTQGQGRQSRPVAGGPGAPPAARPPASPSPQRQAGPPQ
			ATROTSVSGPAPPKASGAPPGGQQRQGPPQKPPGPAGPTRQASQ
I			AGPYPRTGPPTTQOPRPSGPGPAGRPKPQLAQKPSQDVPPPATA AAGGPPHPQLNKSQSLTNAFNLPEPAPPRPSLSQDEVKAETIRS
Ĺ	1 1		LRKSFASLFSD
6046	212	1075	EGLTGPCERVPFLLGRGPPHGATRAGHRRAVRWAGPESLPPLPR
1	i		SLIMDSPRAGTHQGPLDAETEVGADRCTSTAYQEQRPQVEQVGK
			QAPLSPGLPAMGGPGPGPCEDPAGAGGAGAGGGPDT.VTVTVTVCCA
1	, ,	j	FTVALRARRGADLSSLRALLGOALPHO\ AOLGOLGVI a DGPDGU
1	1 1	i	WVP1PEEESLQRAWODAAACPRGLOLOCRGAGGPDVI.VOVVACV
1	[SISAQGPEDLGFRQGDTVDVLCEVDOAWLEGHCDGPTGTEDECE
6047	49		VVPAGPRMSGAPGRLPRSQOGDOP
""	1 1	1405	PVLVTSLRMREADTLRPPQLMEVSADIISTVEFNHTGELLATGD
1			KGGRVVIFQREPESKNAPHSQGEYDVYSTFQSHEPEFDYLKSLE
	1	1	IEBKINKIKWLPQQNAAHSLLSTNDKTIKLWKITERDKRPEGYN LKDBEGKLKDLSTVTSLQVPVLKPMDLMVEVSPRRIFANGHTYH
	ľ		INSISVNSDCETYMSADDLRINLWHLAITDRSFTP\NIVDIKPA
			NMEDLTEVITASEFHPHHCNLFVYSSSKGSLRLCDMRAAALCDK
1		1	HSKLFEEPEDPSNRSFFSEIIS\SVSDVKFSHSDRYMLTR\DYL
1.			TVKVWDL\NMEARPIETYQVHDYLRSKLCSLYENDCIFDKFECA
ļ .	1		WNGSDSVIMTGA\YNNFFRMFDRNTKRDVTL\EASRESSKPRAV
ſ		ľ	LKPRRVCVGGKRRRDDISVDSLDFTKKILHTAWHPAENIIAIAA
6048			TNNLYIFQDKVNSDMH
6048	1	3194	GIRTPKFCDSPTSDLEMRNGRGRGKRMRPNSNTPVNETATASDS
1		1	KGTSNSSKTRAGANSKGRRGSONSSEHRPPASSTSEDVKASPSS
	ı		ANKRKNKPLSDMELNSSSEDSKGSKRVRTNSMGSATGDT.DGTV1/
]	1	İ	EPTVLDRNCPSPVLIDCPHPNCNKKYKHINGLKYHQAHAHTDDD
<u> </u>	ĺ	1	SKPEADGDSEYGEEPILHADLGSCNG\ASVSQK\GSLSPARSAT
1 1		1	PKVRLVEPHSPSPSSKFSTKGLCKKKLSGEGDTDLGALSNDGSD
1		İ	DGPSVMDETSNDAFDSLERKCMEKEKCKKPSSLKPEKIPSKSLK
	1		SARPI/APLAIPPQQIYTFQTATFTAASPGSSSGLTATVAQAMP
	ļ		NSPOLKPIQPKPTVMGEPFTVNPALTPAKDKKKKDKKKKESSKE
		1:	LESPLTPGKVCRAEEGKSPFRESSGNGMKMEGLLNGSSDPHQSR
		1:	LASIKAEADKIYSFTDNAPSPSIGGSSRLENTTPTOPLTPLHVV
			TONGAEASSVKTNSPAYSDISDAGEDGEGKVDSVKSKDAEQLVK
l		1:	EGAKKTLFPPQPQSKDSPYYQGFESYYSPSYAQSSPGALNPSSQ
ļ	1	1:	AGVESQALKTKRDEEPESIEGKVKNDICEEKKPELSSSSQQPSV
}		1;	IQQRPNMYMQSLYYNQYAYVPPYGYSDQSYHTHLLSTNTAYRQQ
l		1 :	YEEQQKRQSLEQQQRGVDKKAEMGLKEREAALKEEWKQKPSIPP ILTKAPSLTDLVKSGPGKAKEPGADPAKSVIIPKLDDSSKLPGQ
i	l	;	APEGLKVKLSDASHLSKEASEAKTGAECGRQAEMDPILWYRQEA
		-	PRMWTYVYPAKYSDIKSEDERWKEERDRKLKBERSRSKDSVPK
			THE THE PROPERTY OF THE PROPER

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide		I WITH THE CELVSTEINE DENAMERS IN THE SECOND
	location	location	Grand Acid, Fathentialanian C. Cl
1		corresponding	n-nistiding, l=180 encine v_r
	corresponding	to first	Leucine, Memethionine Menageration
	to first	amino acid	PEPROLING, OEGLUTAMING Department
ſ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine v_unt + o
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			RDCKEGTSCOCKI DWGEGGG INSERTION)
1	1	1	EDGKESTSSDCKLPTSEESRLGSKEPRPSVHVPVSSPLTQHQSY
	1	i	IPYMHGYSYSQSYDPNHPSYRSMPAVMMQNYPGSYLPSSYSFSP
1 .		1	YGSKVSGGEDADKARASPSVTCKSSSESKALDILQQHASHYKSK
	}		1 25112DVLQCEKDKGGCGAACGCGGGCGGGGGGGGGGGGGGGGGGGGGGGG
ł	ł		SPSQREMSTHHHHHLGYSLLPAOYNLPYAAGLSSTATUAGOOG
6049	215	1000	PIAPPIAAKK
1	223	1089	AMTGVFDRRVPSIRSGDFQAPFQTSAAMHHPSQESPTLPESSAT
	1		DSJX ISPIGGAPHGYCSPTSASYG\ KAT.NDVOVOVOGIDIGARGA
	1		IPARATADISTASSYHOYGGAYNRVPSATMODEREUTEDET THAT
	1		NGKPKKVKKPRTIYSSFOLAALORRFOKTOVLALDEDARINACI
	1		GLIQIQVKIWFQNKRSKIKKIMKNGFMPDFHEDECEDDMACNOD
	1		USPAVWEPQGSSKSLSHHPHAHPPTSNOSPASSVI, FNC A CHIVMC
6050			AASSINSHLPPPGSLOHPLALASCTI.V
9050	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL
1 .			PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD
			RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW
1 1	,		DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHY
			YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDLR
i i			RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN
			FARI TEADEVIL PREATER WITCHWOOD THE PROPERTY OF THE PROPERTY O
			FAEIIEADEVILFERATFLVISHYQCKEQRDAHRFEKISNIIKQ
	1		FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI
6051	566	1718	PSAATLINIRNARKHFEKLERVDGPKQCLLMR
1 1	ı	2720	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL
1 1	f		FINITAPIARAVLLMGKSGSGKTSMRSTIFANVTADDTDDTCADTTD
1 1	I		RIASLQINSSLSTYSLVDSVGNTKTFDVERGHVDFTCNT VI NT V
) }	!		DCGGQUIFMENYFTSORDNIFRNVEVI.TVVFDVFCDFT.FVDMTV
1 1	j		I IVOCUEALLONSPOAKIFCLVHKMDLUOFDODDI TEVERREDE .
1	1		RUSKPLECSCERTSIWDETLYKAWSSIVVOLIDATION DAY
1 1	1		FALL LEADEVILLEERATFLVISHYOCKEODDAHDEDVICKT ****
1 1	1		FALSCSALAASFOSMEVRNSNFAAFIDTETSNTVINGTMCDDCT
6052			PSAATEINIKNAKKHFEKLERVDGPKOCTIMP
0032	566	1718	KGLERTCCAMEESDSEKTTEKENI GPPMDPDLGEDGLCCLCOR
}	į.		PNIAMKAKVLLMGKSGSGKTSMRSITFANVIADDTDDICARTIC
		Į.	RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW
1 1	ļ		DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHY
] [1		YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDLR
1	ſ	ŀ	RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN
]]]	İ	FABIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ
1 1	i		FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI
			PSAATLINIRNARKHFEKLERVDGPKQCLLMR
6053	201	1704	KGTEMNKSRWQSRRRHGRRSHQQNPWFRLRDSEDRSDSRAAQPA
	1		HDSGHGDDRSDSTSCCTACTION TO THE THE STATE OF T
	í	1	HDSGHGDDESPSTSSGTAGTSSVPELPGFYFDPEKKRYFRLLPG
	1	į.	HNNCNPLTKESIRQKEMESKRLRLLQEEDRRKKIARMGFNASSM
			LRKSQLGFLNVTNYCHLAHELRLSCMERKKVQIRSMDPSALASD
	1	i	RFNLILADTNSDRLFTVNDVTVGGSKYGIINLQSLKTPTLKVFM
i	1		HENLYFTNRKV\NSVCWASLNHLDSHILLCLMGLAETPGCATLL
ļ	Ī		PASLFVNSHPAGIDRPG\MLCSFRIPGAWSCAWSLNIQANNCFS
	1	1	IGUSKKVALINVVIGHROSFGTNSDVIAOOFAI.MADI.I ENCORG
i	į	1,	SIFAID RCGNQGKGWKATRLFHDSAVTSVRTLODFOVIMACD
1	[1.9	MAGALKLWDLRTTKCVROYEGHVNEVAVI.DT.RRREPEGTI 120.100
	ļ	1 1	DUCTIKI WSLHDARLLRTIPSPYPASKADIPSVARSSPI COSPO
6054	1	1 4	H-GHLWAVGQDLYCYSYS
1	-	1054	PPIARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIYLH
1		1 5	WSSSQUKKNFFFRRORDISHSIVI,DAAVSQAHDUDVUTVVDDV
		, ,	ATGIVPDWGDSIEVKNEDOIOGIHOACOLAPHULLI ACKEL WAY
ļ		1 -	MITEEIDALVHREIISHNAYPSPIGVGGFPKSVCTSVNNUT GU
- 1	İ	1 0	SIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK
1	ľ	l I	VEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF
1		l v	GHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPE
		l F	KVLEDAWTVVSLD/TSKVSAQFEHTVLITSRGAQILTKLPHEA
			TORVOAQFERTVELTSKGAQILTKLPHEA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
-	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
1	amino acid	sequence	Codon, /=possible nucleotide deletion
<u> </u>	sequence		\=possible nucleotide insertion)
6055	421	2364	PPYFLLSFLAWWLYGQSDRTETDISOSAGPPPGTLOCSALHHDD
		ĺ	GCANCSRFCRDCSPPACQCHTHVFPGNALNGVOPPELSRTLAT.T
1			SSREPPRKKKKSQTETGKERERTSFLTOGGKRFELOHGLAGICM
1			TLLITGDSIVSAEAVWDHVTMANRELAFKAGDVIKVLDASNKDW
ł			WWGQIDDEEGWFPASFVRLWVNHEDEVEEGPSDVQNGHLDPNSD
			CLCLGRPLQNRDQMRANVINEIMSTERHYIKHLKDICEGYLKQC
ļ			RKRRDMFSDEQLKVIFGNIEDIYRFQMGFVRDLEKQYNNDDPHL
1			SEIGPCFLEHQDGFWIYSEYCNNHLDACMELSKLMKDSRYQHFF
1			EACRLLQQMIDIA\IDGFLLTPVQKICKYPLQLAELLKYTAQDH
1			SDYRYVAAALAVMRNVTQQINERKRRLENIDKIAQWQASVLDWE
Į.			GEDILDRSSELIYTGEMAWIYQP\YGRNQQRVFFLFDHQMVLCK
Ī	1		KDLIRRDILYYKGRIDMDKYEVVDIEDGRDDDFNVSMKNAFKLH
1	1		NKETEEIHLFFAKKLEEKIRWLRAFREERKMVQEDEKIGFEISE
1	1		NQKRQAAMTVRKVPKQKGVNSARSVPPSYPPPQDPLNHGQYLVP \DGIAQSQVFEFTEPKRSQSPFWQNFSRLTPFKK
6056	43	3358	SGGRGPVRVRSEQLSPSAEQVSQISQISLGRRPLSSLPPPPPSRA
1		0000	LAPTRAPDTALTIMEVAEVESPLNPSCKIMTFRPSMEEFREFNK
1			YLAYMESKGAHRAGLAKVIPPKEWKPRQCYDDIDNLLIPAPIQQ
			MVTGQSGLFTQYNIQKKAMTVKEFRQLANSGKYCTPRYLDYEDL
1			ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIARLNTVLDVVE
			EECGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHFGED
			KSWYAIPPEHGKRLERLAQGFFPSSSQGCDAFLRHKMTLISPSV
ł			LKKYGIPFDKITQEAGEFMITFPYGYHAGFNHGFNCAESTNFAT
1			VRWIDYGKVAKLCTCRKDMVKISMDIFVRKFQPDRYQLWKQGKD
			IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSKRP
	}		KADEEEEVSDEVDGAEVPNPDSVTDDLKVSEKSEAAVKLRNTEA SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDDKA
			YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPESCS
			SVAESNGVLTEGEESDVESHGNGLEPGEIPAVPSGERNSFKVPS
			IAEGENKTSKSWRHPLSRPPARSPMTLVKOOAPSDEELPRVLST
1 1	'	1	EEEVEETESWAKPLIHLWQTKPPNFAAEOEYNATVARMKPHCAT
			CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEMCF
			IYSEENIEYSPPNAFLEEDGTSLLISCAKCCVRVHASCYGIPSH
! !	i		EICDGWLCARCKRNAWTAECCLCNLRGGALKQTKNNKWAHVMCA
			VAVPEVRFTNVPERTQIDVGRIPLQRLKLKCIFCRHRVKRVSGA
1 1		1	CIQCSYGRCPASFHVTCAHAAGVL\MEPDDWPYVVNITCFRHKV NPNVKSKACEKVISVGQTVITKHRNTRYYSCRVMAVTSQTFYEV
]		1	MFDDGSFSRDTFPEDIVSRDCLKLGPPAEGEVVQVKWPDGKLYG
1 1	1		AKYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKARF
1 1	1		VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKKSQCNIF
			LSGTY
6057	1	853	FVARLKEQEGEGGLGPRKEKGRARGRERRRKMQLTRCCFVFLVQ
] {			GSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKS
1 1	Ì		RPMANSTLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFG
1 [WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNIS
1 1		1	ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVE\RGRR
1 1			TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR LVQKVCPDYNYHSDTPYYPSG
6058	i		HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRARVGSP
			SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR
]	VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD
]			ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR
1 1		1	PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL
1	1		PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/
			RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGRP
COE O			SREAGPWASLNCTLDPSASTP
6059	2	3650	QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT
	İ	1	QMIGDGCDLGLGEEEGGTGLPYPCQFCDK\$FIRL\$YLKRHEOIH
1		1:	SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS
			RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK
	L	<u> </u>	EHLAKSEKBAKKDDFMCDYCEDTFSQTEBLEKHVLTRHPQLSEK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
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NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ı	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	ļ -	\=possible nucleotide insertion)
			ADLQCIHCPEVFVDENTLLAHIHQAHANQKHKCPMCPE\QFSSV
1			\EGVYCHLDSHRQPDSSNHSVSPDPVLGSVASMSSATPDSSASV
1			ERGSTPDSTLKPLRGQKKMRDDGQGWTKVVYSCPYCSKRDFNSL
1			AVLEIHLKTIHADKPQQSHTCQICLDSMPTLYNLNEHVRKLHKN
			HAYPVMQFGNISAFHCNYCPEMFADINSLQEHIRVSHCGPNANP
	<u> </u>		SDGNNAFFCNQCSMGFLTESSLTEHIQ\Q\AHCSVGSAKLESPV
	1		VQPTQSFMEVYSCPYCTNSPIFGSILKLTKHIKENHKNIPLAHS
	1		KKSKAEQSPVSSDVEVSSPKRQRLSASANSISNGEYPCNQCDLK
1			FSNFESFQTHLKLHLELLLRKQACPQCKEDFDSQESLLQHLTVH
İ			YMTTSTHYVCESCDKQFSSVDD\LQKH\LLDMPHPLCCTHCT\L
			CQEVFDS\KVSI\QVHLAVKHSNEKKMYRCTACNWDFRKEADLQ
1			VHVKHSHLGNPAKAHKCIFCGETFSTEVBLQCHITTHSKKYNCK
1]		FCSKAFHAIILLEKHLREKHCVFDAATENGTANGVPPMATKKAE
ŀ	1		PADLQGMLLKNPEAPNSHEASEDDVDASEPMYGCDICGAAYTME
	1		VLLQNHRLRDHNIRPGEDDGSRKKAEFIKGSHKCNVCSRTFFSE
	1		NGLREHLQTHRGPAKHYMCPICGERFPSLLTLTEHKVTHSKSLD
	1		TGTCRICKMPLQSEEEFIEHCQMHPDLRNSLTGFRCVVCMQTVT
			STLELKIHGTFHMQKLAGSSAASSPNGQGLQKLYKCALCLKEFR
İ			SKQDLVKLDVNGLPYGLCAGCMARSANGQVGGLAPPEPADRPCA
			GLRCPECSVKFESAEDLESHMQVDHRDLTPETSGPRKGTQTSPV
			PRKKTYQCIKCQMTFENEREIQIHVANHMIEEGINHECKLCNQM FDSPAKLLCHLIEHSFEGMGGTFKCPVCFTVFVQANKLQQHIFA
1			VHGQEDKIYDCSQCPQKFFFQTELQNHTMSQHAQ
6060	2145	202	SYEIVGKNKLEVNHSQLKALCKCSLPSRLLPLGENLPLLDRGFR
i			KEPRSRGSRERDNMLHLHHSCLCFRSWLPAMLAVLLSLAPSASS
1	ļ		DISASRPNILLLMADDLGIGDIGCYGNNTMRTPNIDRLARDGVK
ł			LTQHISAASLCTPSRAAFLTGRYFVRSGMVSSIGYRVLQWTGAS
			GGLPTNETTFAKILEEKGYATGLIGKWHLGLNCESASDHCHHPL
1			HHGFDHFYGMPFSLMGDCARWELSBKRVNLEQKLNFLFQVLALV
ĺ			ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA
ŀ			DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV
ł			SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV
			EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW
			EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP
1	ŀ		QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR
			GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD
l i			LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ
6061	110		LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ
0001	710	1330	MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN
1			VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK
1 1			ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ
			SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG
, ,		-	HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA
1 1			RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN
1 1			PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY
			KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH
L 1	1		LALHRRRHMLV
6062	71	1079	ETMAKNGPENCEDCHILNABAFKSKKICKSLKICGLVFGILALT
			LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR
į l		į	TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP
1		1	EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI
] [LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE
Į 1		1	EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP
1			INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP
<u> </u>			YPYCYQGGRVICRVIMPCNWWVARMLGRV
6063	71	1079	ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT
[]	Į	LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR
[]	ĺ]	TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP
]]	ļ	j	EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI
			LBICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	l .	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- [to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
-		residue of	S=Serine, T=Threonine, V=Valine.
]	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Gton
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP
ł		İ	INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP
			YPYCYQGGRVICRVIMPCNWWVARMLGRV
6064	913	311	NLPQSLPRPTEHSPPYSLEKMTDLVAVWDVALSDGVHKIEFEHG
- 1	i		TTSGKRVVYVDGKEEIRKEWMFKLVGKETFYVGAAKTKATINID
1	l .		AISGFAYEYTLEINGKSLKKYMEDRSKTTNTWVLHMDGENFRIV
ŀ	1		LEKDAMDINICIONI DEL CERTADESKITNIWVLHMDGENFRIV
1	1		LEKDAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACYIKAV\
6065	1153	641	SSG\KRKEGIIHTLIVDNREIPEIAS
1		041	MSVRVARVAWVRGLGASYRRGASSFPVPPPGAQGVAELLRDATG
	;		AEEEAPWAATERRMPGQCSVLLFPGQGSQVVGMGRGLLNYPRVR
1			BLYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIFVASLAAV
6066			EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG
"""	68	3470	VKENMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGDVRTW
1			BDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIOVHTFDFC
			VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKTVDVMDSS
1			QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWOISDOTCA
}			ISWPLLQKCNDVINAKSICRLAWOPKSGKLLATPVEKSVYLVDD
1 1	1		ESWSHQFDLSDNFISQTLNIVTWSPCGOYLAAGSINGTTTVWNTV
			ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGLLENV
1 1			CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNAVEIP
1	1		SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDISMLKT
i i	1		GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQKPFQS
1			GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSIHHAT
1 1	}		HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSWDSSK
1 1			EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQKEVF
1 1	ł		SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELGKKKK
1 1	Į.		QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLNRGLG
	i		NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGSRFPP
1			TI.DDDAWATI CHELDEGO TAMOVIGA HENDOQUECIPCKGSRFPP
			TLPRPAVAILSFKLPYCQIATEKGQMEEQFWRSVIFHNHLDYLA
1			KNGYEYEBSTKNQATKEQQELLMKMLALSCKLEREFRCVELADL
j j	1		MTQNAVNLAIKYASRSRKLILAQKLSELAVEKAAELTATQVEEE
	1		EEEEDFRKKLNAGYSNTATEWSQPRFRNQVEEDAEDSGEADDEE
1	i		KPEIHKPGQNSFSKSTNSSDVSAKSGAVTFSSQGRVNPFKVSAS
1 1			SKEPAMSMNSARSTNILDNMGKSSKKSTALSRTTNNEKSPIIKP
1	į.		LIPKPKPKQASAASYFQKRNSQTNKTEEVKEENLKNVLSETPAI
1	i		CPPQNTENQRPKTGFQMWLEENRSNILSDNPDFSDEADIIKEGM
1	l l		IRFRVLSTEERKVWANKAKGETASEGTEAKKRKRVVDESDETEN
6067			QEEKAKENLNLSKKQKPLDFSTNOKLSAFAFKOE
1 220,	858	321	LPWQRLGVLLSRGKMAVTGWLESLRTAOKTALLODGRRKVHVLF
i 1			PDGKEMAEEYDEKTSELLVRKWRVKSALGAMGOWOLEVGDDADI.
[GAGNIGPELIKESNANPIFMRKDTKMSFOWRIRNLPYPKDVVSV
			SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T
6068			PTAP
0008	13	1730	GSKMADLANEEKPAIAPPVFVFQKDKGQKSPAEQKNLSDSGEEP
l 1	1	l l	RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL
1	ı		PPFPRELAGRSAGGSSPEGGEDSDREDGNYCPPVKRERTSSLTQ
1	1	,	FPPSQSEERSSGFRLKPPTLIHGQAPSAGLPSQKPKEQQRSVLR
			PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPDTAAW
J	ĺ		RSPSEAADEVCALEEKEPQKNESSNASEBEACEKKDPATQQAFV
Ì			FGQNLRDRVKLINESVDEADMENAGHPSADTPTATNYFLQYISS
		ĺ	SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA
1	1		AAESGSESSQEATPEKESLABSAAAYTKATARKCLLEKVEVIT
- [GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG
- 1			TLOSRISDACODCCIDALILAMENT WAS CONTROL
1	,		TLQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SIRITAM
ļ		İ	DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEQEAK
ĺ	l		MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS
6069	583		
· [PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK
1	İ	į.	RHARVTVKYDRRELORRLDVEKWIDGKLEELYRGMEADMPDEIN
			IDELLELESEERSRKIQGLLKSCGKPVEDFIQELLAKLQGLHR

SEQ	Predicted	Predicted end	Amino agid normant annia
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NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
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1.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	ooquonse	\=possible nucleotide insertion)
	 		Q\PGLRQPSPSP\DGQPSAPFQGPGARTASPLTLLALFPGPPER
1		ł	RPALLCVLSCI
6070	478	858	IRVTVDGEFLHYIFPLQFLDSPEW/RFTETHRGRHF\QVTLTAE
İ			TDCRYVSWRRKKLYLLFAQHRYISRLFSVLIGSDIADKLYALND
]	RVYIGKRYHYDIRLPNFYQMSTPEIRRSPLTQHFQNSRRYW
6071	2	1654	HEARTKGNMALARP\VRLFSLVTRLLLAPRRGLTVRSPDEPLPV
İ			VRIPVALQRQLEQRQSRRRNLPRPVLVRPGPLLVSARRPELNQP
	l		ARLTLGRWERAPLASQGWKSRRARRDHFSIERAQQEAPAVRKLS
			SKGSFADLGAWKPRVLHALQE\AAPEVVQ\PTTVQSSTIPSLLR
ļ	ļ		GRHVVCAAETGSGKTLSYLLPLLQRLLG\HPSLDSLPIPAPRGL
1			VLVPSRELAQQVRAVAQPLGRSLGLLVRDLEGGHGMRRIRLQLS
			ROPSADVLVATPGALWKALKSRLISLEQLSFLVLDEADTLLDES
			FLELVDYILEKSHIAEGPADLEDPFNPKAQLVLVGATFPEGVGQ
1	[ľ	LLNKVASPDAVTTITSSKLHCIMPHVKQTFLRLKGADKVAELVH
l	1		ILKHRDRAERTGPSGTVLVFCNSSSTVNWLGYILDDHKIQHLRL
i	1		QGQMPALMRVGIFQSFQKSSRDILLCTDIASRGLDSTGVELVVN
1	1.		YDFPPTLQDY1HRAGRVGRVGSEVPGTV1SFVTHPWDVSLVQKI
	1		ELAARRRSLPGLASSVKEPLPQAT
6072	1	742	KMERTEMMPTINSQLEFKSKPFPLVSSSRWLVKRGELTAYVEDT
		,	VLFSRRTSKQQVYFFLFNDVLIITKKKSEESYNVNDYSLRDQLL
			VESCONEELNSSPGKNSSTMLYSRQSSASHLFTLTVLSNHANEK
]		VEMLLGAETQSERARWITALGHSSGKPPADRTSLTQVEIVRSFT
	1		AKQPDELSLQVADVVLI\YQRVSDGWYEGER\LRDGERGWFPME
İ	[CAKEITCQATIDKNVERMGRLLGLETNV
6073	620	860	PCRRGLARPLSRRPG/SILVHCAVGVSRSATLVLAYLMLYHHLT
1			LVEAIKKVKDHRGIIPNKGFLRQLLALDRRLRQGLEA
6074	168	1110	PGARCMATELQCPDSMPCHNQQVNSASTPSPEQLRPGDLILDHA
			GGNRASRAKVILLTGYAHSSLPAELDSGACGGSSLNSEGNSGSG
1	ł		DSSSYDAPAGNSFLEDCELSRQIGAQLKLLPMNDQIRELQTIIR
			DKTASRGDFMFSADRLIRLVVEEGLNQLPYKECMVTTPTGYKYE
1 1	i		GVKFEKGNCGVSIMRSGEAMEQGLRDCCRSIRIGKILIQSDEET
1	1		QRAKVYYAKFPPDIYRRKVLLMYPILQTG\NTVIEAVKVLIEHG
1	l		VQPSVIILLSLFSTPHGAKSIIQEFPEITILTTEVHPVAPTHFG
			QKYFGTD
6075	320	1091	PPTCQPQEVEHH\YGYVPILGNKTLPSRCHQCVIVSSSSHLLGT
			KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV
1 1			LRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFP
1 1	ľ		NMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIA
	1		VELCOHVHVYGMVPPNYCSQRPRLQRMPYHYYEPKGPDECVTYI
			QNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT
6076	1721	107	HPSPTEAPRVQHLTMDCTWRILFLVAAATGTHAQVQLVQSGAEV
1	 		KKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGAFDPED
1	1		GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD
1 1	i		HGDYAFDIWGQGTMVTVSSAPTKAPDVFPIISGCRHPKDNSPVV
1 1	1		LACLITGYHPTSV\TVTWYMGTQSQA\QRTFPEIQRRDSYYMTS
		İ	SQLSTPLQQWRQGEYKCVVQHTASKSKKEIFRWPESPKAQASSV
j i			PTAQPQAEGSLAKATTAPATTRNTGRGGEEKKKEKEKEEQEERE
1	1	ĺ	TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD
; l			AHLTWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLPRSLWNA
1 1			GTSVTCTLNHPSLPPQRLMALREPAAQAPVKLSLNLLASSDPPE
			A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKP\
]			RSTTFWA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL
H-2			BVSYVTDHGPMK
6077	3687	1268	LLPDMNLQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECIQ
			AGPNCGWCTNSTFLQEGMPTSARCDDLEALKKKGCPPDDIENPR
] [f	}	GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP
]		i	QTPTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN
			EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS
	1		PFSYKNVLSLTNKGEVFNELVGKQRISGNLDSPEGGFDAIMQVA
		1	VCGSLIGWRNVTRLLVFSTDAGFHFAGDGKLGGIVLPNDGQCHL

SEQ	Predicted	Predicted end	Amino anid committee
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
- 1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ı	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			ENNMYTMSHYYDYPSIAHLVQKLSENNIQTIFAVTEEFQPVYKE
			LKNLIPKSAVGTLSANSSNVIQLIIDAYNSLSSEVILENGKLSE
- 1	1		GVTISYQSY\CKNGVNGTGENGRKCSNISIGDEVQFEISITSNK
- [ļ.		CPKKDSDSFKIRPLGFTEEVEVILQYICECECQSEGIPESPKCH
i	1		EGNGTFECGACRCNEGRVGRHCECSTDEVNSEDIGCFTARKENO
1	1	1	FQKSASNHGRVPSAGQCVCRKRDNTNEIYSGKFCECDNFNCDRS
ı			NGLICGGNGVCKCRVCECNFNYTGSACDCSLDTSTCEASNGOIC
			NGRGICECGVCKCTDPKFQGQTCEMCOTCLGVCAEHKECVOCPA
į	j		FNKGEKKDTCTQECSYFNITKVESRDKLPOPVOPDPVSHCKEYD
	ı		VDDCWFYFTYSVNGNNEVMVHVVENPECPTGPDTTPTVACUUAC
	1		IVLIGLALLLIWKLLMIIHDRREFAKFEKEKMNAKWDTGENPIV
6078	+		KSAVTTVVNPKYEGK
0070	1426	180	ETEDVMELLEEDLTCPICCSLFDDPRVLPCSHNFCKKCLEGILE
J		1	GSVRNSLWRPVPFKCPTCRKKTFSYWELIPLOVNYSLKGTVPKY
1	[NKIKISPKMPVCKGH\LGOPLNIF\CL\TDMOLDL/CGIC\DTP
			GEHTKHVFCSIEDAYAQERDAFESLFOSFETWRRGDAT.Spi.DTI
İ			ETSKRKSLQLLTKDSDKVKEFFEKLQHTLDQKKNEILSDFETMK
	1		LAVMQAYDPEINKLNTILQEQRMAPNIABAFKDVSEPIVFLQQM
1	j j		QEFREKIKVIKETPLPPSNLPASPLMKNFDTSQWEDIKLVDVDK
ì			LSLPQDTGTFISKIPWSFYKLFLLILLLGLVIVFGPTMFLEWSL
			FDDLATWKGCLSNFSSYLTKTADFIEQSVFYWEQVTDGFFIFNE RFKNFTLVVLNNVAEFVCKYKLL
6079	1586	141	ATARDLGCARRIDRVVMESTPSRGLNRVHLQCRNLQEFLGGLSP
1			GVLDRLYGHPATCLAVFRELPSLAKNWVMRMLFLEQPLPQAAVA
	1		LWVKKEFSKAQEESTGLLSGLRIWHTQLLPGGLQGLILNPIFRQ
	1		NLRIALLGGGKAWSDDTSQLGPDKHARDVPSLDKYAEERWEVVL
1	1		HFMVGSPSAAVSQDLAQLLSQAGLMKSTEPGEPPCTTSAGPOPT
1	!	i	LLDTPAQLWYFMLQYLQTAQSRGMDLVEILSFLFOLSPSTLGED
1	1		YSVEGMSDSLLNFLQHLREFGLVFORKRKSRRVVDT/DALAINT
1	1 1		SSGVSGAGGTVHQPGFIV\VETNYRLYAYTESELOTALTALTER
	ļ		MLYPFP\NMVV\ARVTR\ESVOOAIASGITAOOTTHFI.PTPAUD
1		ļ	VMLKQTPVLPPTITDQIRLWELERDRLRFTEGVLVNOFI.SOUDE
			ELL\LAHAPKLGVLVFB/NTPAKRLMVVTPAGHSDVKRFWKROK
6080	1	1199	HSS
	1		TETIDHVGEFAMAAQAAGVSRQRAATQGLGSNQNALKYLGQDFK TLRQQCLDSGVLFKDPEFPACPSALGYKDLGPGSPQTQGIIWKR
l i	. 1	ì	PTELCPSPQFIVGGATRTDICQGGLGDCWLLAAIASLTLNEELL
Ì	i i	1	YRVVPRDQDFQENYAGIFHFQPLCPPSP\FWQYGEWVEVVIDDR
1	i i	ŀ	LPTKNGQLLFLHSEQGNEFWSALLEKAYAKLNGCYEALAGGSTV
1 1			EGFEDFTGGISEFYDLKKPPANLYQIIRKALCAGSLLGCSIDVY
]	Į		SAAEAEAITSQKLVKSHAYSVTGVEEVNFQGHPEKLIRLRNPWG
i i		i	EVENSGAWSDDAPEWNHIDPRRKEELDKKVEDGEFWMSI.SDBIRD
].]			QFSRLEICNLSPDSLSSEEVHKWNLVLFNGHWTRGSTAGGCQNY
L			PGSS
6081	3	865	EMLPLLLPLPLLWA/GALAQDARFRLEMPESVTVQEGLC1FVHC
	1		SVFYLEYGWKDSTPAYGHWFREGVSVDOETPVATNNSTOKYOKR
[[į.	1	TQGRFHLLGDPSRNNCSLSIRDARRRDNGSYFFWVARGETKECV
	1	ī	KYSPLSVYVTALTHRPDILIPEFLKSGHPSNLTCSVPWVCFOCT
ł	l		PPIFSWMSAAPTSLGPRTLHSSVLTIIPRPQDHGTNLICQVTFP
		1.	GAGVTTERTIQLSVSWKSGTVEEVVVLAVGVVAVKILJ.Lct.ct.t
6082	283	1288	ILSFHKKKAVRAVEVEENVYAVMG
	-	1240	EARSPGPTQTRTAPGLAAPGLAQPAALRLLLSRPPSAAMDGDGD
	İ	;	PESVGQPEEASPEEQPEEASAEEERPEDQQEEEAAAAA\Y\LDE
 		1;	LPEPLLA/LRVLAALPRHE\LVQACR\LVCLRWKELVDGAPLWL
ſ	1	11	LKCQQEGLVPEGGVEEERDHWQQFYFLSKRRRNLLRNPCGEEDL EGWCDVEHGGDGWRVEELPGDSGVEFTHDESVKKYFASSFEWCR
j		} ;	KAQVIDLQAEGYWEELLDTTQPAIVVKDWYSGRSDAGCLYBLTV
j		1;	KLLSEHENVLAEFSSGQVAVPQDSDGGGWMEISHTFTDYGPGVR
		;	VRFEHGGQDSVYWKGWFGARVTNSSVWVEP
6083	1865	309 I	COWCAERRGLGMSLADELLADLEEAAEEEEGGSYGEEEEEPATE

SEO	Predicted	1 7-24-5-3	~
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide	\n-aranthe, C=CVSCelne
1 -	location	location	Grucamic Acid, F=Phenylalaning C.Clarica
	corresponding	corresponding	n=nistidine, i=isoleucine V-limina
i	to first	to first	L=Leucine, M=Methionine, N-Assassasine
	amino acid	amino acid	P=Proline, O=Glutamine R-Arginia
}	residue of	residue of	S=Serine, T=Threonine, V=Valine
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +=St
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			DVQEETQLDLSGDSVKTIAKLWDSKMFAEIMMKIEEYISKQAKA
1			SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR
1	(FPELESLVPNALDYIRTVKELGNSLDKCKNNENLQQILTNATIM
1	1		VVSVTASTTOCOOLGEREN ED TOTOCKNNENLQQILTNATIM
	1	Í	VVSVTASTTQGQQLSEEELERLEEACDMALELNASKHRIYEYVE
i	1		SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG
		1	AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPPFSVAP\DL
-	İ		RRKAARLVAAKCTLAARVDSFHESTEGKVGYELKDEIERKFDKW
Į.			QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTEIR\KQ
1		1	ANKMSFGETEEDAYQEDLGFSLGHLGKSGSGBUPOTOUNEADER
1			RISATEQRIEQKQSVVYGGKSTIRDRSSGTASSVARTDI.OCI DE
6084	1865		VNPQAABKKVAEANQKYFSSMAEFLKVKGEKSGLMST
1	1003	309	KOWCAERRGLGMSLADELLADLEEAAEEEEGGGVCEPEPEDATA
1	1		DVQESTQLDLSGDSVKTIAKLWDSKMFARTMMKTERVICVONKN
1	1		SEVMGPVEAAPEYRVIVDANNLTVEIENRINTTUVETEDVVCVD
	1		FPELESLVPNALDYIRTVKELGNSLDKCKNNENLQQILTNATIM
	1		VVSVTASTTQGQQLSEEELERLEEACDMALELNASKHRIYEYVE
1	!		SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG
1	i		AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPFFSVAP\DL
j.	J		RRKAARLVAAKCTLAARVDSFHESTEGKVGYELKDEIERKFDKW
1			QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTEIR\KQ
			ANRMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA
J	1		RISKTIORTLOYOGUUVCCVCTTDDDGGCSGRVRQTQVNEATKA
	<u>L</u> . 1		RISKTLORTLOKOSVVYGGKSTIRDRSSGTASSVAFTPLOGLBI VNPQAAEKKVAEANOKYFSSMAEFLKVKGEKSGLMST
6085	2	1456	CORRESCONDANGERSONST
1	1	7	SGPRSPQGNRAVGRISLGGKRNPEVTLLPGVSSERVRRWRRARV
1	1		GVARVKPGNPWKPSPATQVPR/VPAQVYLPGRGPPLREGEELVM
	i i	i	DEEAYVLYHRAQTGAPCLSFDIVRDHLGDNRTELPLTLYLCAGT
1	1 -1		QALSAQSNRLMMLRMHNLHGTKPPPSEGSDEREEEEDERDEEDE
	i		RPQLELAMVPHYGGINRVRVSWLGEEPVAGVWSRKGOVEVENT D
	[]		RODUVVEEPQALAAFLRDEOAOMKPIFSFAGUMGEGENI DUGED
	1		VIGRULTGUCQKNIHLWTPTDGGSWHVDORPRIGUTPGUCDT ON
1	! !	l	SPIEWIVEASCSADASIRIWDIRAADSKACMI.TTATATAUDCDIDTE
1	i		ISWSRREPF LLSGGDDGALKIWDLROFKSGSDVATEVOUR DIM
[1		SVEWHPQDSGVFAASGADHOITOWDLG/TVEDDDFAGDVPADDG
1 1	1	j	LADLPQQLLFVHQGETELKELHWHPQCPGLLVSTALSGFTIFRT
6086	2486		150
1 0000	2419	1357	GAATQHGGAMNLLPCNPHGNGLLYAGFNQDHGCFACGMENGFRV
<u> </u>		i	YNTDPLKEKEKQEFLEGGVGHVEMLFRCNYLALVGGGKKFKYPP
1 1	1		NKVMIWDDLKKKTVIEIEFSTEVKAVKLRR\DKIVVVLDSMIKV
	· ·	1	FTFTHNP\HQLHVFE\TCYNPKGLCVLCPNSNNSLLAFPGTHTG
! !	İ	ļ	HVQLVDLASTEKPPVDIPAHEGVLSCIALNLQGTRIATASEKGT
] }	1	ľ	LIRIFDTSSGHLIQELRRGSQAANIYCINFNQDASLICVSSDHG
1	1	1	TVHIFAAEDPKRNKQSSLASASFLPKYFSSKWSFSKFQVPSGSP
!!	1		CICAFGTEPNAVIAICADGSYYKFLFNPKGECIRDVYAQFLEMT
			DDKL
6087	476	1877	QNSQRTGLPITIFSRSFPLLTGSDLCENMPCTCTWRNWRQWIRP
	1		LVAVIYLVSIVVAVPLCVWBLQKLEVGIHTKAWFIAGIFLLLTI
	ſ	1	DISLAUTION UNITED BLOWS LOKE VG THE KAWPIAGIFLE TI
i		ĺ,	PISLWVILQHLVHYTQPELQKPIIRILWMVPIYSLDSWIALKYP
		1.	GIAIYVDTCRECYBAYVIYNFMGFLTNYLTNRYPNLVLILEAKD
- 1		1	QQKHFPPLCCCPPWAMGEVLLFRCKLGVLQYTVVRPFTTIVALI
1		1.	CELLGIYDEGNFSFSNAWTYLVIINNMSQLFAMYCLLLFYKVLK
}	1	1:	EELSPIQPVGKFLCVKLVVFVSFWQAVVIALLVKVGVISEKHTW
İ		1.	EWQIVEAVATGLODFIICIEMFIAATA\HHVTEQVVDVIOERDD
ſ	1	1,	SCFDSFLAMWDVSDIRDDISEOVRHVGRTVPGHDDVVI.DDDD
		í 1	DUNEHTSLUSSSSODAISIASSMPPSPMGHYOGEGUTUTDOTTO
6088	1604		TTAKISDEILSDTIGEKKEPSDKSVDS
	1684	689	SASGLVRLLQOGHRCLLAPVAPKI, VPPUBGVKKGEPAAER BOVE
		1	LERQRLLRCPPPPVRRSEKPNWDYHAEIQAFGHRLQENFSLDLL
1		l P	(TAFVNSCYIKSEEAKRQQLGIEKEAVLLNLKSNQELSEQGTSF
		5	GOTCLTQFLEDEYPDMPTEGIKNLVDFLTGEEVVCHVARNLAVE
1	l	آم	DITLSEEFPVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI
		,	OMTGKELFEMWKIINPMGLLVEELKKRNVSAPESRLTRQSG\A
			A STATE OF THE PROPERTY OF THE
			—

SEC	Predicted	Predicted end	1200
ID		nuclectide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F-Phenylalanine, G-Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ì	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ł	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	sequence	sequence	(Codon, /=possible nucleotide deletion
			\=possible nucleotide insertion\
1			PTALPLYFVGLYCDKKLIAEGPGETVLVAEEEAARVALRKLYGE
6089	3	<u> </u>	TENRRPWNYSKPKETLRAEKSITAS
""	. 3	3054	TRLGIPGSTISSRPRLCALAAEGHFLGHSWTGSRAGAHTGAPAW
1	1		PSRRLRDLPAGGMWRLRRAAVACEVCOSLVKHSSGTKGSLDLOV
1	1	1	LINEVSKSI INSHHPTLKLORPOLRTSFOOFSSI TNI DI DVI VEC
Ì	1		PIKIGYQPRRNFWPARLATRLLKLRYLILGSAVGGGYTAYKTED
ļ	1	1	QWKDMIPDLSEYKWIVPDIVWEIDEYIDFEKIRKALDGGEDIAW
1	i	1	LAPDFDKIVESLSLLKDFFTSGSPEETAFRATDRGSESDKHFRK
1	J		VSDKEKIDQLQEELLHTQLKYQRILERLEKENKBLRKLVLQKDD
ĺ	{		KGIPFIESLRKSLIDMYSEVLDVLSDYDASYNTQDHLPRVVVVG
ı			DQSAGKTSVLEMIAQARIFPRGSGEMMTRSPVKVTLSEGPHHVA
1	1	1	LFKDSSREFDLTKEEDLAALRHEIELRMRKNVKEGCTVSPETIS
	- 1		LNVKGPGLQRMVLVDLPGVINTVTSGMAPDTKETIFSISKAYMQ
1	1	l .	DPNAIILCIQDGSVDAERSIVTDLVSQMDPHGRRTIPVLTKVDL
1 '	ļ	İ	AEKNVASPSRIQQIIEGKLFPMKALGYFAVVTGKGNSSESIEAI
Į.	l		REYEEEFFQNSKLLKTSMLKAHQVTTRNLSLAVSDCFWKMVRES
1			VEQQADSFKATRFNLETEWKNNYPRLRELDRNELFEKAKNEILD
1			EVISLSQVTPKHWEEILQQSLWERVSTHVIENIYLPAAQTMNSG
			TFNTTVDIKLKQWTDKQLPNKAVEVAWETLQEEFSRFMTEPKGK
1			EHDDIFDKLKEAVKEESIKRHKWNDFAEDSLRVIQHNALEDRSI
1	ĺ		SDKQQWDAAIYFMEEALQARLKDTENAIENMVGPD\WKKRWLYW
]			KNRTQEQCVHNETKNELEKMLKCNEEHPAYLASDEITTVRKNLE
1	1		SRGVEVDPSLIKDTWHQVYRRHFLKTALNHCNLCRRGFYYYQRH
	1 1		FVDSELECNDVVLFWRIQRMLAITANTLRQQLTNTEVRRLEKNV
i	1		KEVLEDFABDGEKKIKLLTGKRVQLAEDLKKVREIQEKLDAFIE
			ALHOEK
6090	194	1560	PVFVPAPGAVLEQAS/ASPPLATQTVVPLQRCKIPELPVQASIL
Į.	1 1		FELQLFFCQLIALFVHYINIYKTVWWYPPSHPPSHTSLNFHLID
1			FNLLMVTTIVLGRRFIGSIVKEASQRGKVSLFRSILLFLTRFTV
1	1 1		LTATGWSLCRSLIHLFRTYSFLNLL/FPLLSVWDVHSVPAAELR
İ	1		P\RKTSLFNHMASMGPREAVSGLAKSRDYLLTLR\RRGSSTQDS
ĺ	1		CMARTPCP/PHACCLSPSLIRSEVBFLKMDFNWRMKEVLVSSML
	1		SAYYVAFVPVWFVKNTHYYDKRWSCELFLLVSISTSVILMQHLL
1	1 1	'	PASYCDLLHKAAAHLGCWQKVDPALCSNVLQHPWTEECMWPQGV
Ì	1		LVKHSKNVYKAVGHYNVAIPSDVSHFRFHFFFSKPLRILNILLL
1	1		LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL
			VLGKAYSYSASPQRDLDHRFS
6091	3279	412	SSRTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG
	1	ļ	WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG
	1	i	PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK
	1 1		VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ
	!	1	LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE
	1 1		PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ
	1	•	LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR
	i i	į	TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN
	i I		KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS
	1		SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE
	1	[TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR
ŀ		[RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA
]	SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA
j		ſ	RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY
Ì		1	KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ
			RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV
[AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN
ľ			CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG
į		ļ.;	ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG
l		1 7	PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS
ſ	4		SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS
		13	SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL
6092	143	3190	AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ
		i	EVPKPENISLRNKLRELCVKLMFLHPVDYGRKAEELLWRKVYYE
			AAAA AAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAA

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ĺ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid		Codon, /=possible nucleotide deletion,
	1	sequence	
	sequence		\=possible nucleotide insertion)
}		1	VIQLIKTNKKHIHSRSTLECAYRTHLVAGIGFYQHLLLYIQSHY
Ì	ľ	t	QLELQCCIDWTHVTDPLIGCKKPVSASGKEMDWAQMACHRCLVY
1	ļ	1	LGDLSRYQNELAGVDTELLAERFYYQALSVAPQIGMPFNQLGTL
ł	ł .	ł	AGSKYYNVEAMYCYLRCIQSEVSFEGAYGNLKRLYDKAAKMYHQ
1	1	j	LKKCETRKLSPGKKRCKDIKRLLVNFMYLQSLLQPKSSSVDSEL
}	1	}	TSLCQSVLEDFNLCLFYLPSSPNLSLASEDEREYESGYAFLPDL
	į.	1	LIFQMVIICLMCVHSLERAGSKQYSAAIAFTLALFSHLVNHVNI
l		1	RLQAELEEGENPVPAFQSDGTDEPESKEPVEKEEEPDPEPPPVT
	1	ł	PQVGEGRKSRKFSRLSCLRRRRHPPKVGDDSDLSEGFESDSSHD
į	1	j	SARASEGSDSGSDKSLEGGGTAFDAETDSEMNSQESRSDLEDME
1	1	1	EEEGTRSPTLEPPRGRSEAPDSLNGPLGPSEASIASNLQAMSTQ
	1	1	MFQTKRCFRLAPTFSNLLLQPTTNPHTSASHRPCVNGDVDKPSE
	1	}	PASEEGSESEGSESSGRSCRNERSIQEKLQVLMAEGLLPAVKVF
į		}	LDWLRTNPDLIIVCAQSSQSLWNRLSVLLNLLPAAGELQESGLA
1]	}	LCPEVODLLEGCELPDLPSSLLLPEDMALRNLPPLRAAHRRFNF
l			DTDRPLLSTLEESVVRICCIRSFGHFIARLOGSILQFNPEVGIF
	1	1	VSIAQSEQESLLQQAQAQFRMAQEEARRNRLMRDMAQLRLQLEV
ŀ	1	\	SOLEGSLOOPKAOSAMSPYLVPDTOALCHHLPVIRQLATSGRFI
	1	1	VIIPRTVIDGLDLLKKBHPGARDGIRYLEAEFKKGNRYIRCQKE
		1	VGKSFERHKLKRODADAWTLYKILDSCKOLT\LAOGAGEEDPSG
ŀ		ŀ	,
1		}	MVTIITGLPLDNPSLLSGPMQAALQAAAHASVDIKNVLDFYKQW
<u> </u>			KEIG
6093	76	1002	ACGRRAMLALRVART/SRWGAL\RGAVWAPGTRPSKRRACWALL
ļ	1	Ì	PPVPCCLGCLAERWRLRPAALGLRLPGIGQRNHCSGAGKAAPR\
ļ	ì		PAAGAGAAAEAPGGQWGPASTPSLYENPWTIPNMLSMTRIGLAP
1	Í		VLGYLIIEEDFNIALGVFALAGLTDLLDGFIARNWANQRSALGS
ł		{	ALDPLADKILISILYVSLTYADLIPVPLTYMIISRDVMLIAAVF
ſ	1	j	YVRYRTLPTPRTLAKYFNPCYATARLKPTFISKVNTAVQLILVA
	ł		ASLAAPVFNYADSIYLQILWCFTAFTTAASAYSYYHYGRKTVQV
l		l	IKD
6094	23	1010	PFLRCLRGDQKAKMSERKVLNKYYPPDFDPSKIPKLKLPKDRQY
(}	(VVRLMAPFNMRCKTCGEYIYKGKKFNARKETVQNEVYLGLPIFR
l	1	}	FYIKCTRCLAEITFKTDPENTDYTMEHGATRNFQAEKLLEEEEK
l	ļ	{	RVQKEREDEELNNPMKVLENRTKDSKLEMEVLENLQELKDLNQR
Į.	1	1	QAHVDFEAMLROHRLSEEERRRQQQEEDEQETAALLEEARKRRL
ł	-		LEDSDSEDEAAPSPLQPALRPNPTAILDEAPKPKRKVEVWEQSV
§			GSLGSRPPLSRLVVVKKAKADPDCSNGQPQA/APHPRSPAEQEG
ł		}	GOPYTPDAWRVLPEPTGCIPGQ
6095	1	1599	TRGRAAERSRGRGHGFLGGGFA\SVVDYFPSEDFYRCGYCKNES
1	1 -		GSRSNGMWAHSMTVQDYQDLIDRGWRRSGKYVYKPVMNQTCCPQ
l	1		YTIRCRPLOFOPSKSHKKVLKKMLKFLAKGEVPKGSCE\DEPMD
1		j	STMDDAVAGDFALINKLDIOCDLKTLSDDIKESLESEGKNSKKE
ł	1		
L	L	<u> </u>	EPQELLQSQDFVGEKLGSGEPSHS

TRADOCS:1416257.1(%CSH011.DOC)

SEQ	Predicted	Predicted end	1 2min = a sid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- 1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
į	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
]	sequence	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
	1		VKVHTVPKPGKGADLSKPPCRKAKEIRKERKRLKLMQQNPAGEL
		İ	EGFQAQGHPPSLFPPKAKSNQPKSLEDLIFESLPENASHKI.EVR
}			VVRSSPPSSQFKATLLESYQVYKRYQMVIHKNPPDTPTESQFTR
1		}	FLCSSPLEAETPPNGPDCGYGSFHQQYWLDGKIIAVGVIDILPN
}	1		CVSSVYLYYDPDYSFLSLGVYSALREIAFTRQLHEKTSQLSYYY
			MGFYIHSCPKMKYKGQYRPSDLLCPETYVWVPIEQCLPSLENSK
İ			YCRFNQDPEAVDEDRSTEPDRLQVFHKRAIMPYGVYKKQQKDPS
5005			EEAAVLQYASLVGQKCSERMLLFRN
6096	2277	575	QRVRAALLSSAMEDSEALGFEHMGLDPRLLOAVTDLGWSRPTLT
			QBKAIPLALEGKDLLARARTGSGKTAAYAIPMLOLLLHRKATGP
1	l		VVEQAVRGLVLVPTKELARQAQSMIOOLATYCARDVRVANVSAA
1			EDSVSQRAVLMEKPDVVVGTPSRILSHLOODSLKLRDSLELLVV
			DEADLLFSFGFEEELKSLLCHLPRIYOAFLMSATFNEDVOALKE
J			LILHNPVTLKLQESQLPGPDQLQQFQVVCETEEDKFLLLYALLK
1			LSLIRGKSLLFVNTLERSYRLRLFLEOFSIPTCVLNGRLPLRSR
1 1			CHIISQFNQGFYDCVIATDAEVLGAPVKGKRRGRGPKGDKASDP
1 .			EAGVARGIDFHHVSAVLNFDLPPTPEAYIHRAGRTARANNPGIV
1 1			LTFVLPTEQFHLGKIEBLLSGENRGPILLPYOFRMEEIEGFRYR
1 1			CRDAMRSVTKQAIREARLKEIKEBLLHSEKLKTYFEDNPR\DLO
1 1			LLRHDLPLHPAVVKPHLGHVPDYLVPPALRGLVRPHKK\GRSCI.
6097			PLVGRPREQSPRTHCAASSTKERNSDPQPSPPEVVGPLWS
8097	1673	192	APGTMSGGKKKSSFQITSVTTDYEGPGSPGASDPPTPOPPTGPP
1 1			PRLPNGEPSPDPGGKGTPRNGSPPPGAPSSRFRVVKLPHGLGEP
1 1			YRRGRWTCVDVYERDLEPHSFGGLLEGIRGASGGAGGRSLDSRI.
1 1			ELASLGLGAPTPPSGLSQGPTSWLRPPPTSPGPOARSFTGGLGO
1 1	i		LVVPSKAKAEKPPLSASSPQQRPPEPETGESAGTSRAATPLPSI
1	1		RVEAEAGGSGARTPPLSRRKAVDMRLRMELGAPEEMGOVPPLDS
1. 1	Í		RPSSPALYFTHDASLVHKSPDPFGAVAAQKFSLAHSMLAISGHL
1	1		DSDDDSGSGSLVGIDNKIEQAMDLVKSHLMFAVREEVEVLKEQI
1			RELAERNAALEQENGLLRALA\SPEQLGSAGPPRGVPR\LGPPA
ł 1	ļ		PNGPFVLSLPSLTIVPLGLPGLASAAWPPLPMPALIVPVFPGVG
1			VQALSNGPWSPGPLPHLLIIPSLDGGGEGFRTGRQQGAPFGEET
6098	160		QPPPSLPGTPQQ
1 0036	168	1074	NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD
		ĺ	EGKIFKNWGTQTEKEDTSNINPROTETSVNASRSPEKCAOOROK
			RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE
			NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLORTNPRKOL.
			\QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR
1	1		TAWEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D
6099			ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD
6699	168	1074	NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD
ļ 1	ŀ	ŀ	EGKIFKNWGTQTEKEDTSNINPROTETSVNASRSPEKCAOOROK
		İ	RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE
		į.	NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLORTNPRKOL
1		j	\QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKUSVP
1 1		ł	TANEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D
			ELTKEKDQIEAALSRMPSPGGRITLOTRLNOEAFGRSFGKD
6100	2	713	FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLY.
1	1	İ	QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLOIWDTAGORSF
		i	RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDAROHSSSNM
	ŀ		VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN
			VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP
<u> </u>	i		SASQRNSRDIGSNSGCC
5101	1		FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR
	ļ		GKMVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAQIAEDKPY
		1	AELWMGTHPRGDAKILDNRISQKTLSQWIAENQDSLGSKVKDTF
			T T T T T T T T T T T T T T T T T T T

SEQ	Predicted	Predicted end	I Amino and account and a second
ID	beginning	nucleotide	Amino acid segment containing signal peptide
No:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
"""	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	scquence	Codon, /=possible nucleotide deletion,
	sequence	boquence	\=possible nucleotide insertion)
	- Dequence		NGNLPFLFKVLSVETPLSIQAHPNKELAEKLHLQAPQHYPDANH
ĺ			
1	Ĭ		KPEMAIALTPFQGLCGFRPVEEIVTFLKKVPEFQFLIGDEAATH
1	1		LKQTMSHDSQAVASSLQSCFSHLMKSEKKVVVEQLNLLVKRISQ
1		[QAAAGNNMEDIFGELLLQLHQQYPGDIGCFAIYFLNLLTLKPGE
ł			AMFLEANVPHAYLKGDCVECMACSDNTVRAGLTPKFIDVPTLCE
1			MLSYTPSSSKDRLFLPTRSQEDPYLSIYDPPVPDFTIMKA\EVP
ł		į	G\SVTEYKDLALDSASILLMVQGTVIASTPTTQTPIPLQRGGVL
6102	70		FIGANESVSLKLTEPKDLLIFRACCLL
0102	/ / /	2415	QTPQATLAANGAEDSRGGEMLPAGEIGASPAAPCCSESGDERKN
			LEEKSDINVTVLIGSKQVSEGTDNGDLPSYVSAFIEKEVGNDLK
			SLKKLDKLIEQRTVSKMQLEEQVLTISSEIPKRIRSALKNAEES
i	i		KQFLNQFLEQETHLFSAINSHLLTAQPWMDDLGTMISQIEEIER
1			HLAYLKWISQIEELSDNIQQYLMTNNVPEAASTLVSMAELDIKL
	,		QESSCTHLLGFMRATVKFWHKILKDKLTSDFEEILAQLHWPFIA
			PPQSQTVGLSRPASAPEIYSYLETLFCQLLKLQTSHELLTEPK\
1	1		HSQKNTLFLPPLLSS/WPIQVMLTPLQKRFRYHFRGNRQTNVLS
1	1		KPEWYLAQVLMWIGNHTEFLDEKIQPILDKVGSLVNARLEFSRG
1	ì		LMMLVLEKLATDIPCLLYDDNLFCHLVDEVLLFERELHSVHGYP
1			GTFASCMHILSEETCFQRWLTVERKFALQKMDSMLSSEAAWVSQ
1			YKDITDVDEMKVPDCAETFMTLLLVITDRYKNLPTASRKLQFLE
i	(LQKDLVDDFRIRLTQVMKEETRASLGFRYCAILNAVNYISTVLA
}			DWADNVFFLQLQQAALEVFAENNTLSKLQLGQLASMESSVFDDM
l			INLLERLKHDMLTRQVDHVFREVKDAAKLYKKERWLSLPSQSEQ
]		AVMSLSSSACPLLLTLRDHLLQLEQQLCFSLFKIFWQMLVEKLD
1	·		VYIYQEIILANHFNEGGAAQLQFDMTRNLFPLFSHYCKRPENYF
L			KHIKEACIVLNLNVGSALTAGKDVLPVQLQGSFPAT
6103	207	2523	ESNSTMTTYLEFIQQNEERDGVRFSWNVWPSSRLEATRMVVPVA
1			ALFTPLKERPDLPPIQYEPVLCSRTTCRAVLNPLCQVDYRAKLW
1	[ACNFCYQRNQFPPSYAGISELNQPAELLPQFSSIEYVVLRGPQM
1	i		PLIFLYVVDTCMEDEDLQALKESMQMSLSLLPPTALVGLITFGR
			MVQVHELGCEGISKSYVFRGTKDLSAKQLQEMLGLSKVPVTQAT
			RGPQVQQPPPSNRFLQPVQKIDMNLTDLLGELQRDPWPVPQGKR
	ŀ		PLRSSGVALSIAVGLLECTFPNTGARIMMFIGGPATQGPGMVVG
1			DELKTPIRSWHDIDKDNAKYVKKGTKHFEALANRAATTGHVIDI
1			YACALDQTGLLEMKCCPNLTGGYMVMGDSFNTSLFKQTFQRVFT
1			KDMHGQFKMGFGGTLEIKTPR\EIKISGAIGPCVSLNSKGPCVS
			ENEIGTGGTCQWKICGLSPTTTLAIYFEVVNQHNAPIPQGG\RG
			A\IQFVTQY\QHSSGQRRIRVTTIARN\WADAQTQIQNIAASFD
[[QEAAAILMARLAIYRAETEEGPDVLRNLDRQLIRLCQKFGEYHK
1			DDPSSFRFSETFSLYPQFMFHLRRSSFLQVFNNSPDESSYYRHH
}			FMRQDLTQSLIMIQPILYAYSFSGPPEPVLLDSSSILADRILLM
	- 1		DTFFQILIYHGETIAQWRKSGYQDMPEYENFRHLLQAPVDDAQE
}			ILHSRFPMPRYIDTEHGGSQARFLLSKVNPSQTHNNMYAWGQES
6104	104		GAPILTDDVSLQVFMDHLKKLAVSSAA
0104	124	732	KVSEYIILSKDKILFHALAMLVLVVSPWSAARGVLRNYWERLLR
	!		KLPQSRPGFPSPPWGPALAVQ\AQPCLQSQQMIPVEVKRI/RSL
j j			LDSIFWMAAPKNRRTIEVNRCRRRNPQKLIKVKNNIDVCPECGH
<u> </u>	·	ĺ	LKQKHVLCAYCYEKVCKETAEIRRQIGKQEGGPFKAPTIETVVL
			YTGETPSEQDQGKRIIERDRKRPSWFTQN
6105	3	989	PLHGACTSLVLQRFCHRRPRPCAPARPEDMRRPAAVPLLLLCF
			GSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHF
, ,	,	}	CGGSLIAEQWVLTAAHCPRNTSETSLYQVLLGARQLVQPGPHAM
, ,			YARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVCLPD
1	İ		PSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDT\PR
			CNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSAGPLV
L			CLVGQSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1 10.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence	sequence	\=possible nucleotide insertion)
			LOVOPSEVGRPEVTPPGPGAP
6106	3	1302	GRPPTAPHTGRPPTANRGDPRLDLKRGCARLLTSIESRGRPAAS
0.00		1302	AGLRRDRCALRRWPLRRAPLARATRRAGSPRRCAPRPRACPOG
1		·	MSRARHQPGGLCLLLLLLCQFMEDRSAQAGNCWLRQAKNGRCQV
			LYKTELSKEECCSTGRLSTSWTEEDVNDNTLFKWMIFNGGAPNC
J	ļ		IPCKETCENVDCGPGKKCRMNKKNKPRCVCAPDCSNITWKGPVC
			GLDGKTYRNECALLKARCKEOPELEVOYOGRCKKTCRDVFCPGS
	•		STCV\VDQTNNAYCVTCNRICPEPASSEQYLCGNDGVTYS\SAC
1	İ		HLRKATCLLGRSIGLAYEGKCIKAKSCEDIQCTGGKKCLWDFKV
i			GRGRCSLCDELCPDSKSDEPVCASDNATYASECAMKEAACSSGV
6107	623	168	LLEVKHSGSCNSISEDTEEEEEDEDQDYSFPISSILEW
1 520,	023	700	SRCSSPRPEPGRGRGK/LSPSEHRKWVEVFKACDEDHKGYLSRE DFKTAVVMLFGYKPSKIEVDSVMSSINPNTSGILLEGFLNIVRK
	ł		KKEAQRYRNEVRHIFTAFDTYYRGFLTLEDFKKAFRQVAPKLPE
			RTVLEVFREV\DRDS\DGHVSF
6108	3	1348	GGSLRFSPPRVPSCSRVFCPVPPGGCGLPSPMSASRPQSPTTPW
0200		1340	CLPRRYMKHKRDDGPEKQEDEAVDVTPVMTCVFVVMCCSMLVLL
			YYFYDLLVYVVIGIFCLASATGLYSCLAPCVRRLP\SASAGESA
			LLAPTIPHNSLPYFHKRPQARMLLLALFCVAVSVVWGVFRNEDQ
1		ı	WAWVLQDALGIAFCLYMLKTIRLPTFKACTLLLLVLFLYDIFFV
Ì			FITPFLTKSGSSIMVEVATGPSDSATREKLPMVLKVPRLNSSPL
	ĺ		ALCDRPFSLLGFGDILVPGLLVAYCHRFDIQVQSSRVYFVACTI
1			AYGVGLLVTFVALALMORGOPALLYLVPCTLVTSCAVALWRREL
			GVFWTGSGFAKVLPPSPWAPAPADGPQPPKDSATPLSFOPPSEE
		i	PATSPWPAEQSPKSRTSEEMGAGAPMREPGSPAESEGRDQAQPS
1			PVTQPGASA
6109	1	1381	CRSRAGAASGGAILEGTKLRRQRVDTNKPLDPLVPSALRAAMLY
1			LEDYLEMIEQLPMDLRDRFTEMREMDLQVQNAMDQLEQRVSEFF
ļ			MNAKKNKPEWREEQMASIKKDYYKALEDADEKVQLANQIYDLVD
1			RHLRKLDQBLAKFKMELBADNAGITEILERRSLELDTPSQPVNN
İ			HHAHSHTPVEKRKYNPTSHHTTTDHIPEKKFKSEALLSTLTSDA
			SKENTLGCRNNNSTASSNNAYNVNSSQPLGSYNIGSLSSGTGAG
}			GI\TMAAAQAVQATAQMKEGRRTSSLKASYEAFKNNDFQLGKEF
1 1			SMARETVGYSSSSALMTTLTQNASSSAADSRSGRKSKNNNKSSS
1			QQSSSSSSSSSSSSSSSSSTVVQEISQQTTVVPESDSNSQVDWT
			YDPNBPRYCICNQVSYGEMVGCDTQDCPIEWFHYGCVGLTEAPK
			GKWYCPQCT\AANKRRGSRHK
6110	77	2464	ACPSAATMSDQDHSMDEMTAVVKIEKGVGGNNGGNGNGGGAFSQ
1	ļ		ARSSTGSSSTGGGGGESQPSPLALLAATCSRIESPNENSNNS
]	ĺ		QGPSQSGGTGELDLTATQLSQGANGWQIISSSSGATPTSKEQSG
			SSTNGSNGSESSKNRTVSGGQYVVAAAPNLQNQQVLTGLPGVMP
1			NIQYQVIPQFQTVDGQQLQFAATGAQVQQDGSGQIQIIPGANQQ
[i	Ì		IITNRGSGGNIIAAMPNLLQQAVPLQGLANNVLSGQTQYVTNVP
			VALNGNITLLPVNSVSAATLTPSSQAVTISSSGSQESGSQPVTS
1			GTTISSASLVSSQASSSSFFTNANSYSTTTTTSNMGIMNFTTSG
1			SSGTNSQGQTPQRVSGLQGSDALNIQQNQTSGGSLQAGQQKEGE
1			Q\NQQTQAAPKSI.SRPQLVQGG\QALQ\AFQAAPLSGQTFTTQA
			ISQETLQNLQLQAVPNSGPIIIRTPTVGPNGQVSWQTLQLQNLQ
,			VQNPQAQTITLAPMQGVSLGQTSSSNTTLTPIASAASIPAGTVT
Į l		,	VNAAQLSSMPGLQTINLSALGTSGIQVHPIQGLPLAIANAPGDH
			GAQLGLHGAGGDGIHDDTAGGEEGENSPDAQPQAGRRTRREACT
			CPYCKDSEGRGSGDPGKKKQHICHIQGCGKVYGKTSHLRAHLRW
] }			HTGERPFMCTWSYCGKRFTRSDELQRHKRTHTGEKKFACPECPK
1 1			RFMRSDHLSKHIKTHQNKKGGPGVALSVGTLPLDSGAGSEGSGT
] }	1		ATPSALITTNMVAMEAICPEGIARLANSGINVKEGGQFCSPINT
<u></u>			SANGF

SEQ Predicted Predicted end Amino acid segment containing sign nucleotide (A=Alanine, C=Cysteine, D=Asparting nucleotide location Glutamic Acid, F=Phenylalanine, G=Cysteine, C=Cysteine, D=Asparting H=Histidine, I=Isoleucine, K=Lysing NO:	.c Acid, E=
NO: nucleotide location Glutamic Acid, F=Phenylalanine, G	.c Actu, B=
didding notal interpretation, o	
Collesponding msmistidine. isisoleucine. kshvsi	
corresponding to first L=Leucine, M=Methionine, N=Aspara	
to first amino acid P=Proline, Q=Glutamine, R=Arginin	ie,
amino acid residue of S=Serire, T=Threonine, V=Valine,	
residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unkno	wn, *=Stop
amino acid sequence Codon, /=possible nucleotide dele	tion,
sequence \=possible nucleotide insertion)	,
6111 1637 797 RVDPRVRGAMAPWGKRLAGVRGVLLDISGVLYD	SGAGGGTATAG
SVEAVARLKRSRLKVRFCTNESQKSRAELVGQL	
VTAPAPAACQILKERGLRPYLLIHDGV\ASEFD	
VVIADAGESFSYONMNNAFOVLMELEKPVLISL	
LMLDVGPYMKALEYACGIKAEVGGKPSPEFFKS	
AVMIGDDIVGDVGGAQRCGMRALQVRTGKFRPS	DEHMPEVKADG
YVDNLAEAVDLLLQHADK	
6112 77 196 MSSHKSFKSKRFLAKKQKPNRPILQWIWLKTGN	
6113 1779 567 WEGRSWAACGVNLQGAWGERSGVRASEAESPGK	
ETMVDHLANTEINSQRIAAVESCFGASGQPLAL	PGRVLLGEGVL
TKECRKKAKPRIFFLFNDILVYGSIVLNKRKYR	SOHIIPLEEVT
LELLPETLQAKNRWMIKTAKKSFVVSAASATER	OEWISHIEECV
RRQLRATGRPA\STEHAAPWIPDKATDICMRCT	
HCRKCRVVVCAECSRQRFLLPRLSPKPVRVCSL	
EEABEQGAGVPRAASHLARPICGRPVEMTMTPT	
PAAWSSTPRGWPGLPSTADPRPAEHLSPSOLHC	
PGLRDPIPWWQVQRWGVALSGLPVPFCWTLCPY	GFTAGNAFPFR
KPQNTHRSW	
6114 818 246 PTSRPRPSPGSPAMSWSACVSAAPSSSWPASSS	
RRRCSPRCGLAAGSMCSCSPSWRCTPVPACWPS:	
GHLPPHADRRALRLPVAAPARGPGPGHPAGPAG	PRPARTPPASP
HGPGRPTVPAPPCPLLAATEPTPSRPHQRWTRB	DRMLGRGSQVT
GRPQWFLRGLVLFSL	
6115 324 71 DVCGRVCAHPHLYTHIHMHICAHAC\IHTHAQL	C/ITASHALAH
SHLYTCMVMLTASHTPSHTHPHTAVHKEHRADVI	
6116 595 1430 TGVMPPGRWHAA/ISSSGPVFEGARA\LQTVKKI	
AARPQTLNRPGQELFRQLFRQLRYHESSGPLETI	
LRPDVLSKAQILELLVLEQFLSILPGELRVWVQI	
WPCWRSCRGTLMGHPGGTRALP\EPRCALDGYRS	
ASPLRSSSALGDHLEPPYETEARDFLAGQSDTPA	
GCPGDQVTPTRSLTAQLQETMTFKDVEVTFSQDF	EWGWLDSAQRN
LYRDVMLENYRNMASLGK	
6117 1433 222 VGVPSPAPPCSWEVGPGGGWTPGILKEGQGGRRY	
GLLSLFPPAAMHPAAFPLPVVVAAVLWGAAPTRO	
SMDFADLPALFGATLSQEGLQGFLVEAHPDNACS	
NGSVFIALLRRFDCNFDLKVLNAQKAGYGAAVVF	
VWNSEEIQQQIWIPSVFIGERSSEYLRALFVYER	KGARVLLVPDN
TFPLGYYLIPFTGIVGLLVLAMGAVMIARCIQHF	RELORNRETE
\EQLKQI\PTHDYQKGDQYDVCAICLDEYEDGDK	
HSRCVDPWLTQTRKTCPICKQPVHRGPGDEDQEE	
GEPROHPASERTPLLGSSPTLPTSFGSLAPAPLV	
SPPSSPVILV	
6118 1044 247 STISCRACTSGATPGAQSHRSARGHAAGGKETAA	TCMEDCETTE
KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEK	
EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTI	
NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQ	
DSQMEFLBIGGSKPFRSYWEMYLSN/ADSLARSF	
ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAY	HITDIHEALA
II	
6119 1217 462 DPRFVTENTTKAPAGERTTGPRSSREGTLRSTME	YLSALNPSDL
LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRT	ſ
QELLAKALETLLLNGVLTLVLEEDGTAVDSRDFF	i i
VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARF	
DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRE	LUKWISTLLQ
GLGHMLLGISSTLRHAVEGAEQWQQKGRLHSY	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence	1 *	\=possible nucleotide insertion)
6120	785	179	LERAGGGGLSSRALVGSGACLSLVARANGKGLPRGRKEFVEAVR
1	1	j	VRYVAFRYRTPRAVCLRLWSCRREVIMSGRGKQGGKVRAKAKSR
1			SSRAGLOFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAE
į		1	ILELAGNAARDNKKTRIIFRHLQLAIRNDEELNKLLGKVTIAQG
			G\VLPNIQAVLLPKKTESQKDEGANDP
6121	1612	107	FVRAOARGSROPVRRPLLGAGSRLRCRSCGRMEPLKVEKFATAN
}]	RGNGLRAVTPLRPGELLFRSDPLAYTVCKGSRGVVCDRCLLGKE
			KLMRCSQCRVAKYCSAKCQKKAWPDHKRECKCLKSCKPRYPPDS
			VRLLGRVVFKLMDGAPSESEKLYSFYDLESNINKLTEDKKEGLR
		Ì	QLVMTFQHFMREEIQDASQLPPAFDLFEAFAKVICNSFTICNAE
1			MQEVGVGLYPSISLLNHSCDPNCSIVFNGPHLLLRAVRDIEVGE
1	[ELTICYLDMLMTSEERRKQLRDQYCFECD\CFRCQTQDKDADML
1		l	TGDEQVWKEVQESLKKIEELKAHWKWEQVLAMCQAIISSNSERL
		1	PDINIYQLKVLDCAMDACINLGLLEEALFYGTRTMEPYRIFFPG
1]		SHPVRGVQVMKVGKLQLHQGMFPQAMKNLRLAFDIMRVTHGREH
1			SLIEDLILLE/AMRRQHQSILRERSQREIRRVSLLNALLRSHT
1	i		LCFVSCVNLSYWKFCSVFV
6122	2	2324	RFRKMADGGAASQDESSAAAAAAADSRMNNPSETSKPSMESGDG
-			NTGTQTNGLDFQKQPVPVGGAISTAQAQAFLGHLHQVQLAGTSL
1	1		QAAAQSLNVQSKSNEESGDSQQPSQPSQQPSVQAAIPQTQLMLA
1	ļ		GGQITGLTLTPAQQQLLLQQAQAQAQLLAAAVQQHSASQQHSAA
1	1		GATISASAATPMTQIPLSQPIQIAQDLQQLQQLQQQNLNLQQFV
	İ		LVHPTTNLQPA\QFIISQTPQGQQGLLQA\QNLLTQLPRQSQAN
		Ì	LLQSQPRI\TLTSQPATPTCTIAATPIQTLPQSQSTPKRIDTPS
			LEEP\SDLEELEQFAKTFKQRRIKLGFT\QGDAGLAMVKLYGND
į.			FSPTTIFRFRALNLSFKNMCKLKPLLEKWLNDAENLSSDSSLSS
ł	1	1	PSALNSPGIEGLSRRRKKRTSIEA\NIRVALEKSFLEN\QKPTS
	ļ	į	EEITMIADQLNMEKGVIRVWFCNRRQKEKRINPPSSGG\TSSSP
	•	i	IKAIFPSPTSLVATTPSLVTSSAATTLTVSPVLPLTSAAVTNLS
			VTGTSDTTSNNTATVISTAPPASSAVTSPSLSPSPSASASTSEA
			SSASETSTTQTTSTPLSSPLGTSQVMVTASGLQTA/AQLLPFKG
1	Ī		AAQLPANASLAAMAAAAGLNPSLMAPSQFAAGGALLSLNPGTLS
			GALSPALMSNSTLATIQALASGGSLPITSLDATGNLVFANAGGA PNIVTAPLFLNPONLSLLTSNPVSLVSAAAASAGNSAPVASLHA
	ļ		TSTSAESIQNSLFTVASASGAASTTTTASKAQ
6123	3	2944	HLLHRWFGTDMOMINFTTGEFQLTEACPYLGTHSEESRFGILHL
0123	3	6344	HLQPLEMKRVGVVFTPADYGKVTSLILIRNNLTVIDMIGVEGFG
[1		ARELLKYGGRLPGAGGSLRFKYPESTLMDCRRQLKDSKQILSIT
i .		ĺ	KNFKVENIGPLPITVSSLKINGYNCQGYGFEVLDCHQFSLDPNT
1		l	SRDISIVFTPDFTSSWVIRDLSLVTAADLEFRFTLNVTLPHHLL
			PLCADVVPGPSWEESFWRLTVFFVSLSLLGVILIAFQQAQYILM
]	EFMKTRORONASSSSOONNGPMDVISPHSYKSNCKNFLDTYGPS
1		1	DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK
	İ		HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI
			SLRYASGINVNLOKNLTLPKNLLNKEENTLKNTIVFSNPSSECS
			MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL
1		ļ	PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK
1	1		PSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKKLQEKREGNL
1			QNLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS
1			SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK
1	ł		KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKKPM
1			VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTGNSLPQY
1			AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE
1			NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLELNDYNAFP
1			EENMNYANGFPCPADVQTDFIDHNSQSTWNTPP\NMPAS\WGNA
1			QFPSSSRPYLKSTPKACLPMSGLFGPI\WAP\QSDVYENCCPIN
	L		E Company of the Comp

SEQ Predicted predicted end nucleotide (A-Alanine, C=Cysteine, D=Aspartic Aci (A-Alanine acid, F=Phenylalanine, G=Glyc (Blutamic Acid, F=Fhenylalanine, G=Glyc (Blutamic Acid, F=Fhenylalanine, G=Glyc (Blutamic Acid, F=Fhenylalanine, G=Glyc (Blutamic Acid, F=Fhenylalanine, G=Glyc (Blutamic Acid, F=Fhenylalanine, G=Glyc (Blutamic Acid, F=Fhenylalanine, G=Glyc (Blutamic Acid, F=Fhenylalanine, G=Glyc (Blutamic Acid, F=Fhenylalanine, G=Glyc (Blutamic Acid, F=Fhenylalanine, G=Glyc (Blutam	d, E= ine, =Stop WTTT\A TVRVRL LSLADK LHTPRF KLVKTG SLLQKV
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence sequence code sequence co	=Stop WTTT\A TVRVRL LSLADK IHTPRF KLVKTG SLLQKV
location corresponding to first amino acid residue of amino acid sequence 6124 1573 corresponding to first amino acid residue of amino acid sequence Corresponding to first amino acid residue of amino acid sequence Codon, /=possible nucleotide deletion, \text{	=Stop WTTT\A TVRVRL LSLADK LHTPRF KLVKTG SLLQKV
corresponding to first amino acid residue of amino acid residue of amino acid sequence codon, /=possible nucleotide deletion, \=possible nucleotide insertion) 6124 1573 236 SEALRLAGERGMGRVQLFEISLSHGRVVYSPGEPLAG GAPLPFRAIRVTCIGSCGVSNKANDTAWVVEEGYFNSS	=Stop WTTT\A TVRVRL LSLADK LHTPRF KLVKTG SLLQKV
to first amino acid residue of residue of amino acid residue of amino acid sequence Terproline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, K=Unknown, * Codon, /=possible nucleotide deletion, -possible nucleotide insertion) PTTEHSD/THMENQA\VVCKEYYPGF\NPFRAYMNLDI NRNANFPLSRDSSYCGNV SDEALRLAGERGMGRVQLFEISLSHGRVVYSPGEPLAG GAPLPFRAIRVTCIGSCGVSNKANDTAWVVEEGYFNSS	=Stop WTTT\A TVRVRL LSLADK LHTPRF KLVKTG SLLQKV
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, K=Unknown, * Codon, /=possible nucleotide deletion, \	WTTT\A TVRVRL LSLADK IHTPRF KLVKTG SLLQKV
residue of amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide insertion) PTTEHSD/THMENQA\VVCKEYYPGF\NPFRAYMNLDI NRNANFPLSRDSSYCGNV 6124 1573 236 SDEALRLAGERGMGRVQLFEISLSHGRVVYSPGEPLAG GAPLPFRAIRVTCIGSCGVSNKANDTAWVVEEGYFNSS	WTTT\A TVRVRL LSLADK IHTPRF KLVKTG SLLQKV
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SVVLTASTDLRGYVVGQALQLHADVENQSGKDTSPVVA	LPQSAL
SYKAKRWIHDVRTIAEVEGAGVKAWRRAQWHEQILVPA	
PGCSLIHIDYYLQVSLKAPEATVTLPVFIGNIAV/NPC	PSEPPA
RPGAASWGPTPGG\PSAPPQEEAEARAAGGPHFLDPV	FLSTKS
. HSQRQPLLATLSSVPGAPEPCPQDGSPASHPLHPPLCI.	STGATV
PYFAEGSGGPVPTTSTLILPPEYSSWGYPYEAPPSYEQ	SCGGVE
PSLTPES	
6125 1 904 KTCPKLTCAFTVSVPDSCCRVCRGDGELSNEHSDGDIF	ROPANR
EARHSYHRSHYDPPPSRQAGGLSRFFGARSHRGALMDS:	QQASGT
IVQIVINNKHKHGQVCVSNGKTYSHGESWHPNLRAFGI	
TCNVTKQECKKIHCPNRYPCKYPQKIDGKCCKVCPG/KI	
PGQSFDNKGYFCGEETMPVYESVFMEDGETTRKIALET	
EVHVWTIRKGILQHFHIEKISKRMFEELPHFKLVTRTT	
PTEGEAQISQMCSSRVCRTELEDLVKVLYLERSEKGHC	
6126 1224 389 RLLSEAPCPRSRRFQMNPEWGQAFVHVAVAGGLCAVA	
DSVSVQVGYEHYAEAPVAGLPAFLAMPKNSLVNMAYTLI	
HRGGAMGLGPRYLKDVFAAMALLYGPVQWLRLWTQWRR	
WLTLPIFAWPVAWCLYLDRGWRP\WLFLSLECVSLASY(
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6127 1335 463 VLPRRCLVFVVNTMDSSREPTLGRLDAAGFWQVWQRFDI IEEKELDAFFLHMLMKLGTDDTVMKANLHKVKQQFMTTQ	
GRIRMKELAGMFLSEDENFLLLFRRENPLDSSVEFMQI	
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NKDGRLDLNDLARILALQENFLLQFKMDACSTEKRKGDI	
YYDVSKTGALEGP\EVDGFVKDMMELVQPSISGVDLDKI	
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GGAARPEKTABEGPPAAPGSLRHSGPLGPHACPTALPER	
MSSQVVGIEPLYIKAEPASPDSPKGSSETETEPPVALAE	
TRCLPGHKEEEDGEGAGPGEQGGKLVLSSLPKRLCLVC	CODVAS
GYHYGVASCEACKAFFKRTIQGSIEYSCPASNECEITK	RRKAC
QACRFTKCLRVGMLKEGVRLDRVRGGRQKYKRRFEVDPI	
FPAGPLAVAGGPRKTAAPVNALVSHLLVVEPEKLYAMPD	
GHLPAVATLCDLFDREIVVTISWAKSIPGFSSLSLSDQM	
VWMEVLVLGVAQRSLTLQDELAFAEYLVLDEEGARPAGI	
AALLQLVRRLQALRLEREEYVLLKALALANSDSVHIEDE	PRLWS
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KVLAHFYGVKLEGKVPMHKLFLEMLEAMMD	Ì
6129 1764 771 ARFARSAHEGKMPKKKTGARKKAENRREREKQLRASRST	IDLAK
HPCNASMECDKCQRRQKNRAFCYFCNSVQKLPICAQCGK	
KSSDCVIKHAGVYSTGLAMVGAICDFCEAWVCHGRKCLS	
CPLTDAEC\VECERGVWDHGGRIFSCSFCHNFLCEDDQF	
CQVLEAETFKCVSCNRLGQHSCLRCKACFCDDHTRSKVF	
KQPPCPKCGHETQETKDLSMSTRSLKFGRQTGGEEGDGA	
YWKNLSSDKYGDTSYHDEBEDBYEAEDDEEEEDBGRKDS	DTESS
DLFTNLNLGRTYASGYAHYEEQEN	
6130 3 577 GRGGTMREYKVVVLGSG\GVGKSALTV\QFVTCTF1EKY	DPTIE

Deginning nucleotide location corresponding cofirst amino acid amino	SEQ	Predicted	Predicted end	Dring agid gormonh
No. nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence	1 -			Amino acid segment containing signal peptide
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corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence acid sequence acid			1	Giutamic Acid, F=Phenylalanine, G=Glycine,
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SAYVPSALCCUSRASILTGKYPHHHWUNTLEGNCSSKWGKI QENTFPA ILRSMCGUTFY AGKYLMFYDAGGGLEHPIGW SYWALEKNSKYYNYTLSINGKARKHGENYSVULTULANUSI DPLDYKSNYER PPRMTATU APHSPWTAAPQYOKAFONVFAPEN KNFNIHGTKKHLIROAKTPMTNSSIOFLDNAFEKRROTLLEVO DLUSKLVKRLEFTGELMTYT FYTSDNGHAFKRGESPIDTAGLY BFDIKVPLLVRGPGIKPNOTSKMLVANIDLOFTILDIAGYDINK TOMDGMSLLPILRGASNITWRSDVULFYGGSGNYUTPTCPSLS PGVSQCFPCVCEDATMNYACVENSALMMLGYCGFDDGEVFV EVYRLTADPDGITNIAKTIDEELIGKMNYRMMLGSGSPTTCT FGVPDGYSKPPPELMFSNGSVFRRFSKHLLLAFGGSGPTTCT FGVPDGYSKPPPELMFSNGSVFRRFSKHLLLAFGGESGPTCTC FGVPDGYSKPPPELMFSNGSVFRRFSKHLLLAFGGESGPTCTC FGVPDGYSKPPPELMFSNGSVFRRFSKHLLAFGGESGPTCTC FGVPDGYSKPPPELMFSNGSVFRRFSKHLLAFGGESGPTCTC FGVPDGYSKPPPELMFSNGSVFRRFSKHLLAFGGESGPTCTC FGVPDGYSKPPPELMFSNGSVFRRFSKHLLAFGGESGPTCTC FGVPDGYSKPPPELMFSNGSVFRRFSKHLLAFGGESGPTCTC FGVPDGYSKPPPELMFSNGSVFRRFSKHLLAFGGESGPTFCTC FGVPDGYSKPPPELMFSNGSVFRRFSKGSKKKVLPFTSKKD PKFELQKBAVTMBUNATLLEFHLVVSLEEBMFDGLILHHL FGRIAALKLEEDIALTAGKKLLTVUSLEGGKKKVLPFTSKKD PKFELGKBAVTMFVNGKLDRIGGLEVONLDTOPADCUTLLLIGGLEGFP LHLEFYLLFPSSPAELHBAVTALELL/IGGRBQLDFLJKLABEKVNA VKRAIVNFVNGKLDRIGGLEVONLDTOPADCUTLLLIGGLEGFP LHLEFYLLFPSSPAELHBAVTALELL/IGGRBQLDFLJKLABEKVNA VKRAIVNFVNGKLDRIGGLEVONLDTOPADCUTLLILIGGLEGFP LHLEFYLLFPSSPAELHBAVTALELL/IGGRBQLDFLJKLABEKVNA VKRAIVNFVNGKLDRIGGLEVONLDTOPADCUTLLILIGGLEGFP LHLEFYLLFPSSPAELHBAVTALELL/IGGRBQCPFLAKKNA VKRAIVNFVNGKLDRIGGLEVONLDTOPADCUTLLILIGGLEGFP LHLEFYLLFPSSPAELHBAVTALELL/IGGRBQCPFLAKKNA VKRAIVNFVNGKLDRIGGLEFTUGGPPVVNNCPSDRSTK KTLVTLIANNAGNEPLVQGGGGLILTONPAPGIGFMTVQFVLR PVOVMONANHVTSPVBGPFFTTGGFPFPVNGCGOTKSTPSTTTT TAGOPTSIGGLAVOSBGGSNGTTNFRLAPSFPSPANAPSFFFTTTTT TAGOPTSIGGLAVOSBGGSNGTTNFRLAPSFPSPANAPSFFTTTTT TAGOPTSIGGLAVOSBGGSNGTTNFRLAPSFPSPANAPSFFTTTTT TAGOPTSIGGLAVOSBGGSNGTTNFRLAPSFPSPANAPSFFTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT				GVAAGTER PNVVI J. I. TDDODEVI GGMTDI VYTYDI TGTMOMOG
OBENTFPALLSMCGYOTFF\AGKINEYGAPDAGGLEHVPLGW SYWALEKNSKYNNTISINGKARKHGRYSVDYLTUVLANGEL DFLDYKSNFEPFMMTATP\APHSPMTADTQNCKFCNNYAPRIN KNFHIRTNKHLIRDGATFWRINSSIDLBAPRKRRQFLLSVD DLVSKLVKRLEFTGELINTTIFTSDNGYHTGQFSLPIDKRCLY BFDIKVPLLVRGGGIKPROTSKHLVANITDLDFTILDIAGYDLINK TQMDGMSLLPILRGASKLTWRDDVLVEGGGRNVTDPCTCSLE PGVSQCFPDCVCEDAYNNTYACVRTMSALMNLQYCFDDQEVPL VYNALTADPDQITHAIATIDFELLGKMYLMMLGQSGPTCRT PGVPDGYSFPDPLMFSNRGSVBTRRPSKHLL AGGLDPGLVPEDDRFTRNLIPPGTGGGRNVTDPTCSELS PGVSQCFPDCVCEDAYNNTYACVRTMSALMNLCYCFDDQEVPL VYNALTADPDQITHAIATIDFELLGKMYLMPTGSKGSGPTCRT PGVPDGYSFPDPLMFSNRGSVBTRRPSKHLL AGGLDPGLVPEDDRFTRNLIPPGTGGFPALSRPLFSGVSSGA WEARMEPELYDLLQLPKGVEPPAEEELSKGGKKKYLPPTSRKD KFFELGKALVLMERMINATLADELLYSLEEDMPPGLUHHL FORLAALKLEABDIALTATSQKHKLTVULEAVRRS\CSMRGRP SGA/WSSIPNKDLLSTHLVALAKRFOPDLSPILHPL FORLAALKLEABDIALTATSQKHKLTVULEAVRRS\CSMRGRP SGA/WSSIPNKDLLSTHLWALAKRFOPDLSPINVQVBVITI ESTKSGLKSEKLVKDLTEYSTRKEEPPFQUFDSLYHRLV VKRALVNEWNGCDRELGLSVQHKDTQFADGVILLLIGGLEGFF FORGSMADTDLFMSCESELEPPWQRSDVLEFNAPNA VKRALVNEWNGCDRELGLSVQHDTQFADGVILLLIGGLEGFF FORGSMADTDLFMSCESELEPPWQRSSQVETSTSTVDTATVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSGAONDSTK KTLVTLIANNAASPHLVYGLFCKHTGABPANFAPNA FTUNTOVSQQPVSAPVPIAAHASVAGHLSTSTTVSSGAONDSTK KTLVTLIANNAASPHLVYGGGGGPLILONPAPGLGTMVTOVYLK PVOVMONANHTYSSPVSAGPIFTTOGFPVRNVRPVQNAMNQVG IVLNVOQGGTVRPITLVPAGTGTVKFTVVPVSTSGATPVPRG STMPVRPTNTFTTVIPALTITRSTPVQSSGOGTKSTPSTTFT TATQPTSLGGLAVQSRGOSNQTTKPKLAPSFPPAVSIASFYT VKRFGVTVEGNSNEVAKLVNTLNTTFSLGGSPGPVVVSNNSAM\ GSGRTSGPESSMKVTSSIPVPLQDGGGKLCPRCAAGFRVTEAL RGGMCYCCPPAVFVGKKGKSLDSEBPYAANPSPSHEATHAVAS /THPSSTPIPALSPPY/TKVPPRENNGDAVGTKLIMLNDDFYY GROGKVAQCHNPFKAATFFCPHCTKUNTIRFMRMCHHYE LDQONGEVDGHTICGHCYROFSTPPQLOCCLENVERPPESTTYC KICEMAPERSPPLFJAMMKHHYPYNSKSTILATSMPLVFTYTYCSLCRYST CKSRAYANKMSVMGQTCLECSFEIPPPPHFFTYTYCSLCRYST OKONAMAKHLVFRPSHRSSSILPRGLTWIAARSHGYDZVHDR NKNNYYPP SPSFTYNKATHSSACTLARGNGTDRAVHDR NKNNYPP SPSFTYNKATHSSACTLARGSGYSILKACKTGTVTOS SVGDAMAKHLVFRPSHRSSSILPRGALGALAPISAGHLTPLPPAGR YNKNYYPP SPSFTYNKATHANTHYSMCHAHLTPHARRA VANHTLERVARRSONDELSCHTLANGROCHEROUR NVANTERSPROAG	ı			SAVVPSALCCPSPASTITCKYPHATHAAMYT POLYGRANGWITS
SYNVALEKISKYYNYTISIRGKARKIGENYSUDULTDULANUSL DFLDYKANEPEPPHMITAP QAHSPHTAADQYKARGONYAPARN KNPHIHGTNKHULIRQAKTPHTMSSIQFLUNAPRKRYQTLISUD DLUYKLVUKLIEFTGELKINTYI FYTSONYHOGGSILPIDKRQLY BFDIKVPLLVRGPGIKPNQTSKMLVANIDLQPITLDIAGYDLINK TQMDGMSLIP HLRGASNLTWRSDVLVEYQGGGRUVDPTCBLIS BFDIKVPLLVRGPGIKPNQTSKMLVANIDLQPTILDIAGYDLINK TQMDGMSLIP HLRGASNLTWRSDVLVEYQGGRUVDPTCBLIS BFDIKVPLLVRGPGIKPNQTSKMLVANIDLQPTILDIAGYDLINK TQMDGMSLIP HLRGASNLTWRSDVLVEYQGGRUVDPTCBLIS BFDIKVPLLVRGPGIKPNTSALENULGYCEFDDGEVFO EVYNLTADPDQITNIAKTIDPELLGKKMYRLMULGCSGPTCRT BGVPDGVKPFPDRKMFSNGSVETRFSKHLL ARGLEPGGLVPBDFRFTRNLLIPGIQGPPFALSRPLFSCVSSGR AWBENBPEBLIVDLLQLKGVEPPADESKGKKKVLPFTSKL BKFBELQKDA\VMBRINATLLPEHIVVRSLEEDEMFDGLILHHL FQRLAALKLIAEDLATATSGORKKLTVULEBVBRSG\CSWRSGRR SGA\WSSIFNKDLISTHHLUVALAKFSKGKKKVLPFTSKL VRRAINVFNOKLDRIGLSVGNLDTOPADGVILLLLIGGLEGFF LHLKEFYLIPNSPAEMHNVTLAELL/IGGGPADLVC/LALK/ TUNKDAKSTIRVLYGLFCKHTOKAHRRTPHGAPN VRRAINVFNOKLDRIGLSVGNLDTOPADGVILLLLIGGLEGFF LHLKEFYLIPNSPAEMHNVTLAELL/IGGGPADLVC/LALK/ TUNKDAKSTIRVLYGLFCKHTOKAHRRTPHGAPN FVUWMNANHTTSSPVASQPIFITTQGFPVRNVFVDYSOMTVPRG STHVAPTTNTFTTVIFATLTTRSTVPQSGSOTXSTFSTSTTP TANOPTSIGGLAVGSROGONTOTTRFLAFPSPPANSALSPTV VKRPGVTGENSNVAKVISTLNTTESTVPQSGSOTXSTFSTSTTTP TANOPTSIGGLAVGSROGONTOTTRFLKNNIFRMHMENHYE LDQGNGEVDGHTICGGLAVGSROGNOTTRFLKNNIFRMHMENHYE LDQGNGEVDGHTICGCCXRGFSTFPOLOCHLENVHSPFESTTKC KICCHAFFSSFPLFLGFWKNNIFRCHENFRHYAK /THPSSTPIPALSPPJ/TKVPEPRENVGDAVGTKLIMLUDDFYY GROGKVAGULTNFFKVARTSFRCHCIKRNNIFRMHMENHYE LDQGNGEVDGHTICGCCXRGFSTFPOLOCHLENVHSPFESTTKC KICCHAFFSSFPLFLGFWKNNIFRCHENFRHYAK /THPSSTPIPALSPPJ/TKVPERNSNIFRHMENHYEHY CKRCXVQFLFAKKIE BLKQHHTTFFRUNSIFRHMENHYEHY SGOGGSTVPVSSNDTFPSALQBAPLTSSMDPLPVFI/FPVGNS IQKRAVRKMSVMGROTILEGCSFPTPPDFHFFTYVHSLGRVSTI ASGOGGRTVPVSSNDTFPSALQBAPLTSSMDPLPVFI/FPVGNS IQKRAVRKMSVMGROTILEGCSFPTPPDFHFFTYVHSLGRVSTI SGOBMAKHUFFFSHRSSSILPRALGCNTEGOGESPVTOGEG LASGGGGGGGWKKEGLEKLAWUPTGCGOLP VWESTLPQKATKIGSLEGGFVLSTSWAWRFMLHATPARAA VAHTLPKOVAENAGLF IDFORQHINDLPLSMIVADGETSLFL DTBVLSSDDRKENALQTVGTGGDEWCDVULALLABGTULPTLMFY VAHTLPKUARROGGENLEGKYLSVENTALGCTURGOLP	j			OEPNTEPATURSMCGYOTEF\ AGKYLNEYGA DDACGI PURDI OM
DFLDYKSNEEPFFMMTATE\APHSPMTATD\OPYCREGNVPAERN KNPHIHTNIKHLI IROAKTPMTMSSICIDNAFRKRWGTLISVD DLVSKLVKRLEFTGELNNTYIFTSDNGYHTGGPSILP IDKRGLY BFDIKWPLLVRGEGIKNOTISMLUNDLOFFILD IAGYDLMK TOMOGMSLIP ILRGASNLTWRSDVLVEYGGEGNVTDPTCESLS PGVSQCFPDCVCEDAYRNTYACVRTWSALMNLUGYSEDDDEVDL EVINLITADPDGTTNIAKTIDPELLGKMYNYELMHLGSCSSPTCRT PGVFDGVRFDPRLMFSNRGSVWTRRFSKHLU. ARGLUPPGLVPEDDRFTRNLIPFGTGGFPFALSRPLFSCVESGK AWEAMEPELYDLLQLPKGVEPPAEEELSKGGKKKYLPPTSRKD PKFSELGKPALVLHABE WANTALLEELUNSLEEDMMSGLLHHL FORLAALKLEABDIALTATSQKHKLTVVLERVBRS\CSWRSGRP SGAJWESIFNKDLISTIHLUVALAKRYSLEEDMMSGLLHHL FORLAALKLEABDIALTATSQKHKLTVVLERVBRS\CSWRSGRP SGAJWESIFNKDLISTIHLUVALAKRYSLEEDMMSGLLHHL FORLAALKLEABDIALTATSQKHKLTVVLERVBRS\CSWRSGRP SGAJWESIFNKDLISTIHLUVALAKRYSLEEDMMSGLLHHL FORLAALKLEABDIALTATSQKHKLTVVLERVBRS\CSWRSGRP SGAJWESIFNKDLISTIHLUVALAKRYSLEEDMMSGLLHHL FORLAALKLEABDIALTATSQKHKLTVVLERVBRS\CSWRSGRP SGAJWESIFNKDLISTIHLUVALAKRYSLEEDMMSGLHHHL FORLAALKLEABDIALTATSQKHKLTVVLERVBRS\CSWRSGRP SGAJWESIFNKDLISTIHLUVALAKRYSLEEDMMSGLHHHL FORLAALKLEABDIALTATSQKKKLTVVLERVBRS\CSWRSGRP VKFELVYLORGEGPLITORADEVINGVORT THINKDAKSTLRVLYGLFCKHTVALDEVPROPTORVENVOR VKERTULTUNGOGGGPLITORAPROLORITORY FUGGMANDHVTSSPVASGPIFITTOGFPVRNVRPYONAMOVC IVLNVOQGGOFDATTIVAPRGTGPVRPVORYSOMTEVRP PVOVMONANHTVSSPVASGPIFITTOGFPVRNVRPYONAMOVC IVLNVOQGGOFTETTTVPREGSGOOTKSTTSTSTTTP TATQTTSLGGLAVQSRGOSNGTTRPKLAPSFPSPPAVSIASFVT VKREGVTJEGENSEVAKLVANTINTTPSGPSPPAVSIASFVT VKREGVTJEGENSEVAKLVANTINTTPSGPSPPAVSIASFVT VKREGVTJEGENSEVAKLVANTINTTPSGPSPPAVSIASFVT GRGGKVAGUNTPFKAATSFRCHICTKANTSRAMHHHHY GRGGKVAGUNTPFKAATSFRCHICTKANTSRAMHHHY GRGGKVAGUNTPFKAATSFRCHICTKANTSRAMHHHY GRGGKVAGUNTPFKAATSFRCHICTKANTSRAMHHHY LDQOMSEVDGHTICGHCYROFSTPPOLOCICLENVIBPTSTTYC KICCHAPFSPFIFITASSFPIPALSFPIPALSFPPANS /THESSTPIPALSFPIPALSFPIPALSFPIPALSFPPTYVGSLCTFVT SVGDAMAKHUFMPSHRSSSILPRDHPFTTVHCSLCRYST CCSRAYANHINNHVPRSKRSSSILPRDHPFTTVHCSLCRYST CCSRAYANHINNHVPRSKRSSSILPRDHPFTTVHCSLCRYST SVGDAMAKHUFMPSHRSSSSILPRGLATHITSMPLEVFLTYPORS IAKRWERMSVMRGOTCLECSFFIPPPPHFFTTVHCSLCRYST CCSRAYANHINNHVPRSKRSYNIAGAGTHAEHLTPHARA VANHTLER	1			SYWYALEKNSKYYNYTISINGKARKHGENYCUDYLODULANUCI
KNPNIHGTNEHMLIRGAKTPWINSIGFLUNFERKROTILLSVD				DFLDYKSNFEPFFMMTATP\APHSPWTAAPOVOKAFONUPARDN
DLVSKJVKRLEFTGELINTTY;TYTSINGYHTGGFSLPIDRKGLY BFDIKVPLLVRGGEGRNVTDKMINDLGPTLIDAGYDLINK TOMDGMSLLPILAGASNITMRSDUJVSYQGEGRNVTDPTCPSLS PGVSQCPPDCVCEDAYNNTYACVRTMSALWNLQYCEFDDGSVFV EVYNLTADPDQITNTAKTIPPELLGKMNYRLMMLQSCGSGPTCRT PGVFDGYRFDPGYRFDPRLMFSNRGSVRTRRFSKILL 6132 96 1241 AAGLIPPGLYPEDFBERTRNLLPFG1QSPPFALSRFLFSCVESGR AWEAMEPEFLYDLLQLPKGVSPPAEEELSKGGKKKYLPTTSRKD PKFEELGKPA\VIMBRINATLLPHVYRSLEEDMFDGILIHHL FQRLAALKLEAEDIALTATSQKHKLTVURSLEEDMFDGILIHHL FQRLAALKLEAEDIALTATSQKHKLTVURSLEEDMFDGILIHHL FQRLAALKLEAEDIALTATSQKHKLTVURSLEEDMFDGILIHHL FQRLAALKLEAEDIALTATSQKHKLTVURSLEEDMFDGILIHHL FQRLAALKLEAEDIALTATSQKHKLTVURSLEEDMFDGILIHHL FQRLAALKLEAEDIALTATSQKHKLTVURSLEEDMFDGILIHHL FQRLAALKLEAEDIALTATSQKHKLTVURSLEEDMFDGILIHHL FQRLAALKLEAEDIALTATSQKHKLTVURSLEEDMFDGILIHHL FQRLAALKLEAEDIALTATSQKHKLTVURSLEEDMFDGILIHHL FQRLAALKLEAEDIALTATSQKHKLTVURSLEEDMFDGILIHHL FQRLAALKLEAEDIALTATSQKHKLTVURSLEEDMFDGILIHHL FQRLAALKLEAEDIALTATSQKHKLTVURSLEEDMFDGILIHHL FQRLAALKLEAEDIALTATSQKHKLTVURSLEEDMFDGILIHHL FQRLAALKLEAEDIALTATSQKHKLTVURSLEEDMFDGILIHHL FQRLAALKLEAEDIALTATSQKHKLTVURSLEEDMFDGILIHHL FQRLAALKLEAEDIALTATSQKHKLTVURSLEEDMFDGILIHHL FQRLAALKLEAEDIALTATSQKHKLTVURSLEEDMFDGILIHHL FQRLAALKLEAEDIALTATSQKHKLTVURSACCH VKRRAIVNFVNORKLORGHERFBHGKURSLEYDTLAAVCHSCHEAE VKRRAIVNFVNORKLORGHERFBHGKURSLEYDTLAAVCHSCHEAE VKRRAIVNFVNORKLORGHERFBHGKURSLEYDTLAACH FURGHAATCH FURGHAATATTURSACHTURSLEHTLATTVSSSGAQNEDSTK KTIVTLIANNANGMBLVQGGGGPLITURDAPGSGAQTKSTPSTSTTT TTVSVSQQPVSAPVPIAAHASVASQGFVLTNANANDSSAALATSCTTVT VKRPGVTGENSHAVENSTAPPTPTLPPAGSGAGGTNEGVTANANNANG FURUMANNANTATURSLEEDHAATSTTTVSSSGAQNENDSTK FRETTTTTVSSTGAANTATTVSSGAGTSTTTVSSCAGANTATTVSTAATTVSSGAGTSTTTVSTSTTTVSSTGAATTVSTAA	1	1		KNFNIHGTNKHWLIRQAKTPMTNSSIOFLDNAFRKRWOTTISUD
BEPIKVPLLYRGPGIKPNOTSKMUANIDLGPTILDIAGYDLINK TOMOSMSLIPILKGASNILTMENDULVSYQGEGRUTUPDTCESLS PGWSQCPPDCVCEDAYNTYACVETMSALMULQYCEPDDQEVFV EVYNLTADPDQITNIAKTIDPELLGKMYKLMLQSCSGPTCRT PGWFDGYRFDPRLMFSNRGSVETRRPSKHLL AAGLLPPGLVPEDPRRTRNLLPFGIQGPPFALSFRLFSCVSSGR AWEMBFEFLYDLLQLPKGVEPPAELSRFLFSCVSSGR PKFEELQKDA,VLMBBINATLLPFHIVVRSLEEDMFDGLILHHL FORLAALKLEAEDIALTATSQKKKLTVULEGAVINGS\CSWBSGRP SGA,WESIFNKDLISTLHLIVALAKRQCPDLSLPTNVQVEVITI ESTKSGLKSEKLVEQLTEYSTDKDEPPKDVFPBLFKLAPEKVNA VKRAIVNFVNQKLDBGLSVQNLDFDAOVILLLIGQLEGFF LHLKEFYLYPNSPARMLHNVTLALELL/TGRGPAGLPC/LALK/ TIVKKDAKSTLRVLYGLFCKHTQKAHRDETPHGAPN 6133 Z 4256 FVHGSMADTDLFMCEEFEBLEPPGKTSDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAHASVAGHLSTSTTVSSSGAONSDSTK KTLVTLIANNNAGNETVQGGGQCHIOPAPGPVFSQMTVPRG PVQVMQNANHVTSSPVASQPPFTTTGGFPVRRVPVQNAMNQVG IVLNVQQGTVRPITLVPAPGTQFVKPTVGVPQVFSQMTVPRG STMPVRPTTNTFTTVIFATLTIRSTTPQSGSQCYKSTFSTSTTFT TATQFTSLGQLAVQSPGQSNQTTNPKLAPSFSPPAVSIASFVT VKRPGTVGFGSNSEVAKLNVTLNTIPSLGQSPGPVVSNONSARI GSGRTSGPESSMKVTSSIPVPDLQDGGRKICPCCNAQFFVTBAL RGMCVCCPEMVEYQKKGKSLDSEPSVPSAKPPSPEKTPAVS /THPSSTPIPALSPPY/TKVPSPNENVGDAVQTIKLINLDDFFY GRBGCKVAQLINFFKVATSFRCHCTKRLKNIFMMHKHHVE LDQONGEVTGHTICHCYCKFVFNCNAPFQQHYMENQKNVTH\ CNKCRVQFLFAKDKIEHKLQHKKTFRFKCDEGLKPGTKVTIFA SRGQPRTYPVSSNDTFPSALQEABLTTSMDPLEVFITTYC CCSRAYANHMINNIVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAHLLYPNSENSSSILPGLACHITANSVSGIKLACTSCTFVT SVGDAMAHLLYPNSENSSSILPGLACHITANSVSGIKLACTSCTFVT SVGDAMAHLLYPNSENSSSILPGLACINTOPQDEGSPTOCPPE LASGGGGGGVKKEGLSVKKUNTLAISRRGQTRDRVHOR NVNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPLPSPS STATPPFPTPTHPQALALPPLATEGBECLINVDDQDEGSPTOCPPE LASGGGGGGGGGGGGKGLSVKKLNYLAGKTGOLPPUPTRIP RIFRWLRRFGASGGENLBGKYLSFEABEKLAERVLTQREQOLP VMETLEFQKATKTGRSELGSVKKLNSTERKLACHTUTTRACOLP RIFRWLRRFGASGGGRNLBGKYLSFEABEKLAERVLTQREQOLD VMETLEFQKATKTGRSELGSVKKLNSTERKLACHTCTTCAAFFIRNPO RRIFRWLRRFGASGGGRNLBGKYLSFEABEKLAERVLTQREQOLD VMETLEFQKATKTGRSELGSVKKLNSTERMLATHTHATRA VAHTLPKOVAENAGLPIDFVQQVVALALLADGTVLDFISIFL DTBVLSSDDRKERBALGTVGTGEPMCDVVALALLADGTVLDFISIFL RGQMDDZDAMMDDSILLELAERGSVSDELMINSMTSMENTSTUFSTLIFT	1			DLVEKLVKRLEFTGELNNTYIFYTSDNGYHTGOFSLPIDKROLY
TOMOGMSLIP ILRGASNITMRSDULVEYGGERGNYTDPTCBSLS PGVSQCPPOCVEGDAYNNYACVASALMICQVCGPDQCEFD4 BVYNLTADPDQTNTAKTIDELLGKMNYRLMMLQSCSGPTCRT PGVPDPGYFPDGYFPDGYFPDGYFPGYFPDGYFPG BVYNLTADPDQTYPTAKFINDELLGKMNYRLMMLQSCSGPTCRT PGVPDPGYFPDPKFRNRSVRTRFFSKTLLFSCVESGM AWEAMEPEFLYDLLQLPKGVYPPABEELSKGGKKKYLPPTSRKD PKFEELGKPA\VIMBUMATLLIPFGJGSPFFALSRELFSCVESGM AWEAMEPEFLYDLLQLPKGVYPPABEELSKGGKKKYLPPTSRKD PKFEELGKPA\VIMBUMATLLIPFGJGSPFFALSRELFSCVESGM AWEAMEPEFLYDLLQLPKGVYPPABEELSKGGKKKYLPPTSRKD PKFEELGKPA\VIMBUMATLATSKKHKLTVVLEAVNRS\CSMRSGRP SGA\WSSINNKOLLSTLHLLVALAKROPDLSIPTNVQVEVITI ESTKSGLKSEKLVEQLTEYSTDKDEPPKDVFDELFKLAPEKVAN VKRALVNFVNQKLDRLGLSVQNLDTGFADGVLLLLLIGQLEGFF LHLKEFYLTPNSPABMLHNVTLALELL/TGGPAGLPC/LALK/ TIVNKDAKSTLRVLVGLFCKHTQKARRDRTPHGAPN VKRALVNFVNGKLDRLGLSVQNLDTGFADVLLLLLIGQLEGFF LHLKEFYLTPNSPABMLHNVTLALELL/TGGPAGLPC/LALK/ TIVNKDAKSTLRVLVGLFCKHTQKARRDRTPHGAPN VKRALVNFVNGKLDRLELL/TGGPAVNSVDKT TTVSVSQQPVSAPVPLAAHASVAGHLSTSTTVSSGAQNDSTK KTLVTLIANNARAGNELVQCGGGGLLITONPAPGLGTMVTQPVLR FVVWMNANHVTSSEVDSQFTTTUGFPVRNVVDVFSGMTPVRPG STMPVSPTTNTFTIVFAPTLISTDGSQCOTKSTPSTSTTP TATOPTSLGOLAVQSPGGSNCTTNPKLAPSFPSPAVSIASPVT VKRGGVTGNSPTTNFTVTVFATLTISTOSGSQCOTKSTPSTSTTP TATOPTSLGOLAVQSPGGSNCTTNPKLAPSFPSPAVSIASPVT VKRGGVTGNSVNTSSIVPTLQDGGGKKICPRCNAQFRVTEAL RGGMCCCCPERVEYQKGKSLDSEBSVPSAARPPSPEKTAPVAS /THESSTIPPLISTPY/TKVPERDNVGDAVQTKLIHLUDDFYY GROGKVAQLINFFKVATSFRCHCTKLIKNIFFMHMKHHYB LDQNGSEVDGHTICCHCYRGFSTPDFNHSPYSTTKC KICEMAFESEPLFLQHMKDTHKPREMDVLOCHLENVHSPYSTTKC KICEMAFESEPLFLQHMKDTHKPREMDVLOCHLENVHSPYSTTKC KICEMAFESEPLFLGHMKDTHKPREMDFLFVTLYPFVGRS IQKRAVRMSVMGGNCTLCSCSFFI IPPSNHSPYTYTLYPFVGRS IQKRAVRMSVMGGNCTLCSCSFFI IPPSNHSPTYTHSLGCRYST CCSRAYAHHMINNIVPRKSPKYLALFKNSVSGIKLACTSCTPVT SVGDAMAKHLVFNPSHRSSILPRGLTWINSHSCRGTTRRVKIDR RIKMYSPPSPFTNKAATVKSAGATPAREPELLTPLAFALPAPSP STATPPFPTPTHQALALPPLATEGRECLNVDDQDGSPTTQEPE LASGGGGGGGVKGGLSVKLKVRYLCCNTFGAAGHFRNPQ RRIKRWERFGAAGGENLBGKKLSFEABEKLABWVLTQREQOLP WESTLEPQKATKIGRSLEGGFKISYEWAVFMLHHHLTPHARRA VAHTLPKOVAENAGLFINFONDUTALILLBEISLFL DIEVLSSDDKKEMALQTVSTGEPGMCUVALALLADGTVLDTLITLFY		ļ .		EFDIKVPLLVRGPGIKPNQTSKMLVANIDLGPTILDIAGYDLNK
PGVSQCFPDCVCEDAYNTYACVETMSALMNLQVCEPDDGEVFV EVINLTADPDGITNIAKTIDPELLKEKMYNYRMMLQSCSGPTCRT PGVPDCGYRPDPLMFSNGSVETRRFSKHLL AGILPPGLVPEDPRTTRNLLFFGTQGFPFLSKFGKKKYLPPTSKK PKFEELQKPA\VLMEWINATLIPEHLVVRSLEEDMFDGILHHL FGRLAALKLEREIDLATATSQCKKKYLPPTSKK PKFEELQKPA\VLMEWINATLIPEHLVVRSLEEDMFDGILHHL FGRLAALKLEREIDLATATSQCKKKYLPPTSKK SGA/WESIFNKDLLSTLHLLVALAKRFOPDLSLPTNVQVEVITI ESTKSGLKSEKLVEGLITEYSTDKDSFPKOVPDELFKLAPKVNA VKRAIVNFVNQKLDRIGGLSVQNLDTQFADGVILLLIGGLEGFF LHLKEFYLTPNSPAENLHNVTLALELL/IGGCPAQLEC/LALK/ TIVNKDAKSTLRVLYSLFCKHOKAPROTHORAPN 6133 2 4256 FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQCPVSAPVPIAAHASVAGHLSTSTVSSSGANDSTK KTLVTLIANNNAGNELVQQGGQFLILTONPAPGIGGTMVTOPVLR PVQVMQNANHVTSSPVASQPIFITTOGFPVRNVRPVQNAMNQVG IVLNVQQGQTVRFTLTVPAPGGGFLILTONPAPGIGGTMVTOPVLR PVQVMQNANHVTSSVASQPIFITTOGFPVRNVRPVQNAMNQVG IVLNVQQGQTVRFTTNTPTTVIFATLTIRSTVPQSQSQQTKSTPSTSTTP TATQPTSLGCLAVQSPGGSNQTTMPKLAPSFPSPPAVS IASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSGPVVVSNNSSAN\ GSGRTSGPBSSNKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVPYQKKKKSLDSPVSDAKNPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLDDFYY GRDGKVAQLITMFFVANSFRCHCTTRLKNNIRFNNHMKHNUE LDQQNGEVDGHTICCHCXGPSTFPQLQCHLENWISPYSSTTKC KICCMAFSSEPLFLQHMKDTKKPGEMPYVCQVCQYRSSLYSEVD VHFRMHEDTRILLCPYCLKVPKNCNAPQQHYMRGKRNAVYH\ CNCCTQVQPLFAKDKIEHKLQPHKKTFRKPKQLEGLKPGTKVTIRA SRQQPRTVPVSSNNDTPPSAQEAAPDITSSNDLPVFULSCKTSTST CCSRAYANHMINNIPPRKSPKYLALFENSGIKLACTSCTFVT SVGDAMAKHLVMPSHRSSSILPRGTTWIAHSRAGTRDRVIDR NVKNMYPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPTPTHQALALPFLATSGABCLANDDQDESSPYTORFE LASGGGGSGVGKKEQLSVKKLKLRVLFALCCTTEQOALP RRITRWLRRFQASQGENLEGKYLSFEREEKLAEWULTCREQOLP VEETLEFQKATKIGRSLEGGKYLSFEREEKLAEWULTCREQOLP VEETLEFQKATKIGRSLEGGKYLSFEREEKLAEWULTCREQOLP VEETLEFQKATKIGRSLEGGKYLSFEREEKLAEWULTCREQOLP VEETLEFQKATKIGRSLEGGKYLSFEREEKLAEWULTCREQOLP VEETLEFQKATKIGRSLEGGKYLSFEREEKLAEWULTCREQOLP VEETLEFQKATKIGRSLEGGKYLSFEREEKLAEWULTCREQOLP VEETLEFQKATKIGRSLEGGKYLSFEREEKLAEWULTCREQOLP VEETLEFQKATKIGRSLEGGKYLSFEREENLAEWULTCREQOLP VEETLEFQKATKIGRSLEGGKYLSFEREENLAEWULTCREOLF VAHTLPKDVAENAGLFIDFV		<u> </u>		TQMDGMSLLPILRGASNLTWRSDVLVEYQGEGRNVTDPTCPSLS
EVYNLTADPOQITNIAKTIDPELLGKMYKRMMLQSCSGPTCRT PGVPDFQYRDPENIKPNGSURFRESKHLL 6132 96 1241 AAGLLPPGLVPEDPRFTRNLLFFGIQGPFFALSRPLFSCVESGW AWEAMSPEFLYDLLQLPKGVEFPAEEELSKGKKKYLPPTSRKD PKFEELQKPA\UMBENIATLIDEHLVVRSLEEDMFOGLILHHL FQRLAALKLEAEDIALTATSQKHKLTVVLEAVNRS\CSWRSGRF SGA\WESIFNKDLLSTLHLLVALAKRFQPDLS_LPTNVQEVITI ESTKSGLKEEKLVEQLTEYSTDKDEPPRDUPDELFKLAPEKVAA VKBALVNFVNQKLDRIGJSVQNLDTQFFAQDUPLLLLLGQLEGFF LHLKEFYLTPNSPAEMLHNVTLALELL/IGSGPAQLPC/LALK\ TIVNKDAKSTLRVLYGLFCKHTOKAHRDRTPHGAPN 6133 2 4256 FVHGSMADTDLFMECEEEELEFWQKISDVIEDSVVEDTYNSVDKT TTVSVSQQEVSAPVPIAHASVAGHLSTSTVSSSGAQNSDSTK KTLVTLIANNAGNPLVQQGGGFLLLTONPAPGLGTNVTQPVLR PVQVMONANHVTSSPVASQPIFITOGFPVRNVPPVQNAMNQVG IVLNVQQQTVRPITLVPAFGTGVFVKETVGGFPVSNVDRTVRPG STMPVRFTINTFITVIPATLTIRSTVPQSGQOTKSTPSTSTTP TATQPTSLQGLAVQSFGGSNGTTMPKLAPSFFSPAVSIASFYT VKRPGVTGENSNEVAKLUNTLNTTPSLGQSGGVKSTPSTSTTP TATQPTSLQGLAVQSFGGSNGTTMPKLAPSFFSPAVSIASFYT VKRPGVTGENSNEVAKLUNTLNTTPSLGQSGPBPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGKKCPKNACFRVTEAL REMMCYCCPEMVEYQKKCKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLUDDFYY GRIGGEVAQLTTRFPKVATSFFCHCTTRLKNNTRFNMHMKHUB LDQONGEVDGHTICHCYQFSTPPQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTIKFGEMFYVCQCQYARSIJSEVD VHFRMIHBEDTRILLCPYCLKVFKGNAFQQHYWRHQKR\NVYH\ CNKCRVQFJFAKDKIEHLLOPHCKFYKKGNAFQQHYWRHQKR\NVYH\ CNKCRVQFJFAKDKIEHLLOPHCKFYKKGNAFQQHYWRHQKR\NVYH\ CNKCRVQFJFAKDKIEHLLOPHCKFYKKGNAFQQHYWRHGKR\NVYH\ CNKCRVQFJFAKDKIEHLLOPHCKFYKRGNAFQLEIKGTRDVHDR NVKNMYPPPSPFTNKAATVSAGATPAEPEELLTPLAPALPPPA STATPPPTPTPHPQALALPPLATEGABELNVDDQDEGSPVTOEPE LASGGGSGGVKKEQLSVKKLKVJFFACCTTEGAAEHFRNPQ RIRRWLRRFQASGGENLECKYLSFFERKLAEWULTCREQOLP VEETLEFQKAFKIGRSLEGGKYLSFFERKLAEWULTCREQOLP VEETLEFQKAFKIGRSLEGGKYLSFFERKLAEWULTCREQOLP VEETLEFQKAFKIGRSLEGGKYLSFFERKLAEWULTCREQOLP VEETLEFQKAFKIGRSLEGGKYLSFFERKLAEWULTGREQOLP VEETLEFQKAFKIGRSLEGGKYLSFFERKLAEWULTGREQOLP VEETLEFQKAFKIGRSLEGGKYLSFFERKLAEWULTGREQOLP VEETLEFQKAFKIGRSLEGGKYLSFFERKLAEWULTGREQOLP VEETLEFQKAFKIGRSLEGGKYLSFFERKLAEWULTGREQOLP VEETLEFQKAFKIGRSLEGGKYLSTYSDAWRFMLERHLTPHARAR VAHTLPKOVAENAGLFIDFVQRGIB	j			PGVSQCFPDCVCEDAYNNTYACVRTMSALWNLQYCEFDDOEVFV
6132 96 1241 AGLIPPGLVPEDPRTTENLLFGIQGPFFALSRPLFSCVESGW AWEAMEPEFLYDLLQLPKGVEPPAEELSKGGKKKYLPPTSRKD PKFEELGKPA\UMBWINATILEPHILVRSLEEDMFDGLILHHI FQRLAALKLEAEDTATTATSKKKLTVVLEAVINS\CSWESGRP SGA\WESIFNKDLLSTIHLLVALAKRROPDLSLPTNVQVEVITI ESTKSGLKSRKLVEQLTEYSTUEPPKOVPETFKLAPEKVNA VKEAIVNFVNQKLDRLGLSVQNLDTQFADGVILLLIGGLEGFF LHLKEFYLTPNSPAEMLHNVTLALELL/IGRGPAQLPC\LALK\ TIVNKDAKSTLRVLYGLFCKHTQKARHDRIFHGAPN 6133 2 4256 FVIGSMADTDLFMECEEELEPFWCKISDVEDSVEVDYNSVDKT TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSGAQNSDSTK KTLVTLIANNNAGNPLVQGGGPLILTQNPAPGLGTMVTQPVLR PVQVMQNANHVTSSPVASQPIFTTTGFFVRNVRPVQNAMNQVG IVLNVQQGGTVRFITLVPAFDTVRFTVSVGSGAQNSDSTK KTLVTLIANNNAGNPLVQGGGRLILTQNPAPGLGTMVTQPVLR PVQVMQNANHVTSSPVASQPIFTTTGFFVRNVRPVQNAMNQVG STMPVRPTTNFTTVIFATLTRSTVPQSGSQQTKSTPSTSTTP TATQPTSLGQLAVQSPGGSQGTKITGRNAQFRVTSALFVT VKRPGVTGENSEVAILVNTLNTISIGLGSPGFVVVSNNSSAH\ GSGRTSGPESSMKVTSSIPVPDLQQGGRRICPRCNAQFRVTSAL RGMCCCCPMVFYQKKGKSLDSEPSVPSAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPSPNENVGDAVQTKLIMLUDDFYY GRDGKVAQLTNFFKVATSFRCPHCTKRLKNNIRRMMKKHIVE LDQQNGEVDGHTICCHCYRGFSTPPCLQCHLENUTSPYESTTKC KICEWAFSSEPLFLOHMKDTHRPGEMPYVQQVQVRSSLYSEVD VIFFMHHEDTRIHLLCPYCLKVFKNCNAFQQHMERICKR NVYH\ CNKCRVQFLFARUK EHKLQHKKTFRKPKQLEGLKPGTKVTIRA SRQQPTVPVSNNDTPPSALQEAPLITSMDPLPYTYHCSLCRYST CCSRAYANIMINNHVPRKSPKYLALFKRSVGGIKLACTSCTFVT SVGDAMAKHLUNFNSHRSSI LIPRGLTHIAHSRHQOTTROPUDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTPHPQALALPPLATEGGELNVDDQDEGSFVTOEPE LASGGGSGGVGKKEQLSVKKRVVVFALCCREQALP RRIRWLRRFQASGGENLEGKYLSFBAEKLAEWULTQREQOLP VMEETLIFQKATKIGRSLEGGFKISFEMEKLAEWULTQREQOLP VMEETLIFQKATKIGRSLEGGFKISFEMEKLAEWULTQREQOLP VMEETLIFQKATKIGRSLEGGFKISFEMEKLAEWULTQREQOLP VMEETLIFQKATKIGRSLEGGFKISFEMEAREMLAEWULTQREQOLP VMEETLIFQKATKIGRSLEGGFKISFEMEAREMLAEWULTQREQOLP VMEETLIFQKATKIGRSLEGGFKISFEMEAREMLAEWULTQREQOLP TOENLISDDRKENALQTVGTGEPMCDVVLAILABGSTULPTLIFTLFYFT VAHTLPKDVAENAGLFIDFVQGIHNGDLPLSMIVAIDETSLFL DTEVLSDDRKENALQTVGTGEPMCDVVLAILABGSTULPTLIFTLYFT	į .	i		EVYNLTADPDQITNIAKTIDPELLGKMNYRLMMLOSCSGPTCRT
AWEAMEREFLYDLIQLEKGYPALERISKGEKKKYLPPISRKD PKFELCKPA\ULMENTATLEPHILVRSLEEDMFDGLILHHI FORLAALKLEAEDIALTATSQKHKLTVVLEAVMRS\CSWRSGRP SGA\WESIFNKDLLSTHLILVALAKREPDPLSLPTNVQWEVITI ESTKSGLKSEKLVEQUTEYSTDKUBEPPKDVFDBLFKLAPEKVNA VKERIVMFVNGKLDRLGLSVQNLDTOPADOZVILLLIGQLEGFF LHLKEFYLTPNSPAEMHNVTLALELL/IGRGPAQLPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTPHGAPN 6133 2 4256 FVIGSMADTDLFMECEEELEPWQKISDVLEDGVYBSVYDKT TTVSVSQQPVSAPVPLAHASVAGHLSTSTTVSSSGQNSDSTK KTLVTLIANNNAGNPLVQQGQPLILTONPAPGLGTMVTQPVLR PVQVMQNAHNVTSSPVASQPIFTTTGGFPVRNVRPVQNMMNQVG IVLNVQQGQTVRFITLVPAPGTGFVRRVTVVPVQSTSMTPVRPG STMPVXPTTMFTTVIPATHSSTVPQSGSQQTKSTPSTSTTP TATQPTSLGQLAVQSPQGSNQTTNPKLAPSFPSPPAVSTASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLQSBGPVVVSNNSSAH\ GSQRTSGPESSMXVTSSIPVPDLQDGGRKICPRCNAQFRVTBAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGKVAQLITVFPKVATSFRCPHCTKRLKNNIRMMHNKHNVE LDQQNGEVDGHTICCHCYRGFSTPFQLCHLENVHSPYESTTKC KICEMFSEPPLECHMKOTHREGEMPYYCQVQVNSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CKKCRVQFLFAKUKIEHKLQHKKTFRKRQLEGLKPGTKVTIRA SRGQFTVPVSSNDTPFSALQEARLITSSMPLPVFLYFTVGSL SKGGRTVPVSSNDTPFSALQEARLITSSMPLPVFLYFTVGSL SKGGRTVPVSSNDTPFSALQEARLITSSMPLPVFLYFTVGSL CKSRAYANHMINNHVPKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVPNFSHRSSSILPRGLTUHAISSRHQTTBRVHDR NVKNMYPPPSFPTNKAATVKSAGATPABPELLTFLLAPALPSPA STATPPPTPTHPQALAPPLAALEGABECLNVDDQDGSSPVTQEPE LASGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRWLRRFQASGGENLEGKYLSFEAEKLAEWULTQREQQLP VNEETLFQKATKIGRSLESGFKISFEWAAPRINKHHIPHARRA VAHTLPKOVAENAGLFIOFDVQQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRENNAGIFGTFOFVQRIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRENNAGIFGTFOFVQRIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRENNAGIFGTFOFFACEREKLAEWULTQREQOLP VNEETLFQKATKIGRSLESGFKISFEWALEWULTRHTQRACH VAHTLPKOVAENAGLFIOFDVQRIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRENNAGIFGTFOFFACEREKLAEWULTQREQOLP VNEETLFQKATKIGRSLESGFKISFEWAKERWILKHHIPHARRA VAHTLPKOVAENAGLFIOFOVAGIHNGLEFYGNGKHTACO				PGVFDPGYRFDPRLMFSNRGSVRTRRFSKHLL
AWEAMEREFIJULIQLERGVERPEREELISKGGKKKYLPPTSRKD PKFELQKRAJVIMEWINATLIPEHIJVRSLEEDMFDGLILHHL FQRLAALKLEAEDIALTATSQKKKLTVVLEAVYRS\CSWRSGRP SGA/WESIFKKDLLSTIHLLVALAKRROPDISLFTHNQVEVITI ESTKSGLKSRKLVEOLTESTRDEPFKVDAPBLFKLARP VKBAIVMFVNQKLDRLGLSVQNLDTQFADQVILLLIGQLEGFF LHLKEFYLTPNSPABHHNVTLALELL/IGRGPAQDPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTQKARHDRTPHGAPN 6133 2 4256 FVIGSMADTDLFMECEEELEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVFIARASVAGHLSTSTTVSSSGAQNSDSTK KTLVTLIANNNACNPLVQQGGILITONPAPGLGFMVTQPVLR PVQVMQNANNIVTSSPVASQPIFTTGGFPVRNVRPVQNAMNQVG IVLNVQQGQTVRPITLVFAPGTGYPVTVGVPQVYSQMTPVRPG STMPVRFTTNTFTTVIFATLTIRSTVPQSGSQTKSTPSTSTTP TATQPTSLGGLAVQSPGGSNGTTNFKLASFFSPPRAVSIASFYT VKRPGVTGENSNEVAKLWNTJPSLGQSPGPVVVSNNSSAH\ GSQRTSGPESSMKVTSIPVFDLQDGGRKICPRCMAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSFEKTAPVAS ACGURTGPESSMKVTSIPVFDLQDGGRKICPRCMAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSFEKTAPVAS GROGKVAQLTNFPKVATSFRCFHCTKRLKNNIRFMHMKHNVE LDQQNGEVDGHTICQHCYRGFSTPFDLQCHLENNUSPYSSTTKC KICEMAFSSEPLFLOHMKDTHKPGEMPYYCQVQVRSSLYSEVD VHFRMTHEDTRHLLCPYCLKVPKNCNAFQQHTMRHGKRNVTYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRQQRTVPVSSNDTFFSALQEAPLTSSMDPLPVFLVFPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFFTYVHCSLCRYST CCSRAYANHMINNHPKRSSPLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHCQTRRPWHDR NVKNMYPPSFFTNKAATVKSAGAFFABFELLTFLLAPALPSPA STATPPPTTPTHPQALAPPLATGABCLINVDQDEGSFVTOPE LASGGGGSGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASGGENLEGKYLSFEAEKLAEWUTQREQOLP VMEETLFQKATKIGRSLEGGFKISFEWAVFRIKHHLTPHARRA VAHTLPKOVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRRENALFURGSFESGFKISFEWAVFRIKHHLTPHARRA VAHTLPKOVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRRENALFURGSFESGFLAEKLAEWUTQREQOLP VMEETLFGKATKIGRSLEGGFKISFEWAVFRIKHHLTPHARRA VAHTLPKOVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRRENALFURGSFESGFKISFEWAVFRIKHTLPHARRA VAHTLPKOVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRRENALFURGSFESGFURSTVOKGMITACC	6132	96	1241	AAGLLPPGLVPEDPRRTRNLLPFGIQGPPFALSRPLFSCVESGW
FORLAALKLEAEDIALTATSOKHKLITVILEAVINS\CSWRSGRP SGA/WESIFNDLISTHILUALARRFOPDLSIPTNVQVEVITI ESTKSGLKSEKLVEQLTEYSTDKDEPPKDVFPELFFLAPEKVNA VKRAIVWFVNOKLDRIGSVQNLDTOFADGVILLLIGGLEGFF LHLKEFYLITPNSPAEMHANVTLAELLI, IGGRPGQLDPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTPHGAPN 6133 2 4256 FVIGSWADTDLFMSCEEEELEPWQKISDVIEDSVVEDTNSVDKT TTVSVSQQPVSAPPVIRANSVGHLSTSTVSSSGAGNSDSTK KTLVTLIANNNAGMPLVQQGQFLILTQNPAPGLGTMVTQPVLR PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG IVLNVQQGQTVRPITLVPAFTQFPQVKPVVEQVPVSYGMTPVRPG STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP TATQPTSLQQLAVQSPQSNQTTMITHSTVPAKLAPSFPSPSVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLQGSPGPVVVSNNSSAH, GSQRTSGPESSMKVTSSIPVPDLQDGGRKICPRCMAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSFEKTAPVAS /THPSSTP1PALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNIPKVATSFRCHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYGSTPPQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMHEDTRHLLCPYCLKVFKKGNAFQQHYMHQKR\NYYH\ CKKCRVGFLFAKKLIEKLCHHKTFRRPKDLEGKLPGTKVTIRA SRQQPTVPVSSNDTPPSALQEAPLTSSMDPLPVFLYFPVQRS IQKRAVKMSVMGRQTCLECSFEIPPPNHFPTTVHCSLCRYST CCSRAYANIMINNHVPRSKYSSILAFERNSGIKLACTSCTFVT SVGDAMAKHLVPNPSHRSSSILPRGLTWIAHSRGQTRDRVHDR NVKNMYPPPSFFTNKAATVKSAGATABEPBELLTPLAPALPSPA STATPPTTPTPQALALPPILATEGABCLINDDQDQEGSPVTQBPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASGGENLEGKYLSFBABELLAEWVLTQREQOLP VMEETLFQKAATKIGRSLEGGFKISYEMVAFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEGFKISYEMVAFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEGFKISYEMVAFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEGFKISYEMVAFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEGFKISYEMVAFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEGFKISYEMVAFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEGFKISYEMVENTERMURSTRVUKQKHTACO	i i			AWEAMEPEFLYDLLQLPKGVEPPAEEELSKGGKKKYLPPTSRKD
FORLAALKLEAEDIALTATSOKHKLITVILEAVINS\CSWRSGRP SGA/WESIFNDLISTHILUALARRFOPDLSIPTNVQVEVITI ESTKSGLKSEKLVEQLTEYSTDKDEPPKDVFPELFFLAPEKVNA VKRAIVWFVNOKLDRIGSVQNLDTOFADGVILLLIGGLEGFF LHLKEFYLITPNSPAEMHANVTLAELLI, IGGRPGQLDPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTPHGAPN 6133 2 4256 FVIGSWADTDLFMSCEEEELEPWQKISDVIEDSVVEDTNSVDKT TTVSVSQQPVSAPPVIRANSVGHLSTSTVSSSGAGNSDSTK KTLVTLIANNNAGMPLVQQGQFLILTQNPAPGLGTMVTQPVLR PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG IVLNVQQGQTVRPITLVPAFTQFPQVKPVVEQVPVSYGMTPVRPG STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP TATQPTSLQQLAVQSPQSNQTTMITHSTVPAKLAPSFPSPSVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLQGSPGPVVVSNNSSAH, GSQRTSGPESSMKVTSSIPVPDLQDGGRKICPRCMAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSFEKTAPVAS /THPSSTP1PALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNIPKVATSFRCHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYGSTPPQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMHEDTRHLLCPYCLKVFKKGNAFQQHYMHQKR\NYYH\ CKKCRVGFLFAKKLIEKLCHHKTFRRPKDLEGKLPGTKVTIRA SRQQPTVPVSSNDTPPSALQEAPLTSSMDPLPVFLYFPVQRS IQKRAVKMSVMGRQTCLECSFEIPPPNHFPTTVHCSLCRYST CCSRAYANIMINNHVPRSKYSSILAFERNSGIKLACTSCTFVT SVGDAMAKHLVPNPSHRSSSILPRGLTWIAHSRGQTRDRVHDR NVKNMYPPPSFFTNKAATVKSAGATABEPBELLTPLAPALPSPA STATPPTTPTPQALALPPILATEGABCLINDDQDQEGSPVTQBPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASGGENLEGKYLSFBABELLAEWVLTQREQOLP VMEETLFQKAATKIGRSLEGGFKISYEMVAFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEGFKISYEMVAFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEGFKISYEMVAFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEGFKISYEMVAFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEGFKISYEMVAFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEGFKISYEMVAFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEGFKISYEMVENTERMURSTRVUKQKHTACO				PKFEELQKPA\VLMEWINATLLPEHIVVRSLEEDMFDGLILHHL
ESTKSGLKSEKLVEQLTEYSTDKDEPPKUAPDELFKLAPEKVANA VKRAIVNFVNQKLDRIGLSVYQNLDTQFADGVILLLLIGQLEGFF LHLKEFYLTPNSPARMLHNVTLALELL/IGRGPAQLPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTHFGAPN 6133 2 4256 FVHGSMADTDLFMECEEELEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPILAHASVAGHLSTSTTVSSSGAONSDEK KTLVTLIANNNAGNPLVQQGGQFLILTQNPAPGLGTMVTQPVLR PVQVMQNANHYTSSPVASQPIFITTGGFPVRNVRPVQNAMNQVG IVLNVQQGQTVRPITLYAPBGTQFVVETVVGPQVYSQMTPVRPG STMPVRPTTNTFTTVIFATLTIRSTVPQSQSQOTKSTFSTSTTP TATQPTSLGQLAVQSPGGSNQTTNPKLAPSFFSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGRKLCPRCNAGPRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLINTFKVATSFRCPHCTKRLKNNIFMMKHHVE LDQQNGEVDGHTICCHCYRGFSTPGLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLPAKURIEHKLQHKKTFKKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPFSALQEAPLITSSMDFLPVFLYFPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTTVHCSLCRYST CCSRAVANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTMIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGAPTPABPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTCEPE LASGGGGGGGVGKKEQLSVKLUVLFALCCUTTQAAEHFRNPQ RRIFRWLRRPQASGGENLEGKYLSFEAEEKLAEWUTGREQQLP VNEETLFQKATKKGRSLEGGFKISYEWAVRFMLRHLITPHARRR VAHTLPRDVAENAGLFTDFVQRVIHNODLPLSMIVAIDETSLFL UTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRWQKHTACQ	İ			FORLAALKLEAEDIALTATSOKHKLTVVLEAVNRS\CSWRSGRP
VKRATVNFVNQKLDRLGLSVNLDTQFADGVILLLLIGGLEGFF LHLKEFYLTPNSPAEMLHNVTLALELL/IGRGPAQLPC/LALK/ TIVNKDAKSTLRVLYCLFCKHTQKAHRDRTPHGAPN 6133 2 4256 FVHGSMADTDLFMECESEELEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAAHASVAGHLSTSTVSSSGAQNSDSTK KTLVTLIANNNAGNPLVQQGGQELILTONPAPGLGITMYTQPVLR PVQVMQNANHTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG IVLNVQQGQTVRPITLVPAFGTQFVKPTVGVPQVFSQMTPVRPG STMPVRPTTNTFITVTVPATLTIRSTVPGSGQGYTKSTPSTSTTP TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT VKRPGVTGENSENSEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\ GSGRTSGPESSMKVTSSIPVPDLQDGGKKICPSCNAQFRVTEAL RCHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVCDAVQTKLIMLVDDFYY GRDGGKVAQLINTPFKVATSFRCPHCTKRLKNNIFFMHMKHIVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKRGEMPYVCQVCQYRSSLYSEVD VHFRMTHEDTRHLLCPLKVFKKGNAPQQHTWRHQKRKNVTYN\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQRTVPVSSNDTTPPSALQEAPLTSSMDPLPVFLYPPVQRS IQKRAVKRSWMGRGCLEGSPEIDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGGTRDRVHDR NVKNMYPPSFPTNKAATVKSAGATPABPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGABCLNVDDQDEGSPVTQEPE LASGGGGSGGVKKEQLSVKKRVVLFALCCNTEQAAEHFRNPQ RRIRRMLRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQOLP VNEETLFQKATKIGRSLEGGFILSYEMAVRFMKRHHLTPTHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENARLFURGTGFBEMCDVVLAILADGTVLPTLVFY RGQMDDPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ	1 .	[SGA/WESIFNKDLLSTLHLLVALAKRFQPDLSLPTNVQVEVITI
LHLKEFYLTPNSFAEMLHNVTLALELL/IGRGPAQLPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTFHGAPN 2 4256 FVIGGMADTDLFWECEEELEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK KTLVTLLIANNAGNPLVQQGGQFLILTOMPAFGLGTWVTQPVLR PVQVMQNANHVTSSPAQSQFLITTOGFPVRNVRPVQNAMNQVG IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPYSGMTPVRPG STMPVRPTTNTFTTVIFATLTIRSTVPQSGSQOTKSTPSTSTTP TATQPTSLGQLAVQSPQSNQTTNPKLAPSFPSPPAVSIASFVT VKRPGVTGENSNEVAKLUNTLNTIPSLQSPGPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVPDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAKKPPSFEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYNGFSTPFQLQCHLENVHSPYESTTKC KICEWAFESFPLFLOHMKDTHKPGEMPYVCQVQCYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKLEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFFIPDFPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVGSIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPABPEELLITPLAPALPSPA STATPPPTPTHPQALALPPLATEGABCLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASGGSNLEGKYLSFEBEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEMAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHMQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQVTGTGBPWCDVVLAILADGTVLPTLVFY RGQMDDPAMMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ	i			ESTKSGLKSEKLVEQLTEYSTDKDEPPKDVFDELFKLAPEKVNA
TIVNKDAKSTLRVLYGLECKHTQKAHEDRTPHGAPN 1 TVSVSQQPVSAPVPIAAHSVAGHLSTSTTVSSSGAONSDSTK KTLVTLIANNNAGNPLVQGGQFLILTONPAPGLGTWVTQPVLR PVQVMQNANHVTSSPVSSQPIFITTQGFPVRNVRPVQNAMMQVG IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG SYMPVRPTTNTFTTVIPATLTIRSTVPQSQSQOTKSTPSTSTTP TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSFGPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPSPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCFHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYRQFSTPFGLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMTHEDTRILLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQPHKLFFKPKQLEGIKFPGTKVTIRA SRGQPRTVPVSSNDTTPSALQEAAPLTSSNDPLEVFLYPFVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNFSHRSSSILPRGLTWIANSRHGQTRDVHDR NVKNMYPPPSFFTNKAATVKSAGATFAEPEELLTPLAPALPSPA STATPPFPTTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLECKYLSFEAERKLAEWUTGREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQTHNODLPLSNIVAIDESISLFL DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQNDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ				VKKAIVNFVNQKLDRLGLSVQNLDTQFADGVILLLLIGQLEGFF
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GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSFEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQDITNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENNHSPYESTTKC KICEWAFESBPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPBSALQEAAPLTSSMDPLEVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ	. [Ī		VKRPGVTGENSNEVAKLVNTLNTTPSI.GOSDCDWWWSNMeenul
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/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVARSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYWRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTVYHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPROVENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO	[RGHMCYCCPEMVEYOKKGKSLDSEPSVPSAAKPPSPEKTADIJAC
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LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSILPRGLIVIAHSRGQTRDRHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTPPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRHLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ	· i			GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPESALQEÅAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ	1		i	LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
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CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPESALQEAAPLITSMDPLEVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPNHFPTYVHCSLCRYST CCSRAYAHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLITWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO	1			VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
SRGOPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTVVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRHLRRFQASQGENLEGKYLSFEAEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ	l			CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGITWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTPHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ				SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
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NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGSGGVGKKEQLSVKKLRVVLFALCCTTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPRDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO	1	1		CUSKAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
STATPPTTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPRVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ	ļ		ł	SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
LASGGGGSGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRNLRRFQASQGENLEGKYLSFEAEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPRVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ	İ	1	I	NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
RRIRRWIRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSWILVAIDEISLFL DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ			İ	STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ	- 1	Ì	}	LASGGGGGGGGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMBLWSTRVWQKHTACQ	- !			RKIKKWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP
DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMBLWSTRVWQKHTACO	ł	į.	ļ	VNLET LFUKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACO			ŀ	VARITHERDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL]	·	PCOMPORANTARIOTICS TO STATE OF THE PROPERTY OF
RSAGPILVMDCHKTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL	1	1	j	REVENUE AND CHEET AND CHEE
		<u></u>		REAGENLYMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL

SEC	Predicted	Predicted end	
ID			Amino acid segment containing signal peptide
NO:	,	nucleotide	[(A=Alanine, C=CVSteine, D=Aspartic Acid p
1	location	location	Giucamic Acid, F-Phenvialanine G-Glucino
ł		corresponding	H=Histidine, I=Isoleucine, K=Lygine
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
-	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- 1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence	1 -	\=possible nucleotide insertion)
		<u> </u>	DVCIVERVENCY HEXILITIES INSERTION)
1			DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
1 .		1	LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
J	}		LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
6134	2	4052	FYGFEEADLDLMEI
1 020.	· -	4256	FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
1	1	j	TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAONSDSTV
	ŀ		KTLVTLIANNNAGNPLVOOGGOPLILTONPAPGI.GTMVTOPVI.D
	ł		PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
- 1	1	i	IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
			STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
-	İ	1	TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT
		ł	VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
			GOOPTCOPECHIUMCCTPUTCH COCCUSTORY CONTROL OF
i	ı		GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
ľ	ŀ		RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
	ľ		/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
ĺ	[GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
ł	l		LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
	1		KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
1	(VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
1	Ī		CNKCRVQFLFAKDKIEHKLOHHKTFRKPKOLEGI.KPGTKVTTPA
			SRGQPRTVPVSSNDTPPSALOEAAPLTSSMDPLPVFT,VPDVODE
İ	-		IQKKAVRKMSVMGRQTCLECSFEIPDFPNHFPTVVHCSLCPVST
1	1		CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
1			SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGOTPDDVUDD
1]		NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPIADALDSDA
	1 / 1		STATPPPTTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
	1		LASGGGGGGGGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
1	1		RRIRRWLRRFQASQGENLEGKYLSFBAEEKLAEWVLTQREQQLP
i	1 1		VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
]	1		VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
ŀ	1		DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
	, ,		RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
1	1		RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
	1		DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
i	1]	LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
İ]		FYGFEEADLDLMEI
6135	2	4256	
1	1 1		FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
l .			TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
ļ	1		KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
ĺ	1		PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
ļ	i t		IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
1	1 1	. 1	STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
	1		TATQPTSLGQLAVQSPGOSNOTTNPKLAPSPPSPPAVSTASPVT
ļ	, ,		VKRPGVTGENSNEVAKLVNTLNTIPSLGOSPGPVVVSNNSSAU\
1	1	j	GSQRTSGPESSMKVTSSIPVFDLODGGRKICPRCNAOFPVTFAT
		}	RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTADUAG
	1	1	/THPSSTPIPALSPPY/TKVPEPNENVGDAVOTKI.TMI.VDDRVV
		1	GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
	1		LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
	į l		KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
	1	1.	VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
	1.	J.	CNKCBACET EPARDATERIAL CHIRMSON TO COMMUNICATION OF THE COMMUNICATION OF
	1 1		CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
	!		SRGOPRTVPVSSNDTPPSALOEAAPLTSSMDPLPVFLYPPVQRS
	i	1:	IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
	<u> </u>		CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT

SEQ Predicted and mucleotide location corresponding to first the first said of first the first said of first said of first said of first said of first said of first said of first said of sai		SEQ	Predicted	Predicted end	Dmino
No:		ID			(A-Alapino C-Containing signal peptide
corresponding to first amino acid amino acid control to first amino acid control to first amino acid control to first amino acid amino acid amino acid amino acid control to first amino acid control		NO:	nucleotide		Glutamic Acid Fabband C Cl
Leucine, Membeliofinie, Neasparagine, senion acid seide of amino acid sequence side of amino acid sequence sequ			location		H=Histidine T-Toolousing W. V. V.
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amino acid residue of amino acid sequence sequen	ĺ			amino acid	Paproline O-Glutamine Banasinine
### ### ### ### ### ### ### ### ### ##			amino acid		S=Serine, T=Threonine V-Valine
Sequence Codon, /=possible nuclectide insertion) SVGDANARILUPROSHESSIL/REGITELARSEMGOTERVUED SVGDANARILUPROSHESSIL/REGITELARSEMGOTERVUED NYKOWNY PPSSPTNAATUKSAGATRAPPEELLTLAPALPSPA STATPPPTPTHOALALP-LATEGACINVODDEGS-PVTORED LASGGGGGGVEKKEOLSVKILKUV-PLACCHTEGABEIFNPPP RETARRIBERGASGGGENLEKKIS-FRABERLABWUTQGERGOLV VERETLEVARATUKGELGGVETIS-VERNARFMEHHITHARDER VAHTLERVARENGI-TUTUVAFLORVITALETUR-TUTUFF REGONDORAMPOSILLEARESCYSDDEIMEINSTRWOCKTRACO REKOMMUNDCHATHLESEVLANLSASSILPAVEVEDORIUNSPTRAMOCELLIVF REGONDORAMPOSILLEARESCYSDDEIMEINSTRWOCKTRACO REKOMMUNDCHATHLESEVLANLSASSILPAVEVEDORINSPTRAMOCELLIVF REGONDORAMPOSILLEARESCYSDDEIMEINSTRWOCKTRACO REKOMMUNDCHATHLESEVLANLSASSILPAVEVEDORINSPTRAMOMOELLIAS LOVICKETVURFLHKKUREGAREMADTACDSDVLLGUVLVWIGE LOVICKETVURFLHKKUREGAREMADTACDSDVLLGUVLVWIGE RECOLLAGESHESSSTPRORESPETTEPSIJGLEFGESETS PVFERADLILLER SUPERALIZAMEN FVFERADLILLER FVFERADLILLER REGOLKLIGSBHESSSTPRORESPETTEPSIJGLEFGESETS PVFERADLILLER REGOLKLIGSBHESSTPRORESPETTEPSIJGLEFGESSTPRORESPETTEPSIJGLEFTEN A	Į			amino acid	W=Tryptophan V=Tyrosine V=Unknown + ct
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SVGDAMAKILLVPHPSHRSSSILERGITWIANISRIGGTERFUIDE NYKRMYPPPSFTINKATVIKSAGATPAEPELLTPLAPALSPA STATPPPTTHPOALALPFLATEGAECIAVIDODEGS PYTOEPE LASGGGSGGGGGVGKECLSVKRUVIFACCATTGGAAEHFENPO RRIHRALRFGASGGRILEGKTLSFRABEKLAEWULTGREGOLP WRESTLFFKARKIGRSLEGGYKSTSFRAWEHLHTPHARRA VAHTLKEVARNAGLPIDFVORGIHNODPLSHTVAIDEISH, DTEVLSSDDRKKTGRSLEGGYKSTSFRAWEHLHTPHARRA ROGMODPANMPDSILLEAKESGYSDDEIMELMSTKVMCKHTACO RSKKMLVNDCHKRHLSSEVILANIASASTIPANGOESKIAOL DVCIKRTVKMFLHKKWKGOARRHADTACTSDVLLQUVLVHUGSV LGVVICKSFTLVASVLGAPGANGASTSTDVLLQUVLVHUGSV LGVVICKSFTLVASVLGAPGANGASTSTDVLLQUVLVHUGSV LGVVICKSTLVASVLGAPGANGATACTSDVLLQUVLVHUGSV LGVCIKRTVKMFLHKKWKGOARRHADTACTSDVLLQUVLVHUGSV LGVCIKRTVKMFLHKKWKGOARRHADTACTSDVLLQUVLVHUGSV LGVCIKRTVKMFLHKKWKGOARRHADTACTSDVLLQUVLVHUGSV LGVCIKRTVKMFLHKKWKGOARRHADTACTSDVLLQUVLVHUGSV LGVCIKRTVKMFLHKKWKGOARRHADTACTSDVLLQUVLVHUGSV LGVCIKRTVKMFLHKKWKGOARRHADTACTSDVLLQUVLVHUGSV LGVCIKRTVKMFLHKKWKGOARRHADTACTSDVLLQUVLVHUGSV LGVCIKRTVKMFLHKKWKGOARRHADTACTSDVLLQUVLVHUGSV LGVCIKRTVVKMFLAVATACTSCVARCH LGVCIKRTVVKMFLAVATACTSCVARCH RNGAQLANGGTGALASLEPVOVGALVYCKKKKLSFYEXYSQCIKGTACA RNGAQLANGGTRAVDVAGATACTSCVARCH RNGAQLANGGTRAVDVAGATACTSCVARCH RNGALTUMBACHALVTKKMGQCOKSTRAVTATTSCVARCH RNGALTUMBACHALVTKKMGQCOKSTRAVTATTSCVARCH RNGALTUMBACHALVTKKMGQCOKSTRAVTATTSCVARCH RNGALTUMBACHALVTKKMGQCOKSTRAVTATTSCVARCH RNMMLIVAMCLALALLGLFGTAGAGRIGFSFTGAALTATACKGGGLMATACLES LSCPKUMAPGRIGHERKOQFTGAGAGRIGFSFTGAALTATACKGGGLMATACLES LSCPKUMAPGRIGHERKOQFTGAGAGRIGFSFTGAALTATACKGGGLMATACLES LSCPKUMAPGRIGHERKOQFTGAGAGRIGFSFTGAALTATACKGGGLMATACLES LSCPKUMAPGRIGHERKOQFTGAGAGRIGFTGAGAGGGTGATACH LGCRGAVYGGYGSTSBCVAREGUMTACHALVTKHGGACAGGTGFTFTEGGV LGCRGAVYGGYGSTSBCVAREGUMTAGAGGGTGATAGAGGG CCCRGUVFGIUFFGAGAGAGGTFGAGAGGGTGAGAGAGGG CCCRGUVFGIUFFGAGAGAGGGTGAGAGAGGGTGAGAGAGGG CCCRGUVFGIUFFGAGAGAGGGTGAGAGAGGGTGAGAGAGGGTGAGAGAGGGTGA			sequence		\=possible nucleotide insertion)
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VNBETLFQKATKLORS-LEGGFKISYEMAVRFMENHHLIPHARRA VAHTLEKDVARNAGLIFIPVORGIHNOLDIVATILLAGOT VAHTLEKDVARNAGLIFIPVORGIHNOLDIVATILLAGOT RIKEMIVMDCHTHLISEEVLANLASSTLPMVVPAGCSSKIODI DVCIKRTVKNEHIKKKEGSGYSDDETHARSTRVMCKHTACO RIKEMIVMDCHTHLISEEVLANLASSTLPMVVPAGCSSKIODI DVCIKRTVKNEHIKKKEGASGYSDDETHARSTRVMCKHTACO RIKEMIVMDCHTHLISEEVLANLASSTLPMVVPAGCSSKIODI DVCIKRTVKNEHIKKKEGASEMADTACHOLUGIVIVULGISV LGVIGCCPELVQRSFTUNASVLPGPDGNINSPTRNADMGEELIAS LEEGLILISGENESSTTRPRSSPESTIRPESLEQLFRGGVAS EKRGHRISRGOTGRIASLFSSLEPOLGPVIVVVVKKEGALASA DLESEIHOKOGOKRNINSOPGIVKVARRILDDTEDTVVSQRKIO INGEERIKRERTVVVGKLPVTCNKKKLEFKGGLIESVURR SLIPAGGTLSKKLAAIKKHIPDOKINAVVVVKESSAATOALK RNOAJCADGFIRVULASSTSKRRSVORSPRVALIKKKEGVERVGK RNOAJCADGFIRVULASSTSKRRSVORSPRVALIKKKEGVERVGK RNOAJCADGFIRVULASSTSKRRSVORSPRVALIKKKEGVERVGK SLIPAGGTLSKKLAAIKKHIPDOKINAVVVVKESSAATOALK HPLDCGSIMAVRIVDRWRSVNEERFYGOMSPRIKANIKVKUESAITK HPLDCGSIMAVRIVGRORSPRIKADIKVKUESAITK SELMGRKLRVGRORSPRIKADIKVKUESAITK SELMGRKLRVGRORSPRIKADIKVKUESAITK SELMGRKLRVGRORSPRIKADIKVKUESAITK SELMGRKLRVGRORSPRIKADIKVKUESAITK RRAACHABOLULASSTSKRRSVORSPRIKARDVOALINKOITERO MAMILIVAMCIA\LIGHGRGAELIGSVOKSGRVKORX RALKREGGEGREGGAGGGGGGGGVALANICHTERV LECPKOMAPSHCALIKTIKKGOKKSGRVKKGRVX LEKPGGUBHSAQCLATELTCHGSVGGLKKARDVOALINKOITERQ LORGALVGOVGGYSSOVRRIGHTSPRINTSSCRPGGRAIKAVG LERPGGUBHSAQCLATELTCHGSVGGLKKARDVOALINKOITERQ LORGALVGOVGGYSSOVRRIGHTSPRINTSSCRPGGRAILEV LERPGGUBHSAQCLATELTFFFGSEGMIKAVU LEKPGGUBHSAQCLATELTFFFGSEGMIKAVU LEKPGGUBHSAQCLATELTFFFGSEGMIKHALGGFGARENGLUHTIDNI RREGGYFILINGKAALDRAVVARTIFFRGDAVAGLUHTIDNI RREGGYFILINGKAALDRAVVARTIFFRGDAVAGULTITUNI LASMYBTALLISLATIKARGOKADETTTARUL LASMYBTALISATAVRAVRRPGQFIIALSGGSSFFALGTATARAKVA ANDIBATAVRAVRRPGQFIIALSGGSSFFALGTATARAKVA ANDIBATAVRAVRRPGQFIIALSGGSSFFALGTATARAKVA ANDIBATAVRAVRRPGGGRIBALSGGSFFALGTATARAKVA ANDIBATAVRAVRRPGGGRIBALSGGSFFALGTATARAKVA ANDIBATAVRAVRRPGGGRIBALGGGSFFALGTATARAKVA ANDIBATAVRAVRRPGGGRIBALGRAVRSOLULAGGGLATARYGFPR ATTHINJOERCELGABOTOMICKELTTULKTGGVGRRIGGLOVALIKGGILTSKLINGKALGGGRFFALGGLITAKVALGGGILTSKLINGHVINGGULTVINGGULTVOM LORGALAVGG	-		İ		RRIRRWLRRFQASQGENLEGKYLSFEAREKLAEWVLTOREOOLD
VAHTLEKOVARNAGLFIDFVORGIHNGOLPLINTVALETSEL DTEVLSSDIDRERNALGTVOTESPRICOVALLAGFULPTIVEY RGOMOOPANMPDSILLEARESGYSDDEIMELMSTRUKHTEVORGERSKOPL BYGEVERDINTRILLSERSULPMINSASSTIPAVVPAGCSSKIQPL DVCIKRTVKNPLHKKKEGAREMADTACDSDVLLGLULVMLGSV LGVIGCVEPLOVRSFLUNASULPOPDGNINTSPRUNDMOBELIAS LERGLKLISGENSESSTPRRSSPEFTIEPESLHQLFBOESETES FYGFERADLDIMEI 6136 1704 539 FOVMMALBGMSKKRKRENGOGEN PDDGVRGSP PEDVRLGQVAS SLEPGSHHSROGTORLASLFSSLEPOIQPVVPVPKKESALASA DLEBEHHOKOGOKRKNSGPGVKVARKLIDDTEDTVVSORKKIQ INQEERILMBERIVFVGRLEVVTCNKKLKSFYKENGGIESVRFR SLIPAGSHISKKLAJIKRKHHIPPOKNINAVVYKEESAATOALK RNOAGIALGFFLRVULASETSSRDKRSVFVGNLPYKWESAATOALK RNOAGIALGFFLRVULASETSSRDKRSVFVGNLPYKWESAATOALK RNOAGIALGFFLRVULASETSSRDKRSVFVGNLPYKWESAATOALK RNOAGIALGFFLRVULASETSSRDKRSVFVGNLPYKWESAATOALK RNOAGIALGFFLRVULASETSSRDKRSVFVGNLPYKWESAATOALK RNOAGIALGFFLRVULASETSSRDKRSVFVGNLPYKWESAATOALK RNOAGIALGFFLRVULASETSSRDKRSVFVGNLSKKA RNOAGIALGFFLRVULASETSSRDKRSVFVGNLSVK SELMGRKLRVMRSVNKEKFRQONSBFRLKAVSKKRCGINFTSKT ABCHYKKLFJGEKAVLLKTKKKGOKKGGRFKKORKOK 6137 141 2656 RALRKRRGGGGRGGALGSGPOPORIPGRVPERFAPPREEKHG MAMMLIVAMCLALLLGLIGGENGVALTHALGFOLDLAKK YLMGG LLFOLYLDLEAGRGLEGHSFSHAAALTAPKOGOEIMARALES LGFRUMPFHCABHCALALDLINNISHVENEITIMKSTURGGARMLRAV LERPSCHUHSPAAQLATELTTPROESENVANDVALGKOAVAQIL PFRDONKRALDGINNISHVENEVITIMKSTURGGARMLRALES LGFRUMPFHSAAQLATELTTPROESENVANDVALGKGARALES COGRANVOQUGSYSEQVRELQREDSFILIFTPRAGULVHINNI RWEGVPFILMSGKALDERVARTHERPROENTLISHTPRAGULVHINNI RWEGVPFILMSGKALDERVARTHERPROENTLISHTPRAGULVHINNI LASMFNFTELLSLAHRARFULFFROGANNISCHTPRESPSSKEMEGPG LELFGSPLSDYTAYSPVREDAHSVLISHIFHGRKFFTTTHIL LASMFNFTELLSLAHRARFULFFGARMCHEPSISPSSKEMEGPG LELFGSPLSDYTAYSPVREDAHSVLISHIFHGRKFFTTTHIL LASMFNFTELLSLAHRARFULFFGARMCHEPSISPSSKEMEGPGF AATHLBLVDERGCVPLSDPSSNRGGLOALTARTYGFPW AATHLBLVDERGCVPLSDPSSNRGGLOALTARTYGFPW AATHLBLVDERGCVPLSDPSSNRGGLOALTARTYGFPW AATHLBLVDERGCVPLSDPSSNRGGLOALTARTYGFPW AATHLBLVDERGCVPLSDPSSNRGGLOALTARTYGFPW AATHLBLVDERGCVPLSDPSSNRGGLOALTARTYGFPW ATHLBLVDERGVPLTDLKTMESVPRISPSKLOALLVON PPHOQALCAGERGUTTOLKTRUSPRINGERICHTCOLL TLAGAGEKLITTDLK				ł	VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHT.TPHAPPA
BTEVLSSDRKENALQTVGTGSPHODVALAILADGTULPTLIVFY RGQMDQPAMPDSILLARKEGYSDBLMSTKYMQKUTACO RSKGMLVMDCHRTHLSEVLANLGASSTLPRAVPGCSKIQDL DVCIKRYUNSHHKKWRGQARMADTACDSVULQLVLVMLGBV LGVYGCPELVQRSFLVASVLEGPGGNINSPTRYADHQCESLIAS LEGGLKISGENESSTPRPRSSPETTEPESHQLFEGESETTS PYGFERADLDLMEI 6136 1704 539 FGVPMALGGMSKRKBSVQEGENPDDGVRGSPPEDVYLGQVAS SLPRGEHHSRGGTGRLASLFSSLEPQIQEVYYPVPK\ESALASA DLEEZHHCKQGKKRNSQPGVKVADRKLLDDTEDTVVSQRKKIQ INGEERIKNERTVFVGNLPVTCKKKKLSFFKEYGGLESVERR SLIPAGGTISKLAAIKRKHEHDQKNINAYVVFKESAATQALK RNAQIADGFFIRVULASSTSSRNKRSVPVONLPYKVEBSATGK HPILDCGSIMAVRIVRDKMTGIGKOFGVVLFRNTDSVULALKINN SELMGRKLRVNGSVNKSKFKQONSMPKVGPKKOR 6137 141 2656 RAIKKRGCPGRGAIGSGPGQTGREGVEPERPAPEREKHPG MMMLIVAMCLAALLGLPGKAGGLGGHVS\IILAGGCLGDLAKK YUKGGLGVLVLDEAGRGSPGGGGREGVEBPGRANGPKKOR LGYRGMAPSHCAEHKDGFILQLGVYRGLKAEDVQALINDIENQ LGYRGGHBHSAQGLAVFBLOFFGESEMFRVDHIVLGKQAVAQIL PFREDONKRALDGLWNHHVERVELIMKETUABGGTGSHGAMLRVV LGKPFGHBHSAQGLAVFBLOFFTFSEMFRVDHIVLGKQAVAQIL PFREDONKRALDGLWNHHVERVELIMKETUABGGTSFFEETGV IRDVLQNILITENJTLVAMLDEHNUSSAEAVLRHKLOVFOGLEGL QRGSAVVGQYQSYSGVYRGLQKPDSFHSLTPFFAAVLHIDINL RMEGGYPFILMSGKALDBEWGVARILFKHLOVFOALRGL QRGSAVVGQYQSYSGVYRRGLQKDSFHSLTPFFAAVLHIDINL RMEGGYPFILMSGKALDBEWGVARILFKHLGVFOALRGL QRGSAVVGQYQSYSGVYRRGLQKDSFHSLTPFFAAVLHIININ RMEGGYPFILMSGKALDBEWGVARILFKHLGVFOALRGL QRGSAVVGQYQSYSGVYRRGLQKDSFHSLTPFFAAVLHIININ RMEGGYPFILMSGKALDBEWGVARILFKHLGVFOALRGL QRGSAVVGQYQSYSGVYRRGLQKDSFHSLTPFFAAVLHIININ RMEGGYPFILMSGKALDBEWGVARILFKHLGVFOALRGL QRGDEDLYDGGGGGDPDDPVLAAKYRSSELLISKL AND ISATAVBAVRRFGGPHILALGGGSSVALDGQLAKRAKGFFF QQQPGCLUPGGGGGDPDEPQVLAAKYRSSELLISKL AND ISATAVBAVRRFGGPHRANGSLDYLMKMGADGH TASLFPGSFTGLIGGGULVVLTTSPSQPHRRMSLSLJALLYLMYPF DAFIG ELHGELGSLASWTONLKSGVGHFSKLUFGRRTTCAL TDTSHLLSAVKGGEFFSLVGTRSLHELKKKEHFORRTTCAL TDTSHLLSAVKGGEFFSLVGTRSLHELKKKEHFORRTTCAL TDTSHLLSAVKGGEFFSLVGTRSLHELKKEHFFAFI TDTSHLLSAVKGGEFFSLAVGTRSLUFGRAFFTFANIK GALLATURAVRENTERTALGTRANGFCLGANLOWM ENKVLQTADISTARRESILSKFAFAFIGONLKGMGDGLEHEDLINKN ELHGREGDLGLAWNIKETTULKSTURDKHLDVVRDENKRELCANLVGM ENKVLQTADISTARRESILSKRTBAFTGOLBGLKKKLKEFFAFI Q	-				VAHTLPKDVAENAGLFIDFVQRQIHNODLPLSMIVAIDEIST,FI.
RSKOMLVMDCHRTHLSEEVLANLGASSTUPAVPAGCSSKIOPL DVCIKRIVENSHHKKWERQARMADIADEVLICUMVIGEV LGVIGICPELVQRSFLVASVLEGPGRINSPTRNADMOEBLIAS LEEGLKISGENESSTRPRSSPETTEPESHQLFEGESETES FYGFERADLDLMET FOVEMALEGMSKRKRKEVQUEGENPDGVRGSPPEDVRIGGVAS SLERGSHHSRGGTGRIASIFSSLEFOTQEVYYPVEK\ESALASA DLEBEHCKQGQKRKNSOPGVKVADRKILDDTEDTVVSQRKKIO INQEBERLKNERTVFVGNLPVKCNKEKKSFFKEYGGIESVERR SLIPASGTISKKLAAIKRKHHDQKNINAYVVFKESAAAGA DLEBEHCKQGGKRKNSOPGVKVADRKILDDTEDTVVSQRKKIO INQEBERLKNERTVFVGNLPYKVGKKKSFFKEYGGIESVERR SLIPASGTISKKLAAIKRKHHDQKNINAYVVFKESAATOALK RNGAGIADGFEIRVDLASSTSSDRNSFYKOMLPYKVBESAATOALK RNGAGIADGFEIRVDLASSTSSDRNSFYKOMLPYKVBESAATOALK HFLDCGSIMAVRIVRDWTGGKGFGYVLFBNTDSVHLAIKINN SELMGRKILVANSVNKEKFRQGNNFRLKNVGFKKRGKKKRKKRKKGKFKKRFKKFF SLIPASGTISKKLAAIKRKHHDQKNINAYVVFKESAATOALK HFLDCGSIMAVRIVRDWTGGKGFGYVLFBNTDSVHLAIKINN SELMGRKILVANSVNKEKFRQGNNFRLKNVGFKKFRQGLNFTSKT ABGHPKSLFIGHGAVLLKTKKKGQKKSGFKKORKK KHUNGGLEOGFFRANDLASTSSDRNSFALIKK HFLDCGSIMAVRIVRDWTGGKGFGYVFLFBNTDSVHLAIKINN SELMGRKINVACHALLEFRAGGIGFFRYPEERPPPRERRHFG MAMMILVAMCLAILLELGFKAQEIGOHGI ILLAGGGOLAKK YLWGGLEGGFFGVPLEFRAGALTARKGGGSMFKHAALES LSCFKLMAPSHCAHHDGVFLGKAQELGFREYDAILNINDLERQ LGHAGLREAGGIFFFFEUPPFAAVLHTLEKGAVAQGIL PFRQNRKALDGLMNRHEVERVEI INKETVDARGGTSFFEEGV IRDVLQNHLIFEVITUTAMEDJHNVSSAEAVLRHLLQVFQALRGL QRGSAVVGQYSSSCUPRELQKEDSFHLPFFAGVLHVILDINL RHEGYPFILMSGKALDERVGYARILFKNQACCVGSKKHMAAAGS OCLPRQLVFHIGHGDLGSPAVLVSRNLEPPLSPSKKRMEGPFG LALGGSPLSDYYAYSPVEREDABISVLLSHIFPRAGVLYHINL RHEGYPFILMSGKALDERVGYARILFKNQACCVGSKKHMAAAGS OCLPRQLVFHIGHGDLGSPAVLVSRNLEPPLSPSKKRMEGPFG LALGGSPLSDYYAYSPVEREDABISVLLSHIFPRAGVLYHINL RHEGYPFILMSGKALDERVGYARTLFKAGHTHATHYNAPHTYNLAM PVHLQQRLCABEDQGAHTYAREISALGANSFDLIVRLYHAWPT AATHHHUNDERCVPLSDBFSBRNGGGSSPVALHFQUATAHTXGFPW AATHHLMINDERCVPLSDBFSBRNGGGGSPVALHGURTFYTTHINL LASSMFRABETTLVSRVGHEPKKMPISGVLPHSGRUKMGFFFL TDTSHLLSAVKQERFSLVGVLTTSPSCHGRUSLSLDFLINGKGHFGRFTTCAL TLBAGEGLLJUTUTAKTESGVGRISGJCDSWKDMSPQLAEMIK FOSTVETWOQCSKKIKELKSRLCVJKAGGSDPLPBLHBDLHNER ELIKELGGSLASWTONIKERGOJTHATHUVDEDWALKEGOI HARGWBDLCLEVAIR RGGTEDRINGWCHDETSTREDGLIQGTTIS LDRRM	1			ļ	DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
DVC!RETVENPEHHKRMEGOREMADITACDSDULIQUIJUNIJUSEV LGVIGCPEHUQRSFILVASVILGOPUSINFRNADMOGELIAS LEEQLKISGENISESSTRPRSSPETIEPESIHQLFBGESETES PYGFERDLDIMEI 6136 1704 539 FGVWMALBGMSGREKREKSUGEGNPDDGVRGSPPEDYRLGQVAS SLPPGEHHSRGGTGRLASLPSSLBPOIQEVRYPYPK\BSALASA DLEEZHHOKQGQRENINGSPGWAVADRILIDDTEDTVVSGREKIQ INGEERLKNERTVFVGNLPVTCNKKKLKSFFKEVGLISEVRFR SLIPAGGTISKKLAAI KRRIHEDQRININAVVFKESSAATOALK RNGAQIADGFAIRWILAKSTSSRDKRSVFVGNLPYKVESSATEK RNGAQIADGFAIRWILASSTSSRDKRSVFVGNLPYKVESSATEK RNGAQIADGFAIRWILAKSTSSRDKRSVFVGNLPYKVESSATEK RNGAQIADGFAIRWILAKSTSSRDKRSVFVGNLPYKVESSATEK RNGAQIADGFAIRWILAKSTSSRDKRSVFVGNLPYKVESSATEK RNGAQIADGFAIRWILAKSTSSRDKRSVFVGNLPYKVESSATEK RNGAQIADGFAIRWILASSTSSRDKRSVFVGNLPYKVESSATEK RNGAQIADGFAIRWILASSTSSRDKRSVFVGNLPYKVESSATEK RNGAQIADGFAIRWILASSTSSRDKRSVFVGNLPYKVESSATEK RNGAQIADGFAIRWILASSTSSRDKRSVFVGNLPYKVESSATEK RNGAQIADGFAIRWILASSTSSRDKRSVFVGNLPYKVESSATEK RNGAQIADGFAIRWILASSTSSRDKRSVFVGNLPYKVESSATEK RNGAQIADGFAIRWILAKSKGQKNGATURAVVFKESSATER SELMFRKECOFGERGAIGSGFGPQRRFGRVFEERFAFPRERKHFG MANNILVAMCIA\LILOFBRAQELQHUS\LILABGCLGDLAKK YILMQG\LPQLYLDEAGRGSFSFHGAAITAPKQGQELMARALES LSCFKUMAPSHCAEHKDQFLQLSQYRQLKTAEDYQAINKDIERQ LQHAGLIRAGGISFYFTSUPFAYBULHVUMSCAFGFFFEEVGV IEDVUQNILTEVUTUVAHELPHAVUSAGRSFFFEEVGV IEDVUQNILTEVUTUVAHELPHAVUSAGRSFFEEVGV IEDVUQNILTEVUTUVAHELPHAVUSAGRSFFEEVGV IEDVUQNILTEVUTUVAHELPHAVUSAGRSFFEEVGV IEDVUQNILTEVUTUVAHELPHAVUSAGRSFFEEVGV IEDVUQNILTEVUTUVAHELPHAGUVUHUHININA REGGVFTLASSKALDERVGYARILFRRQBESSRUKMEGOPG LLAGSSAVVOQCASSRQVARERDAISVLLAHFRRKFFFITTENL LASMFWTPLLBSLAHKAPRLYPGGAEMGRLLDFEFSGGRLFFS QQCPFGLUFGGQCHAPBERDGGSSFVALFFGLATHATIN AM PPHLQQRLCAEBDGGAHTYAREISALGANSFDLAKHVAN ANTHHINDERCYPLSDBEDSFFGGLAHVTANLAVRINGTBLABLLSPLINGAKV ALVANGRMKREITTLVSRVGHEPKSBV ISGVLPHSGQLVWMDY DAPLG EFSKLTTRWQNAVGGVRQRGKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKQGERFSLVGTNSAGVRMSPQLARMIKQ ILBAGRULATUTURA ROGEIEDLTWVVPDWAVLKSQIIB HLHRQMSDLCLRVAIR ROGEIEDLTWVVPDWAVLKSQIIB HLHRQMSDLCLRVAIR ROGEIEDLTWVVPDWAVLKSQIIB HLHRQMSDLCLRVAIR ROGEIEDLTWVVPDWAVLKSQIIB HLHRQMSDLCLRVAIR ROGEIEDLTWVVPDWAVLKSQIIB LUBRNSNI	1				RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
LGYIGNCPELVQRSTLVASVLPGPDGNINSTTRADMQCELLIAS LEGULKISGHEGSSTPRRSSPETITEPESIHQLFGGESETES FYGFERADLDIMET FYGFERADLDIMET FYGFERADLDIMET FYGFERADLDIMET FYGFERADLDIMET FYGFERADLDIMET FYGFERADLDIMET FYGFERADLDIMET SLPRGEHHSRGTGRLASLFSSLEPQIQFVYVPVPK\ESALASA DLEEZHGXGGRRKNSQPGVKADRKLIDDTEDTVVSQRKKIQ INGEERKIKNERTVYVCNILPVICHKKKSFYKEYGGISSVERF SLIPAGGTLSKKLAAIKRKHPDQNINAYVVYKERSATGALK RNGQIADGFRIRVDUASETSSRKVYVONLDYKVBESATGALK RNGQIADGFRIRVDUASETSSRKVYVONLDYKVBESATGALK RNGQIADGFRIRVDUASETSSRKVYVONLDYKVBESATGALK RNGAQIADGFRIRVDUASETSSRKVYVONLDYKVBESATGALK RNGAQIADGFRIRVDUASETSSRKVYVONLDYKVBESATGALK RNGAQIAGGFRIRVBESVAVIKKKYGQKKSGRPKKQRKQR SELMGRKLAVMSSVANKEKPKQQNSVYVONLDYKVBESATGAL SELMGRKLAVMSSVANKEKPKQQNSVYVONLDYKVBESATGAL SELMGRKLAVMSSVANKEKPKQQNSVYVONLDAVKVBESATGALK AEGHPKSLFIGGRAVLLKTKKKGQKKSGRPKKQRKQR SELMGRKLAVBSVALLKTKKKGQKKSGRPKKQRKQR MNMMLIVAMCLA\LLGLGPGRGELGFSFFRAPFFRERKHPG MNMMLIVAMCLA\LLGLGPGRGELGFSFFBAPFFRERKHPG MNMMLIVAMCLA\LLGLGPGRGELGFSFFBAPFFRERKHPG LGLAFGRAGGIFFFSVPPPAVEDIARNINSSCRPDGGMLKAVLES LSCPKDMAPSKCALAFROQFICLSGVKTAEDVQALMKDIEAG LGLAFGREGGIFFFSVPPPAVEDIARNINSSCRPDGGMLKAVLES LSCPKDMAPSKCALAFROQFICLSGVKTAEDVQALMKDIEAG LGHAGLREAGGIFFSSPPAVEDIARNINSSCRPDGGMLKAVLES LEFFGDHBPSAQQLATELOTFFGSVTATGEVTSGVKTAGVAQQIL PFFDQNRKALDGLMNRHVERVEII IMKETVDARGGSLMKALLES LEFFGDHBPSAQQLAVARELICHTBRUAGKLDFFFSTSFFEYBY QCAPBGLVFHIGHGDLSSPALVSRNGRLLDFFSSTSFFEYBY QCAPBGLVFHIGHGDLSSPALVSRNGRLLDFFSSTLFFFAVILTHENL LASMMYPPLLESLAHKARPLYPGARGKLDLFFFSLOGARLFFFDL ANDIEATAVRAVRRPGGPIHLALSGSSFVALFGCDATAHYGFFR ARTHLMVDBRCVPLSDFESNFGLAMLLGGWRIPTYNINA AV AVLVWGRNKREITTLVSRVGHEPKKWPLSGVLPHSGQLVWYMDY DAFIG TOTSHLLSAVKGQERFSLVOTRSLIHELINKGVKDLCAMMING PGSTVETWOCCKKIKELGSRLOVLKAGSEDPLVILIGNGDDGH TASSFFSSFTALTGRAKGVAGGGCGRKKURLGCAMLUQM PRINLOGALDISTERMIETALRSCLESLKOVLKAGSEDPLARMING ELIKELGSLASMYTONLHELDTMALDFSNKLJCLARMING PRINLOGARDISTERMIETALRSCLESKYVVYDVCDGBCGGRRALGCOQD LQRDISCHAMSPALLITHVILVSDVAVYLKEQUE HIHRQMSDLCLRVATRARIESELSKFVVYDVCDGBGGGGRRALGCOQD LQRDISCHAMSPALLITHVILVSDVAVYLKEQUE LUDRINSULTATARIASELSKFVVYDVCDGBGGGGRRALGCOQD LQRD	1				RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
6136 1704 539 FYGEREADLDLMEI FYGEREADLDLMEI FYGEREADLDLMEI GERENDENGERFRESVEGEENPDEGGRAS PEDTYRLGQVAS SLPREGERHSRGGTGRLASLFSSLEPOIGPTVEVPK\ESALASA DLEEEIHQXQGGRRMSQPGVKVADRKLLDDTEDTVYDGRKXIQ INQEERRIKNERTVFVGNLEVTCNKKKLKSFFKFYGGISVBFR SLIPARGTISKKLAJKRKHFDQVALPNTDVGNLEVGRKXIQ RNGAQIADGFRIRVDLASETSSRDKRSVFVGNLDYKVERSAJEK HFLDCSIMAVRIVDLASETSSRDKRSVFVGNLDYKVERSAJEK HFLDCSIMAVRIVDLASETSSRDKRSVFVGNLDYKVERSAJEK HFLDCSIMAVRIVDLASETSSRDKRSVFVGNLDYKVERSAJEK HFLDCSIMAVRIVDRAMTGIGKGFVLPRITDSVHLAIKINN SELMGRKLRVMRSVNKEKFKQQNSOPRIKNVSKRKGGLMFTSKT AEGHPKSLFIGEKAVLLKTKKKGQKKSGRFKKRKX KROGLIADGFRIRVDLASETSSRDKRSVFVENDYSKRGGLMFTSKT AEGHPKSLFIGEKAVLLKTKKKGQKKSGRFKKRKKA KROGLIADGFRIRVDLASETSSRDMRSVFVENDYSKRGGLMFTSKT AEGHPKSLFIGEKAVLLKTKKKGQKKSGRFKKRKKA KROGLICHTUNALLTALLLALLALLALLALLALLALLALLALLALLALLAL	1				DVCIKRIVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
6136 1704 539 FOURMALEMBIGKRIKRSVQBGENPDDJVRGSPPEDYPLGQVAS SLPRGEHHSRGTGRLASLPSLEPOLOPVYVPVPK\ESALASA DLEELHOKQGGKRKKNSOPGVWADKKILDTEDTVVSGRKKIQ INQEERLKNERTVFVUNLPVTCNKKKLKSFFKEYGGLISVMFR SLIPABGTLSKKLAAIRRKHPDQKNINAYVVFKESAATQALK RNSAQIADDFRIFTUNLSSETSSREVYVONLPYVKMESAATQALK RNSAQIADDFRIFTUNLSSETSSREVYVONLPYVKMESAATQALK RNSAQIADDFRIFTUNLSSETSSREVYVONLPYVKMESAATQALK RNSAQIADDFRIFTUNLSSETSSREVYVONLPYVKMESAATQALK RNSAQIADDFRIFTUNLSSETSSREVYVONLPYVKMESAATQALK RNSAQIADDFRIFTUNLSSETSSREVYVONLPYVKMESAATQALK RNSAQIADDFRIFTUNLSSETSSREVYVONLPYVKMESAATQALK RNSAQIADDFRIFTUNDAMTIGKGGYVLFBRITSVHLALKINN SEMMERKERVSREVNKSKPKQOKKSGRFKKGKKX ABCHPKSLFIGEKAVLLKTKKKGQKKSGRFKKGKKX ABCHPKSLFIGEKAVLLKTKKKGQKKSGRFKKGKKX ABCHPKSLFIGEKAVLLKTKKKGQKKSGRFKKGKKX ABCHPKSLFIGEKAVLLKTKKKGQKKSGRFKKGKKX YLMGGLLFQLADGLAGSGFPGPGRFRFAVPERERKHFG MWNMLIVAMCLA\LLGLPGKAGLIGSFPFAPPRERKHFG MWNMLIVAMCLA\LLGLPGKAGLIGSFPFAPPRERKHFG MWNMLIVAMCLA\LLGLPGKAGLIGSFPFAPPRERKHFG MWNMLIVAMCLA\LLGLPGKAGLIGSFPFAPPRERKHFG LLGFRAMPSKLCARHKOQFLOLGSGUKTATEDYGAGLVAYOLL PFRADOMRALDGLWNRHHVERVEIIMKSTUDASGRFSFYEFYGV IRDVLOMLITEVILLVAMELPHNVSSAAVLRHKLQVFOALTARL RREGYPFILMSGKALDERVGYARILFRNQACCUGEKKMAAAQG OCLPRQUMHIGGGLSPAULVSRRPLDLHFRINGACCUGEKKMAAAQG OCLPRQUMFIGGGLSPAULVSRRPLDLHFRINGACCUGEKKMAAAQG OCLPRQUMFIGGGLSPAULVSRRPLDLHFRINGACCUGEKKMAAAQG OCLPRQUMFIGGGLSPAULVSRRPLDLHFRINGACCUGEKKMAAAQG OCLPRQUMFIGGGLSPAULVSRRPLDLHFRINGACCUGEKKMAAAQG OCLPRQUMFIGGGLSPAULVSRRPLDLHFRINGACCUGEKKMAAAQG OCLPRQUMFIGGGLSPAULVSRRCLLDFRINGALDFFTENL LASMFWPTLLESLAHKAPRLYPGGRLDLFFSPLSSRLFFFFT OQQFBOLVPGGFGCPMSDFOVLAKXRSSLVSAMSEELISKL AADIBAATAVRAVRRPRGPGPBPMSDFOVLAKXRSSLVSAMSEELISKL AADIBAATAVRAVRRPGGPGPMSDFOVLAKXRSSLVSAMSEELISKL AADIBAATAVRAVRRPGGBGSPGRAVGRANGLLDFWRMSLGLISKL AADIBAATAVRAVRRPGGGGRFSVLVATTSSGRAMPKRMSLGLAMMYDV PVHLQQRLCAEBDQGAHTYARSISALGAMSSFDLVLLGMGADCHG TASSFPGSFTGLIGGGLVVTTTSSGRAMPKRMSLGLAMMYDV AVLVVGGRMRETTLUSSRVGRAMSLCAMLVOM FOSTVETWOCKKK KELKSSLOVLKAGSGDDVLKERDLEMMYN PVHLQQRLCAEBOGAHTYACUSTAMVVFREKKKELCAALVOM FOSTVETWOCKKK KELKSSLOVLKAGSGDDVLKAGLDAMIGCL LLGRIBGCHALDTTDLKKELLTHV	1				LEVOLVI SCHUSPOONDERDOODELIAS
FOVEMALEGNISKAKRESSUSSCENPDDGVRGSPPEDYRLGGVAS SLEPEGHHSRGGTGRLASLFSSLEPUGYVPVEVK KSALASA DLEEHHOKGGKRKNSGPGWANDRILLDDTEDTVVSGRKRIQ INGEERALNERTVFVGRLFVTCKKKLKSFFKEYGGLESVEFR SLEPAGGTANDAIKK RINGAGTADGFRTRVDLASETSSRDKRSVFVGRLDYKVBESAATOALK RNGAGTADGFRTRVDLASETSSRDKRSVFVGRLDYKVBESATCAL RFILDCSSIMAVBUVEVKESAATCAL RRHGKTUNDLASETSSRDKRSVFVGRLDYKVBESATCAL RHGKTUNDERSTENDKRSVFVGRLDYKVBESATCAL REGENERALBVMBSVNKEKFKQGNSNDPRLKOVSKFKQGLNFTSKT AEGHPKKLFTGEKAVLLAFTKKGKKKSGRKSGFKKGRKGK RNGAGTADGFRTRVDLASETSSRDKRSVFVGRLDFYSKT AEGHPKSLFTGEKAVLLAFTKKGGKKSGFRKGRKGK RNGAGTADFRCGSFFACHTKORGKKSGFRKGRKGK RNGAGTADFRCGSFFACHTKORGKKSGFRKGRKGK RNGAGTADFRCGSFFACHTKORGKKSGFRKGRKGK RNGAGTADFRCGSFFACHTKORGKKSGFRKGRKGK RNGAGTADFRCGSFFACHTKORGKT RAERKRECGFGRGRGALGSFFOCHREKORGK RNGAGTADFRCGSFFACHTKORGKT RAERKRECGFGRGRANGENGCHAST RAERKRECGFGRGRANGENGCHAST RAERKRECGFGRGAMERV LEKFFGHDHSSAGGLFFSVDLFOLASITATE RNGACCOGLMAKALES LSCFKDMAPSHCARHKOCFLOLASY RNEAMLY RAERGFT RNGACCOGLMAKALES LSCFKDMAPSHCARHKOCFLOLASY RNEAMLY RAERGFT RNGACCOGLMAKALES LSCFKDMAPSHCARHKOCFLOLASY RNEAMLY RAERGFT RNGACCOGLMAKALES LEKFFGHLHSSAGT RNEAMLY RAERGFT RNGACCOGLMAKALES LEKFFGHLHSSAGAVAN RNEAMLY RNGACCOGLMAKALES RAERGFT RNGACCOGLMAKALES RAERGFT RNGACCOGLMAKALES RAERGFT RNGACCOGLMAKALES RAERGFT RNGACCOGLMAKALES RAERGFT RNGACCOGLMAKALES RNGACCOGLMAKAL	1			•	EVGERRADI DI MET
SLPRGEHHRGGTGRIASLFSLEPGIQETYVPVPK\BSALASA DLEEEHHQKGGGKRNSOGPGWADRKILDDTEDTVSQRKKQ INQEERLINGETTUFVGRILPVTCMKKLKSFFKEYGQIESVWFR SLIPAEGTISKKLAAIKKHIPPQKNINAVVVFKESAATQALK RNGAQIADGFRIRVDLASETSSRKRSVFYGRILPVTQMESATGALK RNGAQIADGFRIRVDLASETSSRKRSVFYGRILPVTQMESATATQALK RNGAQIADGFRIRVDLASETSSRKRSVFYGRILPVTQMESATATQALK RNGAQIADGFRIRVDLASETSSRKRSVFYGRILPVTQMESATATQALK SELMGRKLEVMBSVNKEFKGOGNSPPLKNVSRFYGQINFTSKT AEGHPKSIPIGRKAVLLKTKKKGGKKSGRFKKQRKQK AEGHPKSIPIGRKAVLLKTKKKGGKKSGRFKKQRKQK RALRKRCGFGRGADIGSGFGPQRGRGRVPTERPAPPERERHFG MMMLIVAMCLA\LLGIPGKAGGLGGHVS\IILAGGIGDLAKK YLMQGLIFGLYLDEAGRGHSFSFHGAALTAFRQGGEMAKALES LSCPKDMAPSHCABHKODFIGLGYRQLKTAEDYOALMKDIEAQ LCHAGLREAGGIFYFSVBPPAYEDIARNINSSCRPGRGAMLRVV LEXFPGDNRKALDGLMNRHHVERVELIMKETVDAEGRGAMLRVV LEXFPGDNRKALDGLMNRHHVERVELIMKETVDAEGRTSFYEEYGV IRDVLQNILITEVLTLVAMELPHNVSSAEAVLRHKLQVFOALRGL QRGSAVVGYQGYSSSGQVRRELRGSFHSLTPTFAGVLVHIDNL RHEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHMAAAQS OCLPRQLVFHGHGDLGSFAVLVSRNILFRSLPSSWKEMGOPPG LRLFGSPLSDYYASFPVREDABISVLLSHIFHGRKNFFITTENL LASMFWFPLLESLAHRAFRLYBGGAENGRLIDFEFSSGRLFFS QQDFBGLVPGGFGGPMSDFPOVLARYRSSSLVSABSEELISKL AMDIBATAVRAVRRFGQPHLALSGGSSPVALFQQLATAHGFFN AHTHLWLVDERCVPLSDPBSNYCGLAHLLDVRIFYNIN\AM PVHLQGRLCAEEDGGAHIYARISTSLIGANSSFDLVLLGMGADGH TASIFFOSFTSLDGEQLAVVLTTSPSCPHRRMSLSLPLINGAKY ALVMGRNKREITTLVSRVGHEPKKWPISGVLPHSQQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWODFTTSVENLFR L TITSHLLSAVKGGRFSLVQTRSLLHELKNKEHHFQRRFTTCAL TLEAGEKLLLTTDLKYRGERSLVQTRSLLFBCRNITWVVPKEQIE HLHRQMEDLCLRVATIKQSEIDRLNTMVVPRENNELCAMILVQM ENKVLQTADISIEMHEKLQKDCMEEINLFSENKLGLKGMGDQL IKASNKSRAABIDDKLNKINDBWGHLFDVIGSRVKKLKETPAFI QQLDKKNSNLRTAKLAR IESELSKPVVYDVCDDQEIQKRLARGOD LQRDIEQHSAGVESVFNICDVILHIBSDACANSTECDSIQQTTRS LDRRMNICAMSMERRMKIEETWRLMQKFLDDYSRFEDMLKSAR RTAACROSSEVLYTSAKEELKSRFOROHERLICDELINGVY	Γ	6136	1704	539	
DLEEEHGKGGGKRINSOGGWAVADRILLDTEDTUVSGRXIQ INQEERRIKNETIVVGKLPUVGKKKLKSFFKEYGGIESVERR SLIPAGGTI,SKKLAAIKRKIHPDQRNINAYVVFKEESAATQALK RNGAQIADGFRIRVDLASETSSRDKRSVFGMLPYKYEESAATQALK RNGAQIADGFRIRVDLASETSSRDKRSVFGMLPYKYEESAATQALK RNGAQIADGFRIRVDLASETSSRDKRSVFGMLPYKYEESAATQALK RNGAQIADGFRIRVDLASETSSRDKRSVFGMLPYKYEESAATGALK SELMGRKLRVMBSVNKEKFKQONSNPLKNVSKPKQGLOFTSKT AEGHPKSLFIGRKAAVLLKTKKKKSGFFKKQRKQK AEGHPKSLFIGRKAAVLLKTKKKKKSGRFKKQRKQK MAMMLIVAMCLA\LLGLPGRGHSPGREGRPAPPERRHFG MAMMLIVAMCLA\LLGLPGRGHSPFGRALTAPKQGGLMAKALES LSCPKDMAPSHCABHKDQFLQLSQVRQLKTAEDYQALMKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSCRPGGRAMLRVV LEKPFGHDHFSAQQLATELCTFFEEMWYDHYLJKGQAVAQIL PFRDQNRKALDGLWNRIHHVERVEIINKETVABEGTSFYBEYGV IRDVU,ONLITEVLIVAMELPHAVUSSAEAVLHKLQVFQALRGL QRGSAVVGQYQSYSEQVRELQRPDSFHSLFFTFAGVLVHIDNL RWEGYPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRGLVFHIGHGDLSSPAVLVBHIFFPSLPSSWKEMEGPPG LALFGSPLSDYYAYSPVRERDAHSVLLSHIFFGRRNFFITTENL LASWMFWPPLLESLAHKAPRLYPGGABNGRLLDFFFSGGLFFF QQQPEQLVPGGGFGPPMSDFQVLRAKYRESSLVSAMSGEELISKL ANDIBATAVRAVRRFGGFHLALSGGSSVALFQGLATAHVGFPW ATHLMIJVDERCVPLSDPESNFGQAHLGHVURTYPYNTH\AM PVHLQQRLCABEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKY AVLVMGRMKREITTLVSRVGHEPKKKPISGVLPHSGQLVWMDY DAFLG 6138 4587 934 FSKKITDRWQNAVQGVRQRRGDVDGLVRQWQDFTSVENLFRFL TDTSHLLSAVKGQERFSLVQTRSLHELKKKEHFQRRRTTCAL TLEAGERLLLTTDLKTKESSVGRISQLQDSWKMMEPQLABMIKQ FQSTVETWMDQCEKKIKELSRLOVAKAGSBPDLPELHEDHNEKE ELIKELSGSLASHTONLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIR KQEIEBRLNTWVFNEKNKELCAMLVQM ENKVLQTADISIEBMIEKLQKDCMEETINLSSKKLGLKGMGDQL IKASNNSRAABIDDKINKINDRWGHLFDVIGSRVKLKETPRFI QQLDKKNSNLRTHLARIBISSLSKPVVDVCDDQGEIQKRLAEQOD LQRDIEQHSAGVESVFNICDVLLHDSDACANTEECDSIQQTTRS LDRRMRNICAMSMERRMILEETWRLWQKFLDDYSRFEDULLSGAE ENXROASEFLYSTAKEELERRETTSLUSGRVENDELGEGOL LQRDIEQHSAGVESVFNICDVLLHDSDACANTEECDSIQQTTRS LDRRMRNICAMSMERRMKLEETWRLWQKFLDDYSRFEDULLSGAE ENXROASEFLYSTAKEELERRETTSLOKGTLOELINNOY	1				SLFRGEHHSRGGTGRIASLFSSLFDOTORUVURUUV TGALAGO
INGEBERLKNERTYPVONLPYTCHKKKLESFFKEYGQIESVEFR SLIPEAGTISKKLAAIKRKHAPOKNINATVYVYKEESAATQALK RNGAQIADGFRIRVDILASETSSRDKRSVFVONLPYKVBESAIEK HFLDCGSIMAVRIVDILASETSSRDKRSVFVONLPYKVBESAIEK HFLDCGSIMAVRIVDILAMIGIGKGFGYVLPENTDSVHLALKINN SELMGRKLRWMRSVNEKFKQNSMFRIKNVSPKYGKINFTSKT ABCHPKSLFIGERAVLLKTKKKGQKSGRFKKQKKOF RALKRKRCGGFGRGAIGSGGPRGRGTWFERPAFPRERKHFG MMMILIVAMCLA\LLGLPGKAQELQGHYS\IILAGEGLGDLAKK YLWQG\LFQLYLDEAGGGBFSFHGAAATTAPKQGQELMAKKALES LSCFKUMAPSHCAEHKODF\USGYVGLKTAEDVQALNKOI LEAQ LCHAGLREAGGIFYFSVPPFAVEDIAMINSSCRPGPGAMLRVV LEKPFGHDHPSAQQLATELGFPQREEMYRVDHYVJGKQAVAQIL PFRQDNKKALDGLWNRHVERVEIIMKETUDABGRTSFYBEYGV IRDVLQNILITBVLTLVAMELPHNVSSABAVLRHKLQVFQALRGL QKGSAVVGQYQSYSSQVRELGKPDSFHSLIPTFAGVLUWI HDNL RMEGVPFILMSGKALDERGVGATILFKNQACCVQSEKHWAAAQS CCLPRGLVFHIGHGDLGSPAVLVSRNLFRPSLPSSKEMBGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESIAHKAPRLYPGGABNGLLDFEFSGGLFFS QQCFGLVPGFGGPGPMPDGFQVLRAKYRESSLYSAMSGELISKL ANDIBATAVRAVRRPGGGPHLALGGGSSPVALFQQLATAHYGFPW AHTHLMLVDERCVPLSDPESNFGQLQAHLLQHVIFYYNIH\AM PVHLQGRLCAEEDGGAHLYAREISALGANSSFDLVLLGMGADCH TASSFPOSFTGLDGEQLVVLTTSSSQPHRMSLSJPLINRAKKV AVLVWGRNKKRITTLVSRVGHEPKKWPISGVLPWWYDDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWGDFTTSVENLFRFL TDTSHLLSAVKGGRFFSLYGTRSLHELKNKEIHFGRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDWSMMBPGLAEMIKQ PQSTVEFWDQCEKKIKELKSRUVKRSEIHFGRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLOWWYMOYPHENKRELCAMLVQM ENKVLGTADISIEBEMIEKLQKDCMEBINLFSSNKLQLKGMGDQL IKASNKSRAJBIDDKLNKINDRWGHLFDVIJGSRVKKLKETPAFI QQLDKNSNLRTRLARIESELSRUVVYDVCNDQEGICKRLAEQOD LQRDIEQHSAGVESVFNICTUVLLAHDSDACAMSTECDSIQQTTRS LDRNMRNICAMSMERBMKLEETWRJUKFLDDJSRFBBWLKSAB RTAACROSSEVLYTSASELEKEPAGDOLDDFSRDWLKSAB	1				DLEEEIHOKOGOKRKNSOPGVKVADRKILDDTRDTVAGORZETA
SLIPASGTISKKLAAIKRIHPOOKIINAYVUPKEESAATOALK RNGQIADGFRIPVOLASETSSRDKRSVPVGNLPYKVBESAIEK HPLDCGSIMAVRIVRDKMTGIGKGFGYVLFBNTDSVHLALKINN SELMGRKLRVMRSVNIKEKYQQNSPFRLKVUSKPKQGLNFTSKT AECHPKSLFIGEKAVLLKYKKKGKKSGRKKKORKOK AECHPKSLFIGEKAVLLKYKKKGKKSGRKKORKOK AECHPKSLFIGEKAVLLKYKKKGKKSGRKKORKOK AECHPKSLFIGEKAVLLGURKKGGKKSGRFKKORKOK MINNLIVAMCLA\LLGLPGKAQELGYPERPAPPRERKHPG MINNLIVAMCLA\LLGLPGKAQELGYPSEPPAPPRERKHPG MINNLIVAMCLA\LLGLPGKAQELGYPSEPPAPPRERKHPG MINNLIVAMCLA\LLGLPGKAQELGYPSEPPAPPRERKHPG MINNLIVAMCLA\LLGLPGKAQELGYPSEPPAPPRERKHPG LSCPKUMAPSHCAEHKOQFLQLSQYRQGEKABDYGGEMAKLES LSCPKUMAPSHCAEHKOQFLQLSQYRQGEKABDYGGAMLRVV LEKPFGHDHFSAQQLATELGTFFGEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWRRHVERVEIIMKTUDAGGRTSFYREYGY LEKPFGHDHFSAQQLATELGTFFGEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWRHHVERVEIIMKTUDAGGRTSFYREYGY GRGSAVVGGYQSYSEQVRRELQKPDSFHSLTPTFAGULVHIDNL RMEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSFAVLVSRNLFRESLPSSWKEMBGPPG LALFGSPLSDYYAYSPVBERDAHSVLLSHIFHGRKWFFITTENL LASWMFWFLLESLSLAHKAPRIYPGGABNGKLIDFEFSSGRLFFFS QQOPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRPRGGPHLALGGGSPVALFQOLATARYGFFW AHTHLWLVDEEKCVPLSDPESFRGQHLAHGAGSPVALFQOLATARYGFFW AHTHLWLVDEEKCVPLSDPESFRGQLOAHLQHVIFYYNIH\AM PVHLQQRLCAEEDGGAHYAREISALGAMSSFDLVLLGMGADGH TASLFPQSFTGLDGGQLVVLTTSSPGPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVCHEBYKKWPISGQLWYMDY DAFLG FSKLTDBWQNAVGGVRGKGDVDGLVRQWODFTTSVENLFFFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRTTTCAL TLEAGERLLLITTDLKYKESVGRISGLODSWKDMSPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLOTHKADLTHVLVEDVMYLKEQIE HLHRQWEDLCLRVAIRKQEEDGLONKHELOTHMENKELCAWLVQM ENKVLGTABISIEMHIEKLQKOMEBINLFSSNKLQLKQMGPQL IKASNKSRAAEIDDKLNKINDRWHLFDUGSRVKKLKETPAFI QQLDKNNSNLRTHLARIESSLSKPVVYDVCDDGEIQKRLAEQQD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWNICAMSSERMKLEETWRJUKFLDDYSKFEDWLKSAB RTAACPNSSEVLYTSSAKELKERAFGROGHERLTOLBLINKGSAB RTAACPNSSEVLYTSSAKELKERAFGROGHERLTOLBLINKOY	1				INQEEERLKNERTVFVGNLPVTCNKKKLKSFFKEVGOIFGVDER
RNGAQIADGFRIRUDLASETSSRDKRSVFVGNLPYKVEESALEK HFLDCGSIMARRITURDATTGIGKGFGVLFRNTDSVHLALKINN SELMGRKIRVMRSVNKEKFKQQNSNFRIKRVSKPKQGINFTSKT ABGHPKSLFIGERAVLLKTKKKGKKSGRFKKGKKOK RALPKRRCGGRGRGALGSPORFGGRVEEFRAPPRERKHPG MINNILVAMCIA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQIYLDEAGRGHSFSFHGAALTAPKQGQELMARALES LSCPKDMAPSHCAEHKDQFTQLSQYRQLKTAEDYQAINKDIEAQ LQHAGLREAGGIPYFSVPPPAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFGEEMYRVVHIJCKQAVAQOIL PRRDONKKALDGLWNEHHVERVEIIMKETVDABGRTSFYKEYGV IRDVLONHITEVITLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQVQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNIL RWEGVPFILMSGKALDERWGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRHIFRPSLPSSWKEMEGPPG LELIGSPLSDYAAYSPVRERDHISVLISHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFFSSGRLFFS QQCPBQLVPGGPGFWPGDFQVLRAKYRSSSLVSAWSEELISKI ANDIBATAVRAVRRFGQFILALBGGSSPVALFQOLATARYGFPW AHTHLWLDERCVPLJDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASSFPGSPTGLIGGEQLVVLTTSPSQPHRKRMSLSIPLINRAKKV AVLVUGRMKREITTLVSRVGHEPKKWPISGVLPHSQQLVWYMDY DAFLG 6138 4587 934 EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLVQTRSLHELKNKEIHFQRRRTTCAL TLEAGEKLLITDLKTKESVGRISQLQDSWKDMEPQLAEMIKQ PQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLEPLHEDLHNEK ELIKELGSLASWTONLKELQTMKADITHVLVEBVWVLKEQIE HLHRQWEDLCLGNVAIR KGEIBDLNTWVFPBEKNELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENGLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWGHLFDVIGSRVKKLKETPAFI QQLDKNNSMLRTWLAR IESKPVVDVDCDDGIQKRLAEQQD LQRDIEGHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWELWGFLDDYSGFDWLKSAB RTAACNSSEVLVTSAKEELKRFEAFOROHERITOLEI INKOY	1	i			SLIPAEGTLSKKLAAIKRKIHPDOKNINAYVVFKEESAATOALK
HFLDCGSIMAVRIVDEMTGIGKOFGVLERNTDSVHLALKINN SEEMGRILRWARSUNKEKQONSNPRIKNVSKPKQGINFTSKT AEGHPKSLFIGEKAVLLKTKKKGQKSGPKKRQKCK RALKKRKCGFGRRGALGSGFGFGRFGRVEEERPAPPRERKHFG MMMLIVAMCIAL LLGLIFGAGLIGGHUSY, I LLAGSGLGDLAKK YLWGGLIFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES LSCPKDMAPSHCARHKOQFIQLSGYRQKLKTBEDYQALNKDIEAG LCHAGLREAGGIFYFSUPPPAYBDIARNINSSCRFGFGAMLRV LEERFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDOMKKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGY IRDVLQNHLTEVLTLVAMBLPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGYQSYSEQVREELQKPDSFHSLTFTFAGVLVHIDNI RREGYFFILMSKGALDERVGYARILFKNQACCVQSKKHWAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLSHIFHGRKNFFTTTERL LASMFWFTLESLHKKAPRLVFGGAENGRLDFFFSSGRLFFS QQOPEGLVPGGFGFBMPSDFQVLRAXYRSSLVSAWSEELISKL AMDIEATAVRAVRRFGGPHLALSGGSSPVALFQQDATAHYGFPW AHTHLWLVDERCVPLSDESNPGGLQAHLLGHURTPYYNHIN\AM PVHLQQRLCAEEDQCAHIYARSISAIGANSSFDLVLLGKGADCH TASSLFPGSFTGLDGSGLVVUTTSPSQPHRMSLSLPLINGAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWMDY DAFIG 6138 4587 934 EFSKUTDRWQNAVQGVRQRKGDVDGLVRQWDFTTSVENLFRFL TDTSHLLSAVKGQRFFSLVQTRSLHHELKNKEIHFQRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPGLAEMIKQ PQSTVETWDQCEKKIKELKSLQVLKAGSEDPLPEHLHDLHMEK ELIKELGSLASWTONLKELQTMKAKELGTMKKOPEDLEHREG ELIKELGSLASWTONLKELQTMKAKELGAMLVQM ENKVLQTADISIEBMIEKLGRACHGEINLTWVVFMEKNKELCAMLVQM ENKVLQTADISIEBMIEKLGRACHGEINLTWVFMEKNKELCAMLVQM ENKVLQTADISIEBMIEKLGRACHGEINLFSENKLQLKQMGDQDL IKASNKSRABEIDDKLNKINDRWGHLFDVIGSRVKKLKETPAFI QQLDKNMSNLRTMLARIESKFVVDVDCDQEIOKRLAEQQD LQRDIEGHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWNICAMSMERRMKIEETWELWGFLDDVSRFDWLKSAB RTAACNSSEVLVTSALEGELRFAFFOROHERITOLEI INKOY	ı				RNGAQIADGFRIRVDLASETSSRDKRSVFVGNLPYKVRESATEK
SELMGRILRVMRSVNKEKFKQONSFRILKNVSKPKQOLNFTSKT AEGHPKSLF1GEKAVLLTKKKGQKKSGRPKKQRKQK GRACH SELF1GEKAVLLTKKKGQKKSGRPKKQRKQK MINNLTVAMCLA\LIGLFGKAQELGGHVS\IILAGEDLGDLAKK YLWGG\LFOLYLDEAGGHSFSFHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKD1EAQ LCHAGLREAGGIFYFSVDPFAYFDIARNINSSCRPGPGAWLRVV LEEKPFGHDHFSAQQLATTLGATELGTFFQEEWHYNDHYLGKQAVAQIL PFRDQMRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVITLVAMELPHNVSABADVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVGRELQKPDSFISLTPFFAQVLVHIDNL RMEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLFRQLVFHIGHGDLGSFAVLVSRNLFFRSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVFRDAHSVLLSHIFHGRRNFFITTENL LASWMFWTFLLBSLAHKAPRLYPGGAENGRLLDFFFSSGRLPFS QQQPEQLVPGPGPGPPMPSDFQVLRAKVRESSLVSAWSBELISKL ANDIBATAVRAVRRFGQFHLALSGGSSFVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLQHVRIPYYNIH\AM PVHLQGRLGAEDQGAHIYAREISALGANSSFDLVLLGGGADGH TASLFPQSFTGLDGEQLVVTLTTSPSQFHRKMSLSLPLTNRAKKV AVLVVGRWKREITTLVSRVGHEPKKWPISGVLPHSQQLVWYMDY DAFILG 6138 4587 934 EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKQGERFSLVQTRSLHELKMKEHFQRRTTCAL TLEAGEKLLLTDLLXTRESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPEHEDLHNEK ELIKELEGSLASWTONLKELQTWADLTRRIVLVEDVWAVLKEQIE HLHRQWEDLCLRVAIR KORIEDRLNTWVYBENKRELCAWLVQM ENKVLQTADISIEBMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAABEIDDKLNKINDRWQHFDVUSGSVKKLKETFAFI QQLDKNMSNILTWLARIESELSKPVYTDVUDDGEIGKRLABQQD LQRDIECHSAGWESVFNICDVILHDSDACANETECDSIQQTTRS LDRRWRNICAMSWERRMKIEETWRLWGKELDDYSRFEDWLKSAB RTAACPNSSEYLYTSAKBELKRFLAPFLAFDURLKSAB RTAACPNSSEYLYTSAKBELKRFFAFFORGURKSAB		l			HFLDCGSIMAVRIVRDKMTGIGKGFGYVLFENTDSVHLALKINN
6137 141 2656 RALKKRRGGERRGALGSGPFQRRGPRUPEERPAPPRERKHPG MWMLIVAMCLA\LLGLPGKAQELQGHUS\11LAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSHGAALTAPKQGOELMAKALES LSCPKDMAPSHCABHKDQFLQLSQYRQLKTAEDYQALMKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHSAQQLATELGTFGEEMYRVDHYLGKQAVAQIL PFRDQMKKALDGLWMRHHVEVFFJEEMYRVDHYLGKQAVAQIL PFRDQMKKALDGLWMRHHVEVFFJEEMYRVDHYLGKQAVAQIL RREGVPFILMSGKALDGLWRHFUSPFSEEMYRVDHYLGKQAVAQIL RREGVPFILMSGKALDGLWRHFUSPFSEEMYRVDHYLGKQAVAQIL RREGVPFILMSGKALDGLWRHFUSPSHSLTPTFAGULWHIDML RREGVPFILMSGKALDGLWSRNJFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRRNFFITTENL LASMFWTPLESLAHKAPRLYPGGAEMGRLLDFFSSGRIFFS QQQFBQLVPBGGGPMSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRFGCPHLALGGGSSPVALFQQLATAHYGFPW AHTHLMLUDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH AM PVHLQGRLCAEBDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSFTGLDGGLUVULTTSPSQPHRRMSLSLPLLMRAKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSQLVWYMDY DAFLG 6138 4587 934 EFSKLTDRWQNAVGGVRQRKGDVDGLVRQWGDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYGTRSLHELKNKEHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISGLQDSWKDMEPGLAEMIKQ FQSTVETMDQCSKKIKELSSRLQVLKAQSEDPLELHEDLHNEK ELIKELEQSLASWTONLKELQTMKADLTRHVLVEDVWVLKEQIE HLHRQWEDLCLRVAIRKGSIEDRLNTWVVPNENKBELGWLVYQM ENKVLGTADISIEBMIEKLQKDCMGEINLFSBKLQULKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNNSNLETWLAR ISEELSKPVVYDVCDDGEIGKRLABQOD LQRDIEGHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIESTWRLWGKELDDYSRFEDWLKSAB RTAACPNSSEYLYTSAKBELKRFEAPFGOIHRELTOLELINKOY	1	ł			SELMGRKLRVMRSVNKEKFKQQNSNPRLKNVSKPKOGLNFTSKT
MANNELIVAMCIA-\LIGHPGKAQELQGPUS-\IILAGEOLGDLAKK YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES LSCFKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALMKOIEAQ LCHAGLEAGGIFFYSVPPFAYEDIARNINSSERPBGAMLRVV LEKPFGHDHPSAQQLATELGTFFQEEEMYRUDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETUDAEGRISFYEEYGV IRDVLQNHLTEVLTIVAMELPHNVSSAEAVLRHKLQVFQALRGL ORGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS OCLPRQUVPHIGHGDLGSPAVLVSRNLFRSELDSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLDFEFSSGRLFFS OQQFBGLVPGDFGPDMPDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQPHLALSGGSSPVALFQOLATAHYGFFW AHTHLWLVDERCYPLSDPESNFGGLQAHLLQHVRIPYYNIH\AM PVHLQGRLCAEEDQGAHIYAREISALGAMSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLVHYMDY DAFLG 6138 4587 934 EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKQQERFSLYQTRSLHHELKNKEIHFGRRRTTCAL TLEAGEKLLLTDLKKTKESVGRTISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPEHEDLHNEK ELIKELEQSLASWTONLKELQTMKADLTRHVLVEDMYLKEQIE HLHRQWEDLCLRVAIR KQEIEDRLNTWVFMEKNKELCAMLYQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWGHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESSLSRPVYDVDCDDGEJQKRLAEQQD LQRDIEQHSAGWSVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKILEETKRLWGKFGOLGKRLAEQQD LQRDIEQHSAGWSVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKLEETKRLWGKFGOLGKRAEQQD LQRDIEQHSSEVLYTSAKKELKREKFEAFGROIHERIOGLEINKOV	\vdash	6137	7/1	2656	AEGHPKSLFIGEKAVLLKTKKKGOKKSGRPKKORKOK
TYLWGG\LFQLYLDEAGRGHSFSFHGAALTAPKGGGELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALMKDIEAQ LQHAGLREAGGIFYSEVPPFAYEDIARNINSSCRPGGAMLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHVERVETIMKETVDABGRTSFYEEYGV IRDVLQNHLTBYLTLVAMBLPHNVSAEAVLRIKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPILLESLAHKAPRLYPGGAEMGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPBDFQVLRAKYRESSLVSAMSEELISKL ANDIEATAVRAVRRPGQFHIALGGSSFVALFQOLATHAYGFPW AHTHWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQGLCABEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSFTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFIG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGGERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKSSVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLEELHEDLHNEK ELIKELEGSLASHTONLKELQTWKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEBMIEKLQKDCMEEINLFSENKLQLKGMGDQL IKASNKSRABEIDBKLMKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESESSKPVYYDVCDDQEIQKRLAEQQOD LQRDICHBAGQESVFPICDULHHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETTWRLWQKFLDDYSRFEDWLKSAR RTAACPNSSEVLYTSAKEELKRFEFFORGIHERITOLELIINKOY	1	1207	***	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG
LSCPKDMAPSHCAEHRDQFLQLSQVRQLKTAEDYQALMKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAMLRAV LEKPFGHDHFSAQQLATELGTFFGEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLHKKLQVFQALRGL QRGSAVVGQVGYSYSEQVRRELQKPDSFHSLTFFAGULVHIDNL RMEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGLLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRREDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAEMGRLLDFEFSSGRLFFS QQQPEQLVPGGPGPPMSDFQVLRAKYRESSLVSAMSEELISKL ANDIERTAVRAVRREQGHLALGGGSSPVALFQQLATAHYGFFW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIFYYNIH\AM PVHLQQRLCAEBDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRMSLSLPLINRAKKV AVLVWGRMRREITTLVSRVGHEPKKWPISGVLPHSGQLVWWDDY DAFLG 6138 4587 934 EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIXELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASHTONLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIR KQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEMTERLQKDCMEEINLFSENKLOLKGMGDQL IKASNKSRABEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKMMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQOD LQRDIECHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRWRNICAMSMERRMKIEETTWRLWQKFLDDYSRFEDWLKSAR RTAACPNSSEVLYTSAKEELKRFLEFORGIHERITOLELINKOY	ı		i		MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK
LCHAGLREAGGIFYFSUPFAYEDIARNINSSCRPGPGAWLRVU LEKPFGHDHPSAQQLATELGTFFQEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDABGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RMEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAYLVSRNLFRPSLPSSWKEMEGPPG LRLFGSFLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEGLVPGFGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRPGQPHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH AM PVHLQQRLCAEBDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLITTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPPLHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTABJSIEEMIEKLQKDCMEEINLFSSRKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWGHLFDVIGSSVKKLKETFAFI QQLDKNMSNLRTWLARIESELSRPVVYDVCDDQEIQKRLAEQQD LQRDIEQHSAGVESVFNICUVLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSARE LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSARE RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLGLINKOY	1				LSCPKDMARCHCAEUKROFF OF COURSE
LEKPFGIDHFSAQQLATELGTFFQEEEMYRUDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVUTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHTDNL RWEGVFFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPBGLVPGFGPGPMPBGDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWIVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRMSLSLPLINRAKKV AVLVMGMMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFILG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLHHELKNKEHHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVIKKQEEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQBIEDRLNTWVYFNERNKELCAWLVQM ENKVLQATADISIEBMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWGHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQOD LQRDIEQHSAGVESVFNICUVLHDSDACANTTECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHBRLTOLELINKOY	ı	ļ			LOWAGI DEAGGIEVE CURREN CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF T
PFRDQNRKALDGLWNRHHVERVELIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSAEAVLRHKLQVFQALRGL QRGSAVVGQVQGYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHMAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRFFGGPHLALSGGSSFVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSSLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVIVEDWAVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFMEKNKELCAWLVQM ENKVLQTADISIEBMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEQHSAGVESVFNICDVILHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAR RTAACPNSSEVLYTSAKEELKRFEAFORQHERLTGLELINKOY	ı	- 1			LEKPFGHDHFSAOOLATELGTFFOFFFMVDUDUVLGKOAVA
IRDVLQNHLITEVLTILVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVREELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHMAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSFLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAEMGRLLDFEFSSGRLFFS QQQPEQLVPGGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLLALSGGSSFVALFQQLATLAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVWGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRTTTCAL TLEAGEKLLLTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPBLHEDLHHEEK ELIKELEQSLASWTONLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVPNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQOD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDDRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLELINKOV	1	ł	1		PFRDONRKALDGLWNRHHVERVETIMKETUDEGGPTGEVERVON
QRGSAVVQQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGFGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEBMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQOD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLELINKOY					IRDVLQNHLTEVLTLVAMELPHNVSSAFAVLRHKLOVFOAT RGI
RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGLLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFIG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIDRLNTWVVFNEKNKELGAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQOD LQRDIEQHSAGVESVFNICDVLHHDSDACARETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFOROIHERLTOLEIINKOY					QRGSAVVGQYQSYSEQVRRELOKPDSFHSLTPTFAGVLVH IDNI.
CCLPRQLVFHIGHGDLGS PAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGS PLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAEMGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMBDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQPHLALSGGSS PVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG 6138 4587 934 EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIR KQEIEDRLNTWVVPNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLAR IESELSKPVVVDVCDDQEIQKRLAEQQD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDS IQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLLELINKOY	}				RWEGVPFILMSGKALDERVGYARILFKNOACCVOSEKHWAAAOS
LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATTAVRAVRRFGQPHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH, AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVUDVMVLKEQIE HLHRQWEDLCLRVAIR KQEIEDRLNTWVVPNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTLARIESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLLELINKOY					QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGDDG
QQQPEQLVPGPEGPGPMPBDFQVLRAXYRESSLVSAWSEELISKL ANDIENTAVRAVRRPGQFHLALSGGSSPVALFQQLATAHYGFFW AHTHLWIVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEBQCGAHIYAREISALGANSSFDLVILLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGGERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIR KQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEBMIEKLQKDCMEEINLFSENKLQLKQMSDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQOD LQRDIEQHSAGVESVFNICDVILHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLLELINKOY	l	1			LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFTTTPNI.
ANDIFATAVRAVRRFGQFILLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTONLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIR KQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQOD LQRDIEQHSGAVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLLELINKOY			İ		LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS
AHTHLWIVDERCVPLSDPESNFQGIQAHLIQHVRIPYYNIH\AM PVHLQQRLCAEBDQGAHIYAREISALGANSSFDLVILIGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG 6138 4587 934 EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIR KQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLPSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVVDVCDDQEIQKRLAEQOD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLELINKOV	1	1			QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEET.1 SKI.
PVHLQCRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG 6138 4587 934 EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVPNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVVDVCDDQEIQKRLAEQQD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLELINKOV			1		ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW
TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG 6138 4587 934 EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKILLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIR KQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLAR IESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEQHSGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLELINKOY		ļ	1		PUHLOOPLCAREDOCAUTYARETCE- THE PHYNIH AM
AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG 6138 4587 934 EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGGERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIR KQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEBMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQOD LQRDIEQHSGAVESVFNICTVVLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLELINKOY	ĺ	ĺ	į		TASLEPOSPTCIDGEOLUGITTEPSONUMBER CONTROL
DAFLG DAFLG DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTONLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEBMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLFULARIESELSKPVVYDVCDDQEIQKRLAEQOD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLELINKOY					AVLVMGRMKREITTI.VSPVGHEDEVENDICONI DUCCONI DE
6138 4587 934 EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKILLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIR KQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEQHSGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLLELINKOY	L				DAFLG
TDTSHLLSAVKGGERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVYPNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLPSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQOD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLELINKOY	l	6138	4587	934	
TLEAGEKILLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFMEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLELINKOY	i	}		l	TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFORRRTTCAL.
FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTONLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIR KQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEBMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEQHSGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLLELINKOY				1	TLEAGEKLLLTTDLKTKESVGRRISOLODSWKDMEPOLAEMIKO
ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEBMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLLELINKOY				ł	FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK
HLHRQWEDLCLRVAIR KQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLINKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLLELINKOY		[}	ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVT.KEQTE
ENKVLQTADISIEBMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLLELINKOY		1		İ	HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVOM
IKASNKSRAAEIDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTOLLELINKOY		1			ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLOLKOMGDOL
LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTQLELINKOY				•	IKASNKSRAAEIDDKLNKINDRWOHLFDVIGSRVKKLKETFAFI
LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSEVLYTSAKEELKRFEAFORQIHERLTQLELINKOY			1	1	QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD
RTAACPNSSEVLYTSAKEELKRFEAFOROIHERLTOLELINKOY					LUKULEURSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS
RIAACPNSSEVLYTSAKEELKRFEAFQRQIHERLTQLELINKQY RRLARENRTDTASRLKQMVHEGNQRWDNLQRRVTAVLRRLRHFT			l		HUKKWANI CAMSMERRMKIEETWRLWQKFLDDYSRFBDWLKSAB
I AALMADAKIDIASKUKUMUNUQRRVTAVLRRIRHFT		1	[ALAMOFROSEVLYTSAKEELKRFEAFQRQIHERLTQLELINKQY
	_				AND AND A SKUNG POWER OF THE SHOP OF THE SHARE OF THE SHA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	1	sequence	\=possible nucleotide insertion)
	sequence		
			NOREEFEGTRESILVWLTEMDLQLTNVEHFSESDADDKMRQLNG
	i	1	FQQEITLNTNKIDQLIVFGEQLIQKSEP\LDAVLIEDELEELHR
	Į.	į.	YCQEVFGRVSRFHRRLTSCTPGLEDEKEASENETDMEDPREIQT
	1	1	DSWRKRGESEEPSSPOSLCHLVAPGHERSGCETPVSVDS\IPLE
	ŀ	1	WDHTGRRGGPSSSH\EEDEEAQYY\SALSGKSISDGHSWHVPDS
	į	1	PSCPEHHYKOMEGDRNVPPVPPASSTPYKPPYGKLLLPPGTDGG
			KEGPRVLNGNPQQEDGGLAGITEQQSGAFDRWEMIQAQEL\HNK
	1		
	Į.	}	LKIKQNLQQLNSDISAITTWLKKTEAELEMLKMAKPPSDIQEIE
		ì	LRVKRLQEILKAFDTYKALVVSVNVSSKEFLQTESPESTELQSR
			LRQLSLLWEAAQGAVDSWRGGLRQSLMQCQDFHQLSQNLLLWLA
1		1	SAKNRRQKAHVTDPKADPRALLECRRELMQLEKELVERQPQVDM
		I	LQEISNSLLIKGHGEDCIEAEEKVHVI\EKKLKQLREQVSQDLM
			ALOGTONPASPLPSFDEVDSGDOPPATSVPAPRAKQFRAVRTTE
		1	GEEETESRVPGSTRPORSFLSRVVRAALPLQLLLLLLLLLLACLL
			<u> </u>
			PSSEEDYSCTQANNF\ARSFYPMLRYTNGPPPT
613 <i>9</i>	52	1131	LGDWVWSRTCGVLETPTSVLRRARARGPCPTDSKWALPRLREGE
	ł	l l	TERRPWEASSWKTL/LAGWIGGAASVIVGHPLDTVKTRLQAGVG
		1	YGNTLSCIRVVYRRESMFGFFKGMSFPLASIAVYNSVVFGVFSN
		j	TORFLSOHRCGEPEASPPRTLSDLLLASMVAGVVSVGLGGPVDL
	Į.	i	IKIRLOMOTPPVSGROPRFEVQGSGSCG\EPAYQGPVHCITTIV
	i	1	RNEGLAGLYRGASAMLLRDVPGYCLYFIPYVFLSEWITPEACTG
			PSPCAVWLAGGMAGAISWGTATPMDVVKSRLQADGVYLNKYKGV
	ì		
		j	LDCISQSYQKEGLKVFFRGITVNAVRGFPMSAAMFLGYELSLQA
			IRGDHAVTSP
6140	594	136	RPELELWRLRSRSWRPLGVPRRCHRRNWKEPVRAQPLSVTVWAP
i	i	ŀ	RCQRP/QPPAPEPSSPNAAVPEAIPTPRAAASAALELPLGPAPV
i		j	SVAPQAEAEARSTPGPAGSRLGPETFRQRFRQFRYQDAAGPREA
ļ		1	FROLREL/SPROWLRPDI\RTKEQ\IVEMLVQEQLLAILPEAAR
İ	İ	1	ARRIRRTDVRITG
6141	2	984	AQVGPRSRPCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGSLS
0.4.	1	353	ASRAPARRLVFHAQLAHGSATGRVEGFSSIQELYAQIAGAFEIS
	ĺ	1	PSEILYCTLNTPKIDMERLLGGQLGLEDFIFAHVKGIEKEVNVY
		i	KSEDSLGLTITDNGVGYAFIKRIKDGGVIDSVKTICVGDHIESI
	<u>[</u>		1
			NGENIVGWRHYDVAKKLKELKKEELFTMKLIEPKKAFEIELRSK
}	1	1	AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD
l	1	1	VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP
l		}	DEFVFDVWGVIGDAKRRGL
6142	116	602	EAEGEOVCGAKCCGDAPHVENREEETARIGPGVMESKEERALNN
			LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR
1			FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL
l		l .	REKOLSHSLRAVSTDPPHHDHHDEFC\LMP
	ļ		
6143	2802	270	FRMRIPLHCPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q
			\QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED
			LLLNEWEASKCNIVCTQPRRISAVSLANRVCDELGCENGPGGRN
1	Į.	1	SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM
}	1	ĺ	FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE
		1	KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC
l			QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK
l		}	
	1	1	YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI
ļ	1		FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF
i			TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS
1	l	1	QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD
1	1	1	YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN
}	1	ĺ	AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF
l		l	GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL
I	1	L	TIYNAYLGWKKARQEGGYRSEITYCRRNFLNRTSLLTLEDVKQE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
Ì	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
į	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
-	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	i * *	\=possible nucleotide insertion)
			LIKLVKAAGFSSSTTSTSWEGNRASQTLSFQEIALLKAVLVAGL
1	1		YDNVGKIIYTKSVDVTEKLACIVETAQGKAQVHPSSVNRDLOTH
	1		GWLLYQEKIRYARVYLRETTLITPFPVLLFGGDIEVQHRERLLS
	i		IDGWIYFQAPVKIAVIFKQLRVLIDSVLRKKLENPKMSLENDKI
	j		LQIITELIKTENN
6144	1289	568	SGPGSMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGPYON
i			VSASGGARHGGRGSGGPVICTYGPDLFPLVA\TIGAAFVAKVMS
·			VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDSSS
1			FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRRVDFHDV
İ	•		QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVMTE
			DKGVDLGQKPNPYFYSCCHH
6145	1109	196	GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGPVL
	j i		GPMVYAICYCPLPRLADLEALKVADSKTLLESERERLFAKMEDT
1			DFVGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYALD
1			QGVNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALYPV
			\VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDPQD
			/TKAWLKEHVEPVF\GFP\QFVRF\SWRTAQTI\LEKEAEDVIR
1			EDSASENQEGLRKITSYFLNEGSQARPRSSHRYFLERGLESTTS
			r.
6146	428	781	LKKKGKEKAEAQQVEALPGPSLDQWHRSAGEEEDGPVLTDEQKS
			R/YPGHEAHDQGG\WDARQSIIRKVVDPETGRTRLIKGDGEVLE
			EIVTKERHREINKQATRGDCLAFQMRAGLLP
6147	1	2304	GTRQLPPPSPGSGPGDSPEGPEGEAPERRRKAHGMLKLYYGLSE
1	ļ		GEAAGRPAGPDPLDPTDLNGAHFDPEVYLDKLRRECPLAQLMDS
			ETDMVRQIRALDSDMQTLVYENYNKFISATDTIRKMKNDFRKME
			DEMDRLATNMAVITDFSARISATLQDRHERITKLAGVHALLRKL
1			QFLFELPSRLTKCVELGAYGQAVRYQGRAQAVLQQYQHLPSFRA
1			IQDDCQVITARLAQQLRQRFREGGSGAPEQAECVELLLALGEPA
			EELCEEFLAHARGRLEKELRNLEAELGPSPPAPDVLEFTDHG\S
Į l			SGFVGGLCQVAAAYQELFAAQGPAGAEKLAAFARQLGSRYFALV
ĺ			ERRLAQEQGGDNSLLVRALDRFHRRLRAPGALLAAAGLADAAT
			EIVERVARERLGHHLQGLRAAFLGCLTDVRQALAAPRVAGKEGP
1			GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF
1 1			CSQGVREGLIVGFVHSMCQTAQSFCDSPGEKGGATPPALLLLLS
) i	ľ		RLCLDYETATISYILTLTDEQFLVQDQFPVTPVSTLCAEARETA
			RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLEPRNVRAVMKRV
1 1	ł		VEDTTAIDVQVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG GGDMCIWASHGASSVARASVREPQGNKSPRMNTKRAGECLCPRS
1 (i		CSFSAQDYDIFAPILPVEKORLRVTOEVRAGLVLVLKIRPOTNS
	ŀ		CILPLPHSTGSINSDHVPTK
6148	3056	353	VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ
			KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT
,			SYXAFSTRWNWNEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV
1	ļ		PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT
j	-		SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES
, 1	į		VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE
1	Ì		LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ
1 1	1		LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW
			DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR
, !			LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSOSSVS
			ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG
			ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK
			THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAOOTFVDRLVHLM
į l			KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK
	Ī		IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLRQD
			QLILQIISLMDKLLRKENLDLKLTPYKVLATSTKHGFMOFIQSV
			ZZ*TOTHINTTHEVENTINTENTINTENTINTENTIAL STRUCTURES

SEQ	Predicted	Predicted end	Amino acid cognest
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *=C+==
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion\
	1		PVAEVLDTEGSIONFFRKYAPSENGPNGISAEVMDTVVKSCAGV
1			CVITYILGVGDRHLDNLLLTKTGKLPHIDFGYILGPDPKDT.DDD
1	1	İ	MKLNKEMVEGMGGTQSEQYQEFRKQCYTAFI,HI,RDYSNI, II,NI, D
ı	1		SLMVDANIPDIALEPDKTVKKVQDKFRLDLSDERAVHYMOST.TD
6149			ESVHALFAAVVEQIHKFAQYWRK
6149	1	1413	RVDPRVRENGTANPIKNGKTSPASKDQRTGKKTSVQGQVQKGND
	1	}	ESESDEESDEEPKSSEEEEQDDEEVLOGEOGDENDDDTEPENT.
	•		GHRPLLMDSEDEEEEEKHSSDSDYEOAKAKYSDMSSVYPDPSGS
1	1	1	GPTQDLNTILLTSAQLSSDVAVETPKOEFDVFGAVPFFAVRAGO
1	Į.		PQQEKNEKNLPQHRFPAAGLEOEEFDVFTKAPESKKANDOFCUR
1			VGPEAHTIPGYPKSVDVFGSTPFOPFLTSTSKSESNEDLEGLVB
			FDEITGSQQQKVKQRSLQKLSSRORRTKODMSKSNGKPHHGTPT
1	1		STRKTLKPTYRTPERARRHKKVGRRDSOSSNEFT.TISDSKENIS
	1		VALTDGKDRGNVLQPEESLLDPFGAKPFHSPD\1.SWHPD\10Ct
1	1		S\DIRADHNT\VLPGR\PRQNSLHGSFHSADVLKMDDFGAVP/F
6150	372		LTELVVQSITPHQSQQSQPV\ELDPFGAAPFPSKQ
1	1 3/2 1	37	MSNIKKYIIDYDWKASIEIEIDHDVMTEEKLHQINNFWSDSEYR
1	f l		LNKHGSVLNAVLIMLAQHALLIAISSDLNAYGVVCEFDWNDGNG
6151	1555	521	QEGWPPMDGSEGIRITDIDTSGIF
1		721	DSNQQSVSGTAASTLLHSFKATIYYQGTGHVQQFYGVTSPYSQT
			TPPIVQSYAQPSLQYIQGQQIFTAHPQGVVVQPAAAVTTIVAPG
1			QPQPLQPSEMVVINNLLDLPPPSPPKPKTIVLPPNWKTARDPEG KIYYYHVITRQTQWDPPTWESPGDDASLEHEAEMDLGTPTYDEN
ļ			PMK\ASKKPKTAEADTSSELAKKSKEVFRKEMSQFIVQCLNPYR
i	1		KPDCKVG\RITTTEDFKHLARKLTHGVMNKBLKYCKNPE\DLEC
	1		NENVKHKTKEYIKKYMQKFGAVYKPKEDTEFRVTVGPGWEDGWS
<u></u>			GKTDSRERKSCGPFCSTPVSTVLLMIHHPGBFNPADVN
6152	1366	648	NRTWSTPSTWMGVALPPLCSTGPWPVTRQITARTTCGAVPAKCP
ļ			PWC/DVHEPRCQPPDCHGHGTCVDGHCOCTGHFWRGPGCDFLDC
1			GPSNCSQHGLCTETGCRCDAGWTGSNCSERCPLGWHGDGCODDG
l	[KCEHHCPCDPKTGNCSVSRVKOCLOPPEATTRAGELSEFTDTAM
	[LALTLALAFLLLISTAANLSLLLSRAERNRRLHGDYAYHPLOEM
6153	2		NGEPLAAEKEQPGGAHNPFKD
		3368	GRVGARSPGRAYALLLLICFNVGSGLHLQVLSTRNENKLLPKH
			PHLVRQKRAWITAPVALLEGEDLSKKNPIAKIHSDLAEERGLKI
		j	TYKYTGKGITEPPFGIFVFNKDTGELNVTSILDREETPFFLLTG
'			YALDARGNNVEKPLELRIKVLDINDNEPVFTQDVFVGSVEELSA
	Į		AHTLVMKINATDADEPNTLNSKISYRIVSLEPAYPPVFYLNKDT
			GEIYTTSVTLDREEHSSYTLTVEARDGNGEVTDKPVKQAQVQIR
		ľ	ILDVNDNIPVVENKVLEGMVEENQVNVEVTRIKVFDADEIGSDN WLANFTFASGNEGGYFHIETDAQTNEGIVTLIKEVDYEEMKNLD
!	ł		FSVIVANKAAFHKSIRSKYKPTPIPIKVKVKNVKEGIHFKSSVI
	!		SIYVSESMDRSSKGQIIGNFQAFDEDTGLPAHARYVKLEDRDNW
1	1		ISVDSVTSEIKLAKLPDFESRYVQNGTYTVKIVAISEDYPRKTI
}	1	F	TGTVLINVEDINDNCPTLIEPVQTICHDAEYVNVTAEDLDGHPN
}			SGPFSFSVIDKPPGMAEKWKIARQESTSVLLQQSEKKLGRSEIQ
	}		FLISDNQGFSCPEKQVLTLTVCEVLHGS\GCREAOHDSVVGLGD
	1	į.	AAIALMILAFLLLLLVPLLLLMCHCGKGAKGFTPIDGTTEMLUD
	İ	ĺ	WNNEGAPPEDKVVPSFLPVDQGGSLVGRNGVGGMAKEATMKGGG
1			SASIVKGQHEMSEMDGRWEEHRSLLSGRATOFTGATGAT\MTTP
	•	1	TTITARATGASRDVAGAQAAAVALNEEFLKNYFTDKAASYTEED
- 1			ENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDP FLDDLCI
ļ		1	KFKTLAEVCLGQKIDINKEIEOROKPATETSMNTASHSLCEOTM
		I '	VNSENTYSSGSSFPVPKSLOEANAEKVTOEIVTERSVSSPODOV
		1.	VATPLPDPMASRNVIATETSYVTGSTMPPTTVTIGPGODGE TV
			TERVYAPASTLVDQPYANEGTVVVTERVIQPHGGGSNPLEGTQH

SEQ	Predicted	Predicted end	Amino acid coment
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- }	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
			LQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
1			APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGH
L			SNSTITTSSTRVTKHSTVQHSYS
6154	3660	2146	KKKTKMKNTLQKTVNFGAWPKPTISDKSHLLQMVSKLDLTDAKN
ł	ļ		SDTAHIKSIEITSILNGLQASESSAEDSEQEDERGAQDMDNNGK
i	1	1	EESKIDHLTNNRNDLISKEEQNSSSLLEENKVHADLVISKPVSK
-			SPERLRKDIEVLSEDTDYEEDEVTKKRKDVKKDTTDKSSKPQIK
ł	1	}	RGKRRYCNTEECLKTGSPGKKEBKAKNKESLCMENSSNSSSDED
			EEETKAKMTPTKKYNGLEEKRKSLRTTGFYSGFSEVAEKRIKLL
ł			NNSDERLQNSRAKDRKDVWSSIQGQNPKKTLKELFSDSDTEAAA
	ļ		SPPHPAPEEGVAEESLQTVAEESCSPSVELEKPPPVNVDSKPI
1	1		EEKTVEVNDRKAEFPSSGSNFSA*IPLPYLHLNRLHQSL*QKGS
1]		RQQSSVTVSEPLAPNQEEVRSIKSETDSTIEVDSVAGELQDLQS
I	1		ERE*LASRF*CQCELEQ**SARTRTS*KSLYRSEKSERCSGRRK
			FIKKAEKKP*SNSGKOOKEGK
6155	869	121	HLLPELRGKSWITMKYVFYLGVLAGTEFFADSSVOKEDBADVTV
Į.	i i		YLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMLGNPKSRVRDG
1			TEQTINPIQIVRYWNYSHSAPODDLMI.TKI.AKDAMI.MDVXXOATAY
			P\PTTNVRPGTVCLLSGLDWSOENSGRHPDIRONI.EADVMCDDE
1			CURTEQGKSHRNSLCVKFVKVFSRIFGEVAVATVICKDVLOGIR
			VGHFMGGDVGIYTNVYKYVSWIENTAKDK
6156	5725	3984	GTSTVTMATKKHFSIILNLLGMLLKKDNODTBKLLMTWAY
1 i	1		VMKKSETYAPLFCLPSFHKFCKGLLADTLVRDVNICT.OACCELU
1	! . !		ALSSSLPDDLLORCVDVCRVOLVHRGTCIPOARGVII VCIDI GU
1			FLSNNHTEIQEISLALRSHMSKAPSNTFHPODESD/MTCPTtv {
j			GNSHRIGKUNWLERLFYSCORLDKRDOSTIDPNII, KTDAMI MOM
1 . [j		AIWEAAQFTVLSKLRTPLGRAODTFOTIEGTIRSI.ACUTY MDDO
1 8	i		DVSQWTTADNDEGHGNNOLRLVLLLOYLENTERLMVNAVEGGAN
1 1			ALTSPPKVIRTFLYTNROTCODWITRTRISTMPWGLLACODARM
1 1			VRHGFDLLTEMKTTSLSOGNELEVSIMMVVFALCETHORRATOR
1	į		IAVWSSSIVGKHLLWINSVAOOAEGRFEKASVEYOEUT.CAMTCU
1	1		DCCISSFDKSVLTLASAGCKSASLKHCLNGESRKSVI.cvpmpce
1 1			PEVINYLGNKACECYISTADWAAVOEWONATHDI.KKGTGGTGIN
i I	1	ĺ	LKADFNYIKSLSSFESGKFVECTEQLELLPGENINLLAGGSKEK
6157	946	329	IDMKKLLRNM
j		229	MANRGPSYGLSREVQEKIEQKYDADLENKLVDWIILQCAEDIEH
[[1		PPPGRAHFQKWLMDGTVLCKLINSLYPPGQEPIPKISESKMAFK
		l	QMEQISQFLKAAETYGVRTTDIFQTVDLWEGKDMAAVQRTLMAL
1			GSVAVTKDDGCYRGEPSWFHRKAQQNRRGFSEEQLRQGQNVIGL QMGSNKGASQAGMTGYGMPRQIM*DAASCP
6158	441	1482	IGSLIVICING VI PROCOL PRANCE
			LGSLIVLSLHCKVIFSSQSLERAMKEKAVDLVPILAQNPGLAQN PILEGKDHNQNTGVDPIIDHVQDRKTD/SRSKSPHKKRSKSRER
			RKSRSRSHSRDKRKDTREKIKEKERVKEKDREKEREKEREKE
i 1			KERGKNKORDKEREKDREKDKEKDREREREKEREKE KERGKNKORDKEREKDREKDKEKDREREREKEHEKORDKEKEKE
	l l	I	QDKEKEREKDRSKEIDEKRKKDKKSRTPPRSYNASRRSRSSSRE
			RRRRRSRSSSRSPRTSKTIKRKSSRSPSPRSRNKKDKKREKERD
ł	1		HISERRERSTSMRKSSNDRDGKEKLEKNSTSLKEKEHNKEPD
			SSVSKEVDDKDAPRTEENKIQHNGNCQLNEENLSTKTEAV
6159	53	84	AVIAPLHISLGDRARPYLKNTEKSSTTCSRRRNQSFPPVMSLTH
!	[1	RLHLCKYWGCAVSNVCRFWEGRPLPLMIVVPYTLPVSLPVGSCV
[ĺ	ļ	IITGTPILTFVKDPQLEVNFYTGMDBDSDIAFQFRLHFGHPAIM
J		1	NSCVFGIWRYEEKCYYLPFEDGKPFELCIYVRHKEYKVMVNGQR
		.	IYNFAHREPPASUKMI OUVEDIG TENTE TODOGO TO
			IYNFAHRFPPASVKMLQVFRDISLTRVLISD*GRCVRITAVQEF DVSVSCDCTTAYQPG
6160	1626		AGAKFFP+F*KVADAQPTESEKEIYNQVNVVLKDAEGILEDLQS
			YRGAGHEIREAIQHPADEKLQEKAWGAVVPLVGKLKKFYEFSQR
			- ADDITION OF THE PROPERTY OF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine, .
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LEAALRGLLGALTSTPYSPTQHLEREQALAKQFAEILHFTLRFD
1]		ELKMTNPAIQNDFSYYRRTLSRMRINNVPAEGENEVNNELANRM
İ	İ		SLFYAEATPMLKTLSDATTKFVSENKNLPIENTTDCLSTMASVC
			RVMLETPEYRSRFTNEETVSFCLRVMVGVIILYDFVHPVGAFAK
1			TSKIDMKGCIKVLKDQPPNSVEGLLNALRYTTKHLNDETTSKQI KSMLQ+QLLTLVNKG
6161	455	1569	PVSGSESSLRRAWASILRLMLGPRVAVSILCEDGISH*LLEKH*
	1	1305	KSHVLEPLSSLALEEQCLALSLDWSTGKTGRAGDQPLKIISSDS
1			TGQLHLLMVNETRPRLQKVASWQAHQFEANIAAFNYWHPEIVYS
			GGDDGLLRGWDTRVPGKFLFTSKRHTMGVCSIQSSPHREHILAT
1			GSYDEHILLWDTRNMKQPLADTPVQGGVWRIKWHPFHHHLLLAA
			CMHSGFKILNCQKAMEERQEATVLTSHTLPDSLVYGADWSWLLF
1			RSLQRAPSWSFPSNLGTKTADLKGASELPTPCHECREDNDGEGH
· ·			ARPQSGMKPLTEGMRKNGTWLQATAATTRDCGVNPEEADSAFSL
L			LATCSFYDHALHLWEWEGN
6162	1	586	RTIHATGRAGASPMHRLIVWRLAEANKQHVRCQKCLEFGHWTYE
			CTGKRKYLHRPSRTAELKKALKEKENRLLLQQSIGETNVERKAK
			KKRSKSVTSSSSSSSSSSSSSSSSSSEETSTSSSSEDSDTDESS
1			SSSSSASSTTSSSSSDSDSDSDSSSSSKQ*HQHR*QL*R*TTKEE
		···	EKEIELLHSYWTDGLKTLM
6163	1081	785	RIRSTTEGCAVRLHPTQNTGKARIMILLSVSLGRHWAFTYKFFL
l i			TPVVFVFFFFFFHRKE*VMQKNPMKSREDEWMEKLNNLHVQRAD
			MNRLIMNYLVTEGFKEAAEKFRMESGIEPSVDLETLDERIKIRE
1			MILKGQIQEAIALINSLHPELLDTNRYLYFHLQQQHLIBLIRQR ETEAALEFAQTQLAEQGEESRECLTEMERTLALLAFDSPEESPF
			GDLLHTMQRQKVWSEVNQAVLDYENRESTPKLAKLLKLLLWAQN
			ELDQKKVKYPKMTDLSKGVIEEPK
6164	90	406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR
			SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA
1	ļ		VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS
1 1			NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
1			WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES
			YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
			GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
1			RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE
			LMQTVYSMAPFPFPQLAELREKYTYNITPFPATVKPTSVSGRHS
			KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTTDIN
]	,		ALKROYSRIKKKOOOOVHOVYIRADKGPVTSILPSOVNSSPVIN
į i	Ì		HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS
[1	·	PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEONEASKTNGLGAA
1			EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA
			VQAKLGALELNQRDAAAETELRVHPPCQRHCPEPPSAPEENKAT
	İ		SKAPQGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV
]			HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYQRN
			GGERFG
6165	90	405	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR
	ļ		SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA
			VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS
	ţ		NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
!	İ		WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES
! !		İ	YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
			GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
		İ	RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE
		ľ	LMOTVYSMAPFPFPQLAELREKYTYNITPFPATVKPTSVSGRHS
LL		<u></u>	KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE

SEQ	Predicted	Predicted end	Amino soid -
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
]	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	·	\=possible nucleotide insertion)
			PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTTDIN
ı			ALKRQYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN
ļ			HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS
			PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNGLGAA
1		•	EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA
			VQAKLGALELNQRDAAAETELRVHPPCQRHCPEPPSAPEENKAT
			SKAPQGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV
1			HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYQRN
			GGERFG
6166	2	1206	HKLWRTVAMAGAEWKSLEECLEKHLPLPDLQEVKRVLYGKELRK
1			LDLPREAFEAASREDFELQGYAFEAAEEQLRRPRIVHVGLVQNR
1			IPLPANAPVAEQVSALHRRIKAIVEVAAMCGVNIICFQEAWTMP
1			FAFCTREKLPWTEFAESAEDGPTTRFCQKLAKNHDMVVVSPILE
1			RDSEHGDVLWNTAVVISNSGAVLGKTRKNHIPRVGDFNESTYYM
1			EGNLGHPVFQTQFGRIAVNICYGRHHPLNWLMYSINGAEIIFNP SATIGALSESLWPIEARNAAIANHCFTCAINRVGTEHFPNEFTS
			GDGKKAHQDFGYFYGSSYVAAPDSSRTPGLSRSRDGLLVAKLDL
			NLCQQVNDVWNFKMTGRYEMYARELAEAVKSNYSPTIVKE*PAS
			VPALG
6167	1220	1844	YGIVTGPSLCAGDKQPKKQEKNPVLVSPEFVDEALCACEEYLSN
1			LAHMDIDKDLEAPLYLTPEGWSLFLQRYYQVVHEGAELRHLDTQ
			VQRCEDILQQLQAVVPQIDMEGDRNIWIVKPGAKSRGRGIMCMD
1			HLEEMLKLVNGNPVVMKDGKWVVQKYIERPLLIFGTKFDLRQWF
			LVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDK*APLYLTPEGWS
1 1			LFLQRYYQVVHEGAELRHLDTQVQRCEDILQQLQAVVPOIDMEG
	I		DRNIWIVKPGAKSRGRGIMCMDHLBEMLKLVNGNPVVMKDGKWV
i i	!		VQKYIERPLLIFGTKFDLRQWFLVTDWNPLTVWFYRDSYIRFST
6168	84	4200	QPFSLKNLDK
0200	0.1	1392	VWPVPSVSAMPPKKQAQAGGSKKAEQKKKEKIIEDKTFGLKNKK
)	j		GAKQQKFIKAVTHQVKFGQQNPRQVAQSEAEKKLKKDDKKKELQ
1 1			ELNELFKPVVAAQKISKGADPKSVVCAFFKQGQCTKGDKCKFSH
			DLTLERKCEKRSVYIDARDEELEKDTMDNWDEKKLEEVVNKKHG EABKKKPKTQIVCKHFLEAIENNKYGWFWVCPGGGDICMYRHAL
1 1			PPGFVLKKKKKKKKEDEISL*DLIERERSALGPNVTKITLESF
	ĺ		LAWKKRKRQEKIDKLEQDMERRKADFKAGKALVISGREVFEFRP
		1	ELVNDDDEEADDTRYTQGTGGDEVDDSVSVNDIDLSLYIPRDVD
		ļ	ETGITVASLERFSTYTSDKDENKLSEASGGRAENGERSDLEEDN
			EREGTENGALDAVPVDENLFTGEDLDELEEELNTLDLEE
6169	112	662	APAAAMAERPEDLNLPNAVITRIIKEALPDGVNISKEARSAISR
		1	AASVFVLYATSCANNFAMKGKRKTLNASDVLSAMEEMEFORFVT
		İ	PLKEALEAYRREQKGKKEASEQKKKDKDKKTDSEEODKSRDEDN
!!			DEDEBRLEEREQNEEREVDN*KGRETVAPWKVPLEMRRATCFCE
6170			AFPCWAE
51/5	62	667	STKVMLPNTGRLAGCTVFITGASRGIGKAIALKAAKDGANIVIA
	1		AKTAQPHPKLLGTIYTAAEEIEAVGGKALPCIVDVRDEQQISAA
	İ	1	VEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG
!!!		-	TYLASKACIPYLKKSKVAHIPNISPPLNLNPVWFKQHCGRW*VV
6171	382	941	G*GDGLCLICFELNLCMSDVITICT
		771	HFMQSDVELDCDIEPCGHTKFPPTLPLSTTVIVCSCHPVATAST
			MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRRHAN
j		Í	SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT
			NATLRYTKSK
6172	651		GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR
	.		SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV
		[]	TSHVDDEYRWAGVEDPKVMITTSRDPSSRLKMFAKELKLVFPGA
			TORDE STATE AND A STATE OF THE

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Truntonhon V-Truncing Vavaline,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1	sequence	bequence	\=possible nucleotide insertion)
			QRMNRGRHEVGALVRACKANGVTDLLVVHEHRGTPVGLIVSHLP
1			FGPTAVETI COMMENDED TO THE TOTAL COMMENDE TO THE TOTAL COMMENDED TO THE TOTAL COMMENDED TO THE TOTAL COMMENDED TO THE TOTAL COMMENDED TO THE TOTAL COMMENDED TO THE TOTAL COMMENDED TO THE TOTAL COMMENDED TO THE TOTAL COMMENDED TO THE TOTAL COMMEND TO THE TOTAL COMMEND TO THE TOTAL COMMENDED TO THE
			FGPTAYFTLCNVVMRHDIPDLGTMSEAKPHLITHGFSSRLGKRV
1			SDILRYLFPVPKDDSHRVITFANQDDYISFRHHVYKKTDHRNVE
			LTEVGPRFELKLYMIRLGTLEQEATADVEWRWHPYTNTARKRVF LSTE*AAPRPLGQLL
6173	3	288	
		200 .	SVDHREVQVLSQSMPLTPHQAVLRGERPYMCVECGKCFGRSSHL
			LQHQRIHTGEKPYVCSVCGKAFSQSSVLSKHRTIHTGEKPYECN
			ECGKAFRVSSDLAQHHKIHTGEKPHECLECRKAFTQLSHLIQHQ
			RIHTGERPYVCPLCGKAFNHSTVLRSHQRVHTGEKPHRCNECGK
			TFSVKRTLLQHQRIHTGEKPYTCSECGKAFSDRSVLIQHHNVHT
	l i		GEKPYECSECGKTFSHRSTLMNHERIHTEEKPYACYECGKAFVQ
1 1			HSHLIQHQKVHRKL*PTCVLSVGSALAGVPTSFSISVSTLERSP
6174	1060	959	MCAVYVGRPSARAQSLVNTGQFTQVRSPMSVMSVEKPLE
	2000	233	PRPPGKRWMVAGLGNPGLPGTRHSVGMAVLGQLARRLGVAESWT
			RDRHCAADLALAPLGDAQLVLLRPRRLMNANGRSVARAAELFGL
1			TAEEVYLVHDELDKPLGRLALKLGGSARGHNGVRSCISCLNSNA
			MPRLRVGIGRPAHPEAVQAHVLGCFSPAEQELLPLLLDRATDLI
6175	2204	334	LDHIRERSQGPSLGP*H*WFSKKA
		234	RYFRADPRSRSGOPRAEGLGAFAEGPLRAMAAPVKGNRKQSTEG
1			DALDPPASPKPAGKQNGIQNPISLEDSPEAGGEREEEQEREEEQ
			AFLVSLYKFMKERHTPIERVPHLGFKQINLWKIYKAVEKLGAYE LVTGRRLWKNVYNELGGSPGSTSGATCTRRHY*RLVLPYVRHLK
	1		GBDDKPLPTSKPRKQYKMAKENRGDDGATERPKKAKEERRMDOM
1 1	ľ		MPGKTKADAADPAPLPSQEPPRNSTEQQGLASGSSVSFVGASGC
1	i	i	PEAYKRLLSSFYCKGTHGIMSPLAKKKLLAQVSKVEALQCQEEG
1			CRHGAEPQASPAVHLPESPQSPKGLTENSRHRLTPQEGLQAPGG
{			SLREEAQAGPCPAAPIFKGCFYTHPTEVLKPVSQHPRDFFSRLK
1			DGVLLGPPGKEGLSVKEPQLVWGGDANRPSAFHKGGSRKGILYP
1	1		KPKACWVSPMAKVPAESPTLPPTFPSSPGLGSKRSLEEEGAAHS
	1		GKRLRAVSPFLKEADAKKCGAKPAGSGLVSCLLGPALGPVPPEA
1 1			YRGTMLHCPLNFTGTPGPLKGQAALPFSPLVIPAFPAHFLATAG
1			PSPMAAGLMHFPPTSFDSALRHRLCPASSAWHAPPVTTYAAPHF
<u>li</u>			FHLNTKL
6176	1040	402	PLSALRAMAEVHVIGQIIGASGFSESSLFCKWGIHTGAAWKLLS
, ,			GVREGQTQVDTPQIGDMAYWSHPIDLHFATKGLQGWPRLHFQVW
1	1		SQDSFGRCQLAGYGFCHVPSSPGTHQLACPTWRPLGSWREQLAR
] [AFVGGGPQLLHGDTIYSGADRYRLHTAAGGTVHLEIGLLLRNFD
L1			RYGVEC*GTLPPTSPPSTPRTPSDGGGWHSGQEHRL
6177	1400	992	VPIESLVGKVHNFPLIAFYCCEKGKRQPHKSLHDRCFGEALDPN
	j	1	CSHCYLDQIKRSDFLGFSGYSPHFVAISTNSEHKMQPSSMQQAL
			PSQ*PYWTDPRPALVPCCSHRPDVHRSRPGPGLPGTSGCSDRPP
		1	VCPI
6178	1027	254	STORGGIKGVARAASLVGRRRAGTGMALLLCLVCLTAALAHGCL
ĺ		i	HCHSNFSKKFSFYRHHVNFKSWWVGDIPVSGALLTDWSDDTMKE
	Į		LHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELR
		İ	NIFREQUALIQUALIESRIDCQHRCGIFQYETISCNNCTDSHVA
			CFGYNCESSAQWKSAVQGLLNYINNWHKQDTSMRPRSSAFSWPG
			THRAAPAFLVLPALRCLEPPHLANLSLEDAA*CLKQH
6179	806	276	RGETREMAGNILLSGAGRRIWDWVPLACRSFSLGVPRLIGIRLTL
			PPPKVVDRWNEKRAMFGVYDNIGILGNFEKHPKELIRGPIWLRG
[f		WKGNELQRCIRKRKMVGSRMFADDLHNLNKRIRYLYKHFNRHGK
	1		FR*KRKLRTSEKAHLSPWRRETVLFPVRKRLCIFSVIKWGFFGI
6180	156	1833	DUNTI, KAN CTTUVON DONTEN TONTON TONTON
		2033	DHHILKAASTTHVCARGNIFAIPNTRCLEC*ATATPSSLECQN* SHISLCPL PATTSGLTDNGMIPEVERONIA FOLL DVRGARY
	1		SHLSLCPLPATTSGLTPNSMIPEKERONIAERLLRVMCADLGAL
- 1	1		SVVSGKEFLKLAQTLVDSGARYGAFSVTEILGNFNTLALKHLPR
			MYNQVKVKVTCALGSNACLGIGVTCHSQSVGPDSCYILTAYQAE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ľ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
[residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
	1		GNHIKSYVLGVKGADIRDSGDLVHHWVQNVLSEFVMSEIRTVYV
1			TDCRVSTSAFSKAGMCLRCSACALNSVVQSVLSKRTLQARSMHE
ł	1		VIELLNVCEDLAGSTGLAKETFGSLEETSPPPCWNSVTDSLLLV
1	1		HERYEQICEFYSRAKKMNLIQSLNKHLLSNLAAILTPVKQAVIE
}			LSNESQPTLQLVLPTYVRLEKLFTAKANDAGTVSKLCHLFLEAL KENFKVHPAHKVAMILDPQQKLRPVPPYQHEEIIGKVCELINEV
			KESWABEADFEPAAKKPRSAAVENPAAQEDDRLGKNEVYDYLQE
		•	PLFQATPDLFQYWSCVTQKHTKLAKLAFWLLAVPAVGARSGCVN
			MCEQALLIKRRRLLSPEDMNKLMFLKSNML
5181	169	1032	TRTLLSPVLLPGPRWKPWRRRPMGPLALPAWLQPRYRKNAYLFI
1			YYLIQFCGHSWIFTNMTVRFFSFGKDSMVDTFYAIGLVMRLCQS
1]		VSLLELLHIYVGIESNHLLPRFLQLTERIIILFVVITSQEEVQE
			KYVVCVLFVFWNLLDMVRYTYSMLSVIGISYAVLTWLSQTLWMP
1			IYPLCVLAEAFAIYQSLPYFESFGTYSTKLPFDLSIYFPYVLKI
	·		YLMMLFIGMYFTYSHLYSERRDILGIFPIKKKKM*STAFQCDTR
6182	1769	1004	KDRLWIQCSK*NTGSILVEKFLVF
0.02	1,09	1224	AS*IDYQLNTLLKEFQLTEENTKLRYLTCSLIEDMAAAYFPDCI
1			VRPFGSSVNTFGKLGCDLDMFLDLDETRNLSAHKISGNFLMEPQ
			VKNVPSERIATQKILSVLGECLDHFGPGCVGVQKILNARCPLVR FSHQASGFQCDLTTNNRIALTSSELLYIYGALDSRVRALVFSVR
			CWARAHSLTSSIPGAWITNFSLTMMVIFFLQRRSPPILPTLDSL
			KTLADAEDKCVIEGNNCTFVRDLSRIKPSQNTETLELLLKEFFE
			YFGNFAFDKNSINIRQGREQNKPDSSPLYIQNPFETSLNISKNV
1			SQSQLQKFVDLARESAWILQQEDTDRPSISSNRPWGLVSLLLPS
			APNRKSFTKKKSNKFAIETVKNLLESLKGNRTENFTKTSGKRTI
			STQT
6183	1118	452	HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRTMGCCGCSRGC
1		•	GSGCGGCGSSCGGCGSGCGCGSSCGGCGS
1			RCYVPVCCCKPVCSWVPACSCTSCGSCGGSKGGCGSCGGSKGGC
			GSCGCSQSSCCKPCCCSSGCGSSCCCQSSCCKPCCCQSSCCVPVC
1 1	'		CQSSCCKPCCCQSNCCVPVCCQCKI*GSGPRPSGFSCLVKAFLM VP
6184	1	2191	IVTVREEDGAPAVAPPGVVVSRANKRSGAGPGGSGGGGARGAEE
	· -	~~~	EPPPPLQAVLVADSFDRRFFPISKDQPRVLLPLANVALIDYTLE
	Í		FLTATGVQETFVFCCWKAAQIKEHLLKSKWCRPTSLNVVRIITS
	1		ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR
			LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNRVL
	ļ		HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA
	}		QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS
,	ł		NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG
1	Ì	ļ	PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD
1			NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL
		!	TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK
1	1		DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEEELQQNLWGLKI
			NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLOO
	İ		MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED
			FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGO
			QLRKNQQLQRFIQWLKEAEEESSEDD
6185	791	44	PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG
		- "	IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFOR
			HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF
			GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK
			REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR
<u></u>			GCQEAEMQTPRRLGWGWYHTLTLYLWBEK
6186	569	238	VYGIDSSNTNTHGABERNRKLKKHWKLCHAQSRLDVNGLALKMA
	<u></u>	230	- 101203N IN I HOMBERNKALLKHWALICHAQSKEDVNGLALKMA

SEQ	Predicted	Predicted end	I have a series
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
İ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
<u> </u>	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
J	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid		P=Proline, Q=Glutamine, R=Arginine,
į.	residue of	residue of	S=Serine, T=Threonine, V=Valine
	amino acid	amino acid	Watryptophan, Yatrosine, Xallnknown *-char
		sequence	Codon, /=possible nucleotide deletion
 	sequence		\=possible nucleotide insertion)
1	į.		KERKVKNKVKNKADTEEVFNNSPTNOEKMPTSATIJPDESGSVIS
			NIRNQMETLHSQPHQEENLCFENSFSLINLLPINAVEPTSSQQI
ł	į.	1	PNRETSEANKERRKMTSKSSESNIYSPLTSFITADSELHDIIKD
į		1	LEDCLMVGLHTCGDLAPNTLRIFTSNSEIKGVCSVGCCYHLLSE
ĺ			EFENQHKERTQEKWGFPMCHYLKEERWCCGRNARMSACLALERV
			AAGQGLPTESLFYRAVLQDIIKDCYGITKCDRHVGKIYSKCSSF
	1		LDYVRRSLKKLGLDESKLPEKIIMNYYEKYKPRMNELRAFNMLK
1	1		VVIAPCIETITITORI CVI VPOPPATAVICA INTERINALIZATIONI
İ	1		VVLAPCIETLILLDRLCYLKEQEDIAWSALVKLFDPVKSPRCYA
			VIALKKQQ*FPLKQIIRCISL*DSAGCAEEVSVGDGGPALRDAP PSGSRVGSRYD
6187	1701	771	
1	"""	,,,	DAWGPETRLARILNPDSFIEPRPGRLPELEATRPHMEPKASCPA
1			AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDIPGLEVAVVTT
1			ERAKHFYSPQDIPVTLYSDADEWEMWKSRSDPVIHTDI.PPWant
			LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSKPLLFCPAMNT
			AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGDEGLGAMAEUG
1			TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEWVOAKSVKMDV
1			GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPGLSFFOPGEAA
6188	238		A
0200	236	1534	KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHPSA*GPRWASW
	1		NIGVFICIRCAGIHRNLGVHISRVKSVNLDOWTOFOIOCMOFMG
1 1	' I		NGKANRLYEAYLPETFRRPOIDPAVEGFIRDKVEKKKVMDBcin
	İ		INAFRKEKDDKWKRGSEPVPEKKLEPVVFRKVKMPOKKEDPOLP
	i	1	RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTLEKDIDI.LASV
	į.		PSPSSSGSRKVVGSMPTAGSAGSVPENINI.FPEPGSKSFFTGKK
1 1	I		QLSKDSILSLYGSQTPQMPTQAMFMAPAOMAYPTAYDSFDCVTD
1 1	1		PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGVMCGMOASMMC
1	1		VPNGMMTTQQAGYMAGMAAMPQTVYGVOPAOOLOWNT.TOMTOOM
6189			AGMNEYGANGMMNYGQSMSGGNEOAANOTLSPOMWK
0189	1297	793	LGEPLGDLCELIPGDVQQLOMGEVHPGTGAOGSAAOSVAGEVOT
1 1	1		TQLSHARQRPSCQGSQLIALDLOHMDISROPRWOHVOPVAROVO
1 1	İ		RAQQAQLAEGVAVHLWAGDAVVAEVELLQEVGGGKVFAANACDL
1 1	į	i	VVQDHEGAHAARQATGHALQRVIVQVRRVQPLEAL*RVPSGLPR
1	i		RVRAFMILHNQITGIGREDFATTYFLEELNLSYNRITSPQVHRD
1 1		`	AFRKLRLLRSLDLSGNRLHMLPPGLPRNVHVLKVKRNBLAALAR
1	1		GALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQ
1 1	i	i	LTEIPEGLPESLEYLYLQNNKISAVPANAFDSTPNLKGIFLRFN
1 1		.	KLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKDRGRLGKEKE
		1	EEEEDEVEEEETR
6190	66	1309	ILVGNVSFLLSFAEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQ
1	1		GLHCETCKEGFYLNYTSGLCQPCDCSPHGALSIPCNSSGKCQCK
		ſ	VGVIGSICDRCQDGYYGFSKNGCLPCQCNNRSASCDALTGACLN
1	}	1	CQENSKGNHCEECKEGFYQSPDATKECLRCPCSAVTSTGSCSIK
1 1			SSELEDECDOCKDOWTODWOOTHOUTON
; 1	1	1	SSELEPECDQCKDGYIGPNCNKCENGYYNFDSICRKCQCHGHVY
j l		I	PVKTPKICKPESGECINCLHNTTGFWCENCL*GYVHDLBGNCIK
]	!	1	KVILPTPEGSTILVSNASLTTSVPTPVINSTFTPTTLQTIFSVS
; l		1	TSENSTSALADVSWTQFNIIILTVIIIVVVLLMGFVGAVYMYRE
]	f	∄.	YONRKLNAPFWTIELKEDNISFSSYHDSIPNADVSGLLEDDGNE
6191	1212		VAPNGQLTLTTPIHNYKA
		,	VNLCHGGLLHLSTHHLGIKPSMH*LFFLMLSFPHLTPQQPKCPS
1		[]	MIDWIKKIWYIYTMEYYATIKRNEIMFFAGTWMEMEAIILSKLM
6192	3		QDYMFSLISGS
22.2	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
	i	1.1	KGGLVSDAYGEDDFSRLGGDEDGYEREEDENSROSEDDDSRTEY
	•	[]	PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPRPPG
1	ļ	1 1	RCSNHLQDKIQKLYERKIKEGMDMNYIIORKKEFRNPSTYRKI.T
			QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK

Deginning nucleotide location corresponding corresponding corresponding to first amino acid maino acid maino acid sequence	SEQ	Predicted	Predicted end	I amino poid
No:				Amino acid segment containing signal peptide
Corresponding to first amino acid acid acid acid acid acid acid acid	NO:			Glutamic Acid F-Phonylalanian College
Lofiret amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acid		location	corresponding	H=Histidine, T=Tsoleucine, V=Lycine,
amino acid amino acid amino acid and residue of amino acid and sequence Residue of amino acid and sequence Residue of and sequence Residue of and sequence Residue of and sequence Residue of and sequence Residue of and sequence Residue of and sequence Residue of and sequence Residue of and sequence Residue of activities	ı		to first	L=Leucine, M=Methiorine, N=Asparacine
### ### ### ### ### ### ### ### ### ##	1		amino acid	P=Proline, O=Glutamine, R=Arginine
### ### ### ### ### ### ### ### ### ##			residue of	S=Serine, T=Threonine, V=Valine.
Sequence Codon, /-possible nuclectide insertion) AKKERTKIEFVITIKIGITIANTSTITITASTAVADAGKEKSKM DARI PVITIAGPIILITTATILEAUVTUTTSASGKITVISAUGT IVKKARO ARKERTKIEFVITIKIGITIANTSTITITASTAVADAGKEKSKM DARI PVITIAGPIILITTATILEAUVTUTTSASGKITVISAUGT IVKKARO TREGGENEMAGKENVISSIAUVAEDSEPESDERAGTEAUGSAAEE KOGLVSDAVGEDDFSRILGGEDCVESEEDBINSROSEDDDSTEINE ROGLVSDAVGEDDFSRILGGEDCVESEEDBINSROSEDDDSTEINE ROGLVSDAVGEDDFSRILGGEDCVESEEDBINSROSEDDDSTEINE ROGLVSDAVGEDDFSRILGGEDCVESEEDBINSROSEDDDSTEINE ROGLVSDAVGENDFSRILGGEDCVESEEDBINSROSEDDDSTEINE ROGLVSDAVGENDFSRILGGEDCVESEEDBINSROSEDDDSTEIN BELTVITIAGPTILITTATILEAUVTVITSASGKITVISAUGT IVKARO TREGGENRAGKENVILSSIAUVAEDSEPESDERGE EAVUGNAAEE KOGLVSDAVGEDDFSRILGGEDEDGVESEEDBINSROSEDDDSTEIN ROGLVSDAVGEDDFSRILGGEDEDGVESEEDBINSROSEDDDSTEINE ROGLVSDAVGEDDFSRILGGEDEDGVESEEDBINSROSEDDDSTEIN ROGLVSDAVGEDFSRILGGEDEDGVESEEDBINSROSEDDDSTEIN ROGLVSDAVGEDFSRILGGEDEDGVESEEDBINSROSEDDDSTEIN ROGLVSDAVGEDFSRILGGEDEDGVESEEDBINSROSEDDDSTEIN ROGLVSDAVGEDFSRILGGEDEDGVESEEDBINSROSEDDDSTEIN ROGLVSDAVGEDGESERGUNGVESEEDBINSROSEDBINSROSEDBINSTEIN ROGLVSDAVGENDFSRILGGEDGVESEEDBINSROSE			amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
AKKERTKIEPTVORKMOTTIANISTITITASTAVADAQKRESKM DAAIPVTIAQPTILITTATLPAVVIVITSASGSKTIVISAVGT IVKRAKQ DAAIPVTIAQPTILITTATLPAVVIVITSASGSKTIVISAVGT IVKRAKQ TIKKGKUSISIAGUSISIAGVARDSSPESDORAGIEAVGGAAFE REGULVENAVGEDPSRILGGDEDVESEEDENGEDDOSTERE PRADDPKDMTEARERDPGELVASFESRYRRMSPDEIKIPPEPPG RESNHLDDRIGKJENEKMINSTITITATSATTAJAAQKRESKM PRADDPKDMTEARERDPGELVASFESRYRRMSPDEIKIPPEPPG RESNHLDDRIGKJENEKMINSTITITATSATTAJAAQKRESKM DSAIPVTITAQPTILITTATLPAVVTVTTSASGSKTIVISAVGT IVKRAKQ DSAIPVTITAQPTILITTATLPAVVTVTTSASGSKTIVISAVGT IVKRAKQ SAIPVTITAQPTILITTATLPAVVTVTTSASGSKTIVISAVGT REGULVBANGGEDPSRIGGGEODDSTERE RESNHLDBRIGKJENEKMINSTITITATSATTAJAAQKRESKM DSAIPVTITAQPTILITTATLPAVVTVTTSASGSKTIVISAVGT REGULVBANGGEOFSENDERSTEREK REGULVBANGGEOFSENDERSTEREK REGULVBANGGEOFSENDENSTEREK REGULVBANGGEOFSENDERSTEREK REGULVBANGGEOFSENDENSTEREK REGULVBANGGEOFSENDENSTEREK REGULVBANGGEOFSENDENSTEREK REGULVBANGGEOFSENDENSTEREK REGULVBANGGEOFSENDENSTEREK REGULVBANGGEOFSENDENSTEREK REGULVBANGGEOFSENDENSTEREK REGULVBANGGEOFSENDENSTEREK REGULVBANGGEOFSENDENSTEREK REGULVBANGGEOFSENDENSTEREK REGULVBANGGEOFSENDENSTEREK REGULVBANGGEOFSENDENSTEREK REGULVBANGGEOFSENDENSTEREK REGULVBANGGEOFSENDENSTEREK REGULVBANGGEOFSENDENSTEREN REGULVBANGGEOFSENDENSTEREN REGULVBANGGEOFSENDENSTEREN REGULVBANGGEOFSENDENSTEREN REGULVBANGGEOFSENDENSTEREN REGULVBANGGEOFSENDENSTEREN REGULVBANGGEOFSENDENSTEREN REGULVBANGGEOFSENDENSTEREN REGULVBANGGEOFSENDENSTERE	ļ		sequence	Codon, /=possible nucleotide deletion.
6193 3 950 TRIGGONIMAGKKINULSSLAVYABDSEPESDORAGIEAVGAAFE KOGLUSDANGENDESSLEGEDYSEEGEDENGSAEDDSATEK PRADDEKDITEAKENDESSLEGEDYSEEGEDENGSAEDDSATEK PRADDEKDITEAKENDESSLEGEDYSEEGEDENGSGEDDSATEK PRADDEKDITEAKENDESSLEGEDYSEEGEDENGSGEDDSATEK PRADDEKDITEAKENDESSLEGENGMINGVIOLIGHEK KORGLUSDANGENSENDESSLEGENGENGENGENDATER REGENHLODKINGLYBEK KIEGEMINYLTSTITTEASHADGKERSKE DSALFUTTIAOPTILITTATIPAVUTUTTSAGGKKTVISAUGT IVKKAKO 6194 3 950 TRIGGONMAGKKINULSSLAVYABDSE PERGEAN I EAVIGAAEE REGENBLODKINGLYERK KIEGEMINYLTIGKKERFINESTITK PERADDEKDITEAKENDESSLAVYABDSE PERGEAN I EAVIGAAEE REGENBLODKINGLYERK KIEGEMINYLTIGKKERFINESTITK PERADDEKDITEAKENTUR KORGLINTYLTITATITATITATITATITATITATITATITATITATIT	<u> </u>	sequence		\=possible nucleotide insertion)
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RGGLVSDAYGEDDFSRLGGDEDGYEEEDEDRINGSEDDDSSTEK PRADDPKINTEASKRPOPGLIVASTSKYNMS PBELKT PPEPPO RCSNHLQDKIQKLYERKI KEGMMNNY I I I QRKKEFRNPSI YEKLI QPCALDELGTNY PKDMFDPHGWSEDSYYEALKAQKLEMOKLEK AKKERTRIEFVTGTKRGTTTMATSTTTTTASTAVADAQKEKSKW BSAIPVITIAQPTILITTATLPAVVVTTTSASGSKTTVI SAVGT IVKKAKQ 6195 736 235 VANGLQSNMSKYCOVCDTYLTHDSPSVRKTHCSGRKHKENVKD YQKWMBEDAQSI.IDKTTAPQOGKIPPTPPSAPPPAGAMIPPP PSLPGPPRPGMMPAPHMGPPMMSPPPPPPAGAMIPPPP PSLPGPPRGMMPAPHMGPPMMSPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	6194	3	950	
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RCSNILQDKIQKLYERKIRGHDMYII TQRKEFRNESIYEKLI QPCALDELGTHYPKDMPDPHGNSBEDSYYEALAKAQKIEMDKLEK AKKERIKIEFYTGTKGGTTINATSTTTTASTAVADAQKRKSKW DSAIPYTTIAQPTILITTATLPAVUTTTASTAVADAQKRKSKW DSAIPYTTIAQPTILITTATLPAVUTTTASGEKTTVISAVGT IVKKAKQ 6195 736 235 VANGLQSNMPKFYCDYCDTYLTHDSPSYRKTHCGGRKHKENYKD YYQKWMBEQAQSLIDKTTAAFQQGKIPPTPFSAPPPAGAMIPPP PSLDCPPRFOMMSAPHNGGPPMMPMPPPPGMPVGPAPGMP PMGGMMPMMPDPPMMPPPAPPMWPTRPGMTRPDR 6196 1512 623 KTGKRRSAAYVRNILDNAEQVISNUEARNIGSPRUTPLLQEEDSH QRLLMGIMVSELKDHFLRRLQGVEKKKLEQMULDYISKLDDLIC HIVBTINNEKENILBWULHFNSGARFAVVFNITTPLLQEEDSH QRLLMGIMVSELKDHFLRRLQGVEKKKLEQMULDYISKLDDLIC HIVBTINNEKENILBWULHFNSGARFAVVFNITTRILETAVIRL HIVBTINNEKENILBWULHFNSGARFAVVFNITTRILETAVIRL HIVBTINNEKENILBWULHFNSGARFAVVFNTHTRILETAVIRL HIVBTINNEKENILBWULHFNSGARFAVVFNTHTRILETAVIRL HIVBTINNEKENILBWULHFNSGARFAVFNTHTSILTDLSS NHAVTRLLQNYKKQPRNSMINKSSPSVFFLEINTYFISILTDLSS NHAVTRLLQNYKKQPRNSMINKSSPSVFFLEINTYFISILTDLSS NHAVTRLLQNYKKQPRNSMINKSSPSVFFLEINTYFISILTDLSS NALYPFEGBDAVMBEYTFPONTSLTNADATREPDLRREFGRYG PIVDVYTPLDFYTRRPRGFAVQPEDVADADALAYNINKWVCG ROBEGGFADMYTFONTSPSSTSSPSQRRTRS RSSSWGRNRRSGDSLKESRHRRFSDSDSHRSSPSSGRYRTS RSSSWGRNRRSGDSLKESRHRRFSHSGRSSPSGVFTSSGTKS RSSSWGRNRRSGDSLKESRHRRFSHSGRSSPSGVFTSSGTKS RSSSWGRNRRSGDSLKESRHRRFSHSGRSSPSGVFTSSGTKS RSSSWGRNRRSGDSLKESRHRRFSHSGRSSPSGVFTSSGTKS RSSSWGRNRRSGDSLKESRHRRFSHSGRSSPSGVFTSSGTKS RSSSWGRNRRSGDSLKESRHRRFSHSGRSSPSGVFTSSGTKS RSSSWGRNRRSGDSLKESRHRRFSHSGRSSRS YRKMSW 1912 SEAALSPSTISPACFLLRKLPALEDGTLPHPPTFLANLDSGTW GVPSLLLYFLSGGUVLVTILVWHLLKTPPEPPTPLPEBERQSV REMPHAADDSEGGALDMCCSRRLPGLPQUPTUWSLADEAGADDST GVPSLLLYFLSGGUVLVTILVWHLLKTPPEPPTPLPEBERQSV REMPHAADDSEGGALDMCCSRRLPGLPQUPTUWSLCHDARGE REMPHAADDSEGGALDMCCSRRLPGLPQUPTUWSLCHDARGE REMPHAADDSEGGALDMCCSRRLPGLPQUPTUWSLCHDARGE GVPSLLLYFLSGGUVLVTILVWHLLKTPPEPPTPLPEBERQSV SRQPSTYSEMMERE ISDDELLDUPPLTUVAGEFTUTTUMITNIEMM GVPSLLLYFRAGGUVTUTTUWHLLTPPEPPTPLPEBERQSV PROPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP				PEADDPKDNTEAEKRDPOELVASFSERVRNMSPDETKIDDEDDC
OPCAIDELGTTYPROMEDPHGMSEDSYYEALAKAQKIEMDKLEK AKKERTKIEFVIGTKKGTTTATTTTTATADAQKKRISKM DSAIPVTTIAQPTILTTATLPAVVTVTTSASGSKTTVISAVGT IVKKAKQ VANGLQSNMPKFYCDVCDTYLTHDSPSVRKTHCGGRKHKENVKD YYQKWMEGQQSLIDETTAAFQQGKIPPTPFSAPPPAGAMIPPP PSLESPRFGMMSAPHINGGPPMMPPPPPAGAMIPPP PSLESPRFGMMSAPHINGGPPMMPPPPPAGAMIPPP PSLESPRFGMMSAPHINGGPPMMPPPPPPPDPDEDSH 6196 1512 623 KTGKRRSAAYVENILDNAGVISNLEARNLEPHITLDEEDSH CRLLMGIMVSELKDHFLEHLQCVELHLHLHCIDSGVLLITETAVIRL HUVETNNRKENLHSWULHFNSRGSAAFFAVFHIMTRILEATNSL FLPFLPPGFHTHIHLIGVCCLPHLHLHCYDSVLLITETAVIRL MKDLDNTEKREKLKFSIIVRLPPLIGQKICRLMGHMSSNIISR NQALYPPEGHDXVDAEFVEEAALHTAMLLGL 6197 3 819 ADPEGTESAVMSRYTRPPHTSLFTRNVADATRPEDLRREFGRYG PIVDVTPLDFYTRRREGFAVGDEVRDAEDALYNLNRKWVCG ROIFLQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSGRRTS RSSSWGRNRRSDSLKESRHRRFSYSGSKSRSKSLDRRSTSARQ SRTPRRNFGSRGRSKSLOKSKSIGKSGSKSLPRRSTSARQ SRTPRRNFGSRGRSKSLOKSKSIGKSGSKSLPRRSTSRSKS RSGRRISDSIARSPCKSFKGYTNFETKVQTAKHSHFRSHSRSRS FRIHAADDSGGALDMCCSBRLRGLQPJTVMALDEABGLQDSQ REMPPPPPPPSPSPDPAQKPPPRGAGSHSITVRSSLCLPFASGFL LAGGVLWFSGVGLVTTTLWHLLHTPPPPPPTPLPPEDRRQSV SRQPSTYSEMMEKIBODPLDLVPFTPVDCVMDLKPEADP TSLTVKKSMGLOERGRSSNSVLIKGLEEFPTPVLIKALDEAGGLODSQ SRQPSTYSEMMEKIBODPLDLVPFTPVDCVMLKPEADP TSLTVKSMGLOERGRSSNSVLITLMCTPGCMSEGFCYLMSPRES ARSYLLSASRVLQAEELHERALDPFLLQAEFFEIPMFVDKKY DIPGLVRKNYKTILPRPHSRVCLTSPDDDDLSSYINANVIRG YGGEEKVYIATQGTVSTVADFPBSRVCLTSPDDDDLSSYINANVIRG YGGEKVYIATQGTVSTVADFPBSRVCLTSPDDDDLSSYINANVIRG YGGEKVYIATQGTVSTVADFPBRRVCLTSPDDDDLSSYINANVIRG YGGEKVYIATQGTVSTVADFPBRRVCLTSPDDDDLSSYINANVIRG YGGEKVYIATQGTVSTVADFPBRRVCLTSPDDDDLSSYINANVIRG YGGEKVYIATQGTVSTVADFPBRRVCLTSPDDDDLSSYINANVIRG YGGEKVYIATQGTVSTVADFPBRRVCLTSPDDDDLSSYINANVIRG YGGEKVYIATQGTVSTVADFPBRRVCLTSPDDDDLSSYINANVIRG YGGEKVYIATQGTVSTVADFPBRRVCLTSPDDDDLSSYINANVIRG YGGEKVYIATQGTVSTVADFPBRRVCLTSPDDDDLSSYINANVIRG YGGEKVYIATQGTVSTVADFBRRVCLTSPDDDDLSSYINANDRG GCKHWFTSWPDQKTPDRAPPLLHLURGERAQQGGHCAPII VICKSGIGRTCGTTATSICCQUCRGGVVDTLKTTCQHRQDRGG MTQHCGQVGFVHHWSLYKKQLSHQSPE ARRESULSSSSKKQADDTKKIFFERTLGTGTAFSEVVLAREKA TGKLFAVKGTYRKKGTLDFRUKKGTDLTRALTRIKKKGTDIVADEDTY YL	1			RCSNHLQDKIQKLYERKIKEGMDMNYIIORKKEFRNPSIVEKLT
AKKERTKIEVTGTKKGTTTNATSTTTTASTAVADAQKEKSKM DSA1PVTI1AQPTILITTATLPAVVTVTTSASGSKTTVISAVGT TUKKAKQ VANGLQSNMPKPYCDYCDTYLTHDSPSVRKTHCGGRKHKENYKD YQKWMEGQAQSLIDKTTAAFQQGKIPPTPSAPPPAGANIPPP PSLPGPRFGMMAPHNGGPPMMPMGPPPGMMPVGPAPGMP PMGGMMPMGPPMMPMPAPPMMYTRPGMTRPDR 6196 1512 623 KTGKRRSANYVRNILDNAEQYISMLEARNIGPRITPLLQEEDSH QRLLMGIMUSELKDHFLERLQGVEKKIEGMVLDY1SKLDLLC HIVBTNNRKENLIKSWLHFNSGABFAVFHIMTRILEATNSL PLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLIKFSIIVRLPPLIGGKIGCHADHFMSSNIISR NHVTRLLQWYKKQPRNSMINNSSVEFFLEINYFISILTDIESS NQALYPPGGHDNVDAEFVEBAALKHTAMLIGL 6197 3 819 ADPEGTESAWSFYRPPHTSIFIRVADATRPEDLRREFGRYG PIVDVYIPLDFTTRRPRGFAVQFEDVRDAEDALYNLNKKWVG RQIEIGFAGODKKTFGQMKSKERRPGSPSDHRRSRSPSORRTRS RSSWGNRRRSDSIKKERHRFSYSGKSKGKSLPRBTSARQ SRTPRNFGSRGRSKSKLOKRSKSIGKSQSSSPQXOTSSGTKS RSSGRHSDSIARSPCKSPKKGYTNFFTKVTTAKHSHFREHSRSRS SYRKMSW 6198 111 1912 SEBALSFSTISPACFLLKKLPALEDGTLPHPDTLGNNYGGARSE KENHADDSEGGALDMCCSRRIPGPLOFTUMBALDEAGCLODSQ REMPPPPPPSPSDBAQKPPPRGSSHSLTVRSSLCLFAASGFL LACGVLWFSGYCHIWSOMATNILVSSLLTLIKQLEPTAMLDGGTW GVPSLLLVELSGGLVUTTLUWHLLRTPPEPPTPLPPEDRGNSV SRQPSTYSEWMBERISDPLDLDPVETPVFDCVMDIKPERDP TSJTVKSMGLOERRGSNVSLTLDMCTFGCNEEGFGYLMSPREES ARSYLLSASRVLQAEELHERGLDFFLLQAEFFEIPMNVDKEY DIPGLVRKNRYKTILPPHFBRRVCLTSPDPDDDLSSYIMANNIRG YGGEEXVIJATQGVIVSTLUWRUGSHTGILWMINIERM EKCTEFWPPEQVANDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPQKTPDRAPPLLHLUWMGRHTGILWMINIERM EKCTEFWPPEQVANDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPQKTPDRAPPLLHLURGHTWUNGENFTILVMINIERM EKCTEFWPPEQUSSSSSWKGAGDIKKIFEFETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY BSPNHLYLVMGLVSGGELFDRIVEKGFTERGASTLRQVIDADAY YJLHRGGVSSSSKKOADEJKKIFFETRUGAFTLRQVIDADAY YJLHRGGUYGDESKIMISDPGESKMISKGGD		ļ		QPCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAOKIEMDKLEK
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VANCUSAMENT (CLYCTYTHINSPSVRKTHCSGRKKHENVKD YYQKMMERGQSLIKTTAPCQGKIPTPFFSAPPPAGMIPPP PSLEGPPREGMMPAPQGKIPTPFFSAPPPAGMIPPP PSLEGPPREGMMPAPHMGPPMMPGPPMMPVGPAPGMRP PMGGMMPMMPGPPMMPPARPMVPTREGMTREDR KTGKRSAAYVRILDMAEQVISNLEARNLGPRLTPLLQEEDSH ORLLMGLMVSELKUHFLRHLGGVEKKKLEQWULDYISKLLDLIC HIVBTNWRKHLHSWULHFNSSGSABEFAVFHINTRILEATMSL PLPLPPPGFHTLHTLIGVCLPLHNLHCIDSGVLLLTETAVIRL MKOLDNTEKREKLKFSIIVRLPPLIGGKICRLMDHPMSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDABEFVEEAALKHTANLLGL ADPEGTEZAWSKYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDPYTRPRBGFAVVQPEDVRDAEDALYNLNKKWVCG RQIEIQFAQGDRKTPGMKSKERHPCSPSDHRRSRSPSQRKTRS RSSSWGRNRRSDSLKESRRRFSYSQSKERSKSLPRRSTSARQ SRTPRRNFGSRGSRSKSLGKSSLGKSGSSPSQKOTSSGTKS RSSGRNRRSDSLKESRRRRFSYSQSKERSKSLPRRSTSARQ REMPRANDSSGRGSRSRSKSLGKSSGSSPCKOFSSGTKS RSHGHABDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSR3 YRHKNSW 6198 111 1912 SEAALSPSTISPACFLLRKLPALEDGTIPHPDTLGMNYEGARSE REMHAADDSEGGALDMCCSRRIPGLPQPIVMEALDBAEGLQDSQ REMPPPPPPPSPDAQKPPPRAGASHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAMLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLETPPEPPTPLPPEDRRQSV SRQPSTYSEMMEK HEDDFLDLPVPETPVFDCVMDI KPEADP TSLTVKSMGLQERGSNVSLTLDMCTPGCNEEGFGYLMSPRRES AREYLLSASRVLQABEHERALDPFLLQABFFEIPMFVDPKEY DIPGLWRKNYKTILENPRSVLTSDEDDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRWWQEHTPIIVMITNIEENN EKCTEVWPEQVAYDGVEITVQKVITHEDYRRLHISLKSGTEER GLKYWFTSWPDQKTDRAPPLLHLVREVEEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCQYGFVHHVWSLYSKQLSHGSPE GKLFAVKCIPKKALKGKESSIENEIAVLRKKHENIVALEDIY SSPNILLVLWGLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLLHRMGIVHPGLVEFBILLVYSODESKKHISDFGLISKMEGKDDAV YYLHRMGIVHPGLVEFBILLVYSODESKKHISDFGLISKMEGKDDAV YYLHRMGIVHROLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHROLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHROLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHROLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHROLVSGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHROLVSGELFDRIVEKGFTTENDASTLIRQVLDAV YYLHRMGIVHROLVSGELFDRIVEKGRUSDFGLFWGANDAV	6105			IVKKAKQ
ATTOKKMEQAGSLINTARAPQAGKIPTPFSAPPAGAMIPPP PSLPGPPREPGMRPAPHMAGPPPMMMRPPPPGMMPWGPPAGMRP PSLPGPPREPGMRPAPHMAGPPPMMMRPPPRGMTRPDR 6196 1512 623 KTGKRRSAAYVENILDNAEQVISNLEANNLGPRITPLLQEEDSH ORLLMGLMVSLIKDHFLEAGVEKKKLEGWULDYISKLDLIC HIVETNMRKHALHSWLHHPNSRGSAAEFAVFHIMTRILEATNSL PLPLPPGFHTLHTILGVQCLPLHNHLHCIDSGVULLITETAVIRL MKDLDNTEKMEKLKFSIIVRLPPLIGGKICRIMPHMSSNIISR NHVIRLLQNYKKQPRNSMINKSSPSVEFLPLNYPTEILITDIESS NQALYPPEGHDNVDAEFVEALKHTAMLLGL 6197 3 619 ADPEGTEEAVMSRYTRPNTSLFIRNVADARRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQPEDVRDARDALYNLMRKWVCG RQIBIGFAGGDRKTPGGMKSKERHPCSFSDHRRSRSPSORRTRS RSSSWGRNRRSDSLKESRHRSFSYSQSKSRSKELPRSTSARQ SRTPRRNFGSRGRSRSKSLQKRSKSIENSSPSGRGTSSGTKS RSSSWGRNRRSDSLKESRHRSFSYSQSKSRSKELPRSTSARQ SRTPRRNFGSRGRSRSKSLQKRSKSIEKGSGSSSPGKOTSSGTKS RSSGRHSDSLARSPCKSPKVTPFETKVQTAKHSHFRSHSRSR FRHHAADDSEGGALDMCCSRRLBGLQCPJVMELKKHSHFRSHSSS KRHPPPPPSPSBDAQKPPPRGAGSHSLTVRSSLCLFAASOFL LACGVLWFSGVGHIWSGNATUSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSTYSEMMESKIEDDPLDLDPPTTWFLDGMPTEGADP TSJTVKSMGLQERRGSNVSLTLDMCTFGCNEGGFGYLMSPRESS AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDDDDDLSSYINANYIRG YGGEEKVY LATGGP LVSTVADFWRMWQERTP IJWITTNIEEMM EKCTEYWPEQVAYDGVETTVQKV UNTENVRILBILKSGTEER CLKYMFTSWPDQKTDRAPPLLHLVREVEAAQQGGPHCAPII VHCSAGIGRTGCFIATSICCQQLRGGGVVDILKTTCQLRQRGG MTQHCSQYGFVHHVMSLYSKQLSHGSPE 6199 144 1211 NRENDESSSSWKGAGAELYKFFFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDLY SEPNHLYLVMQLVSGGELFDRIVEKGFTTEKDASTLIRQVLDAV YYLLRMGIVHRULDFYSDEESKIMISGFGTENERAGRGKSTLIRQVLDAV YYLLRMGIVHRULDFYSDEESKIMISGFGTENERAGRGKERGKGNDAV YYLLRMGIVHRULDFYSDEESKIMISGFGTENERAGRGKERG	9195	736	235	VANGLQSNMPKFYCDYCDTYLTHDSPSVRKTHCSGRKHKENVKD
6196 1512 623 KTGKRRSAAYVRNILDNAEQVISNLEARNISPRITPLIQEEDSH ORLIMGIMVSELKOHFIRILQGVEKKIEQMULDYISKLLDLIC HIVBTNMRKHNILSWULHFINSGSAAEFAVFHIMTRILEATMSL PLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKOLDNTEKNEKLKFSITVRLPPLIQGKICRLMDHPMSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLELNYFIEILTDIESS NQALYPPEGDDNVDAEFVEEAALKHTAMLIGL 6197 3 819 ADPEGTESAVWSTYTFPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYTPLDFYTRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIGFAQGDRKTPGVMKSKERHPCSPSDHRRSRSFSQRTTRS RSSSWGRNRRRSDSLKESRHRRFSVSQSKRSKSLEPRSTSARQ SRTPRRMFGSRGRSRSKSLQRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFFTKVQTAKKSHFFSHGRSRS YRKKNSW 6198 111 1912 SEAALSPSFISPACFLLRKLPALEGGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCZBRIPGIPQPIVMEALDBAEGLQDSQ REMPPPPPPPSPSDPAQKPPPRGAGSHSLTVRSSLCLFAASGFL LAGGVLWFSGYGHLWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPPPPTPLPFPEDRRQSV SRQPSTTYSSWMEKEISDDFLDLDPVPETTPVPDCVMDIKPEADP TSSTVKSMGLQERRGSNVSLTLDMCTPGGNEESFGYLMSPRESS ARBYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFUDKEY DIPGLVRKNYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATOGPIVSTVADFWMVWQBHTPLIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKGGTERR GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGGGMIQHCAPTII VICSAGIGRTGCFIATSICCQQLRGGGVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHGSPE 6199 144 1211 NARENGESSSSWKQAEDIKKTFFKSTLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY SEPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRUKQSGELFDRIVEKGFYTEKDASTLIRQVDAV				YYQKWMEEQAQSLIDKTTAAFQQGKIPPTPFSAPPPAGAMIPPP
KTGKRRSARYVENILDNÆGVISNLERARNLSPRITPILQEEDSH ORLLMGLMVSELKDHFLRHLGVVEKKKIEQMUDYISKIDLIC HIVETNMEKHNLHSWULHINSRGSAAEFAVFHINTRILEATMSL FLPIPPGPHTHHTILGVQCLPHINLHHCIDSGVLLLTETAVIRL MKDLDNTERMEKLKFSIIVRLPPLIGQKICRLWDHFMESSNIISR NHVTRLLQNYKKOPRNSMINKSSFSVEFIPLNYFIEIINTELSS NQALYPFEGHDNVDAEFVEEAALKHTAMLIGL 6197 3 819 ADPEGTEZAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDPYTRRPRGFAYVQFEDVRDAEDALYNLNRKWCG RQIEIQFAQGDRKTFGQMKSKERHPCSPSDHRRSRSPSQRRTRS SSSWGRRRSSDSLKERRFSSVSQSKSRSKSLPRRSTSARQ SRTPRRNFGSRGRSKSLQKRSKSIGKSQSSSPQKTTSSGTKS RSSGWRRRSDSLAKSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS REHHAADDSEGGALDMCCSBELJPGLPQFUYMBALDBREGLQDSQ REMPPPPPPPSPSPSPDAOKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLKQLEPTAWLDSGTW GVPSLLLVFLSGGIVLVTTLUWHLLRTPEPPTPTPLPPEDRRQSV SRQPSTTYSSMMEKKIEDPLDLDPVEPTPTPLPPEDRRQSV SRQPSTTYSSMMEKSIEDPLDLDPVEFTPVPFOVMDIKPEADP TSSTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLQAEFFEIPMNFUDPKEY JDTPGLVRKNRYKTILPMPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVY IATQGPIVSTVADFWRWVWQEHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVHTEDYBLRLISLKSGTEER GLKHYWFTSWPDQKTTPDRAPPLLHLVREVEDAAQOGEPHCAPTI VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHVMSLYENGLEHQSPE OKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY BSPNHLYLWWQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRUKYGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRUKYGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRUKYGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRUKYGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRUKYGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRUKYGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRUKYGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRUKYGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRUKYGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRUKYGGELFDRIVLYSODEESKIMISDFGLISKMGKGRD				PSLPGPPRPGMMPAPHMGGPPMMPMMGPPPPGMMPVGPAPGMRP
ORLIMGENSARYUNILDIAGY ISMLEARNIGERLITPLIQUEDSH ORLIMGENSHINGSEKKKIEDMYLDYISKLIDLIC HIVETNWRKENLHSWULHFINSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPHRLLHCIDSGVILLTETAVIRL MKDLIDNTEKNEKLKSFIIVRLPPLIGQKICRLMDHMSSRIISR NHVIRLLONYKKOPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEESALKHTAMLIGL 6197 3 819 ADEGTESAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRRRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGOMSKERHPCSFSDHRRSSSFSQRRTRS RSSSWGRNRRSDSLKESKHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRRNSGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTMFETKVQTAKHSHFRSHSRSRS VRHKNSW FINHAADDSEGGALDMCCSELTGELQPI IVWEALDEAGELQDSQF LACGVLWFSGVGHINSQNATNLVSSLITLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLRRTPFFPTTLPPEDRRQSV SRQPSTTYSEMMEKIEDDFLDLDPVETTVFDCVMDIKPEADP TSJTVKSMGLQERRGSNVSLTLDMCTFGCNEEGFGYLMSPRESS ARSYLLSASRVLQAEELHEKALDFFLLQAFFEITMNFVDPKSY DIPGLVRKNRYKTILPNPERSVCLTSPDPDDPLSSYINANYIRG VGGEEKVYIANGGPIVSTVADFWRWWQEHTPIIVMINIEMN EKCTEYWPEQVAYDGVEITVQKVIHTEDYRLRILISLKSGTEER GLKHYWFTSWPDQKTPDRAPPILHLVREVEAAQOEGFHCAPTI VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHWMSLYKGLUSHGSPSE GLKHYWFTSWPDQKTPDRAPPILHLVREVEAAQOEGFHCAPTI VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHWMSLYKGLUSHGSPSE TGKLFAVKCIPKKALKGKESSIENEIAVLRKKHENIVALEDIY ESPNHLYLLWGGIVGROFTEKDASTLIRQVLDAV YYLHKMGIVHRDLKFPENLLYYSODESKIMISDFLGKMFRGKGD	6196	1512	600	PMGGHMPMMPGPPMMRPPARPMMVPTRPGMTRPDR
HIVETNMERENLHSWULHFNSRGSAAEFAUFHIMTRILEATMSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSCULLTETAVIRL MKDLDNTEKNELKKFSIIVELPPLIGQKICRLMDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTANLLGL ADPEGTEZAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYMLNRKWVCG RQILEIQFAQGDRKTFGQMKSKERHPCSFSDHRRSRSPSQRRTRS RSSSWGRRRRSDSLKESRHRRFSYSQKSRSKSLPRRSTSARQ SRTFRRNFGSRGRSRSKSLQKSKSIGKSQSSSPQKOTSSGTKS RSSGWGRRRSDSLKESRHRFFSYSQKSRSKSLPRRSTSARQ SRTFRRNFGSRGRSRSKSLQKSKSIGKSQSSSPQKOTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW 6198 111 1912 SEAALSFSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE REMHAADDSEGGALDMCCSBRLPGLPQPIVMEALDBAEGLQDSQ REMPPPPPPSPPSDPAQKEPPPRAGGSHSLTVRSSLCLFAASQFL LACGVLWFSGGGHLWSQNATNLVSSLLTLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSTTYSEMMEKIEDDFLDDPVETTYVFDCVMDIKPEADP TSJTVKSMGLQERRGSNVSLTLDMCTFGCNEEGFGYLMSPREES AREYLLSASRVIQAEELHEKALDPFLLQAEFFEIPMNFVDPKRY DIPGLVRKNRYKTILPNPHSRVCLTSBDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWGEHTPIIVMITNIEEMN EKCTEWPERQVADGVEITVQKVIHTEDWRLRLISLKSGTEER GLKHYWFTSWPDQRTPDRAPPLLHLVREVEBAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQLRQEGVVDILKTTCQLRQDRGG NICHCRQYQFVHHWMJVEKGLSHQSPE 6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKCKESSIENEIAVLRKKKHENIVALEDIY ESPNHLYLVMQLVSGGELIFDRIVVEKGFYTEKDASTLIRQVLDAV YYLHKMGIVHRDLKPENLLYYSODESKIMISDFGLSKMFGKGD	0250	1212	623	KTGKRRSAAYVRNILDNAEQVISNLEARNLGPRLTPLLQEEDSH
FLPLPPGFHTLHTILGVGCLPLHNLLHCIDSGULLITETAVIRL MKDLDNTEKNEKLKFS I IVRLPPLIGQKICRLWDHPMSSNI ISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIE ILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRPRGFAVVQFEDVRDAEDALYNLNRKWVCG ROIE IQ FAQGDRKTPGQMKSKERHPCS PSDHRRSRS PSQRRTRS RSSSWGRNRRRSDSLKESRIRRFFSVSQSKSRSKSLDRRSTSARQ SRTPRRNJGSRGRSKSLOKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARS PCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW 111 1912 SEAALSPSFISPACFLLRKLPALEDGTLPHPDTIGMNYEGARSE RENHAADDSEGGALDMCCSRLPGGLPQPIVMEALDEAGELQDSQ REMPPPPPPSPSDPAQKPPPRGASHSLTVRSSLCLFFASQFI LACGULWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTIVWHLLRTPPEPPTPLPPEDRRQSV SRQPSFTYSEMMEKIEDDFLDLDPVETPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEGGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFIPMNPUPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDDPLSSYINANYIRG YGGEEKVYIATGGPIVSTVADFWRMVWGEHTPIIVMTINIEEMN EKCTEVMPEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLLLVREVEEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHWALYEKQLSHQSPE 6199 144 1211 MARENGESSSWKKQAEDIKKIFFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY ESPNILYLVMQLVSGGEIDRIVEKGFYTEKDASTLIRQVLDAV YVLHRMGIVWRDLKPENLLYYSODEEKIMISDFGLSKWFGKGD				QKDDMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC
MKDLDNTEKNEKLKFSITURLPPLIGKICRICHDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYPIEILTDIESS NQALYPFECHDNVDAEFVEEAALKHTAMLIGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRPRRGFAYVQFEDVRDAEDALYNLNRKWVCG ROIEBIQFAGGDRATTGGOMKSKERHPCSPDHRRSSPSGRRTRS RSSWGRNRRSDSLKESRHRSFSYSGCKSRSKSLPRRSTSARQ SRTPRRNFGSRGRSRSKSLOKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRKKNSW 111 1912 SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSBRLPGLPQPIVMEALDEAEGLODSQ REMPPPPPPPSPDPDPDPAGKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSONATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSFTYSEWMEEKIEDDFLDLDPVPETPVPLOVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTTGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDFLSSYINANYIRG YGGEEKYYIATGJPIVSTVADFWMWWQEHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDOKTPDRAPPLLHLVREVEEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQOLRGGGVVDIKTTCQLRQDRGG MIQHCSQYQFVHHVMSLYEKGLSHOSPE 6199 144 1211 MARENGESSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKSKESSIENBIAVLRKIKHENIVALEDIY ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKKDASTLIRQVLDAV YYLHRMGIVHRDLKPENLLYYSODEESKIMISDFGLSKMECKGD	i			FLDLDDCEUTH HTTL CHOOL DE TRUTTE CONTRACTOR DE LA CONTRAC
NHVTRLLQNYKKQPRNSMINKSSPSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAFFVEAALKHTAMLLGL ADPEGTEZAWMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRTRS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRRNFGSRGRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKKSHFRSHSRSRS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE REMHAADDSEGGALDMCCSBRLPGLPQPIVMEALDEAGGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASOFL LACGVLWFSGYCHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSFTYSEWMEKISDDFLDLDPVETPVPDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMMFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRWWQEHTPIIVMITNIEEMN EKCTEYMPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTDRAPPLLHLVREVEBAAQOEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCSQYQFVHHVMSLYEKQLSHQSPE 6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA TGKLFAVKCI?KKALKGKESSIENEIAVLRKIKHENIVALEDIY ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKBASTLIRQVIDAV YYLHRMGIVHRDLKPENLLYYSODESKIMISDFGLSKMRGKGD				MKDLDNTEKNEVI VEGITUDI DDI TOOKIGDI KINANDA
6197 3 819 ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSFSQRRTRS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTFRRNFGSRGSRKSKLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDBIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSR YRHKNSW 6198 111 1912 SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPJIVMEALDEAEGLQDSQ REMPPPPPPSPSDPAQKPPPRGAGSHSLTVRSSLCLFAASOFL LACGVLWFSGYGHTWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGYLUVTTLVWHLLRTPPEPPTPDPEDRRGSV SRQPSFTYSEWMEKIEDDPLDDPVEFTVYDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDDDDPLSSYINANYIRG YGGEEKVYIAHTQCPIVSTVADFFWRWVQEHTPIIVMITNIEMM EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCSQYQFVHIVMSLYEKQLSHQSPE 6199 144 1211 MARENGESSSSWKKQAEDIKKIFFFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKCKESSIENEIAVLRKIKHENIVALEDIY ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRDLKPENILYYSODEESKIMISDFGLSKMEKKGD				MHVTRILONYKKOPPNSMINKSSESVEELDINVETERA TOARGA
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AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEMN EKCTEYWPBEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPILHLVREVEBAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE 6199 144 1211 MARENGESSSSWKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRDLKPENLLYYSODEESKIMISDFGLSKMEGKGD	, 1			TS:TVKSMGIOERRGSMGITI.DMCTDCGMDBGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE 6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRDLKPENLLYYSODEESKIMISDFGLSKMEGKGD	1			AREYLLSASRVI.OAERI.HEKAT.DDELT.OABBERT.DAMBURGES
YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE 6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRDLKPENLLYYSODEESKIMISDFGLSKMEGKGD	1			DIPGLVRKNRYKTII.PNPHSRVCI.TSDDDDDDI.GGVTXXXXXXXXX
EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE 6199 144 1211 MARENGESSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY ESPNHLYLWQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRDLKPENLLYYSODEESKTMISDFGLSKMEGKGD			1	YGGEEKVYIATOGPIVSTVADFWRMUMORUTDTTUMTTWTEELA
GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE 6199 144 1211 MARENGESSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRDLKPENLLYYSODEESKTMISDFGLSKMEGKGD	[[1	1	EKCTEYWPEEQVAYDGVEITVOKVIHTEDYRIRI,TGI.KGGTDDD
VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE 6199 144 1211 MARENGESSSSWKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRDLKPENLLYYSODEESKIMISDFGLSKMEGKGD	[]	1	ł	GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAOOEGPHCAPIT
6199 144 1211 MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRDLKPENLLYYSODEESKLMISDFGLSKMEGKGD		1	}	VHCSAGIGRTGCFIATSICCOOLROEGVVDILKTTCOLRODGC
1211 MARENGESSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRDLKPENLLYYSODEESKIMISDFGLSKMEGKGD				MIQHCEQYQFVHHVMSLYEKOLSHOSPE
TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRDLKPENLLYYSODEESKIMISDFGLSKMEGKGD	6199	144	1211	MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA
ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRDLKPENLLYYSODEESKIMISDFGLSKMEGKGD				TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY
YYLHRMGIVHRDLKPENLLYYSODEESKIMISDFGLSKMFGKGD		İ		ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIROVLDAV
VMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPP		į		YYLHRMGIVHRDLKPENLLYYSODEESKIMISDFGLSKMEGKGD
				VMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ı	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			FYDENDSKLFEQILKAEYEFDSPYWDDISDSAKDFIRNLMEKDP
ĺ			NKRYTCEQAARHPWIAGDTALNKNIHESVSAQIRKNFAKSKWRQ
	1	1	AFNATAVVRHMRKLHLGSSLDSSNASVSSSLSLASQKDCASGTF
		<u>L</u>	HAL*
6200	702	96	LPEVPHSLRPRVKPHLCCAQPAVRVMARLPKLAVFDLDYTLWPF
ŀ			WVDTHVDPPFHKSSDGTVRDRRGQDVRLYPEVPEVLKRLQSLGV
1			PGAAASRTSEIEGANQLLELFDLFRYFVHREIYPGSKITHFERL
	ł	ļ	QQKTGIPFSQMIFFDDERRNIVDVSKLGVTCIHIQNGMNLQTLS
		i	QGLETFAKAQTGPLRSSLEESPFEA
6201	2809	2383	GQTPRVRWKMRRSLRAGKRRQTAGRKSKSPPKVPIVIQDDSLPA
1			GPPPQIRILKRPTSNGVVSSPNSTSRPTLPVKSLAQREAEYAEA
1			RKRILGSASPEEEQEKPILDRPTRISQPEDSRQPNNVIRQPLGP
	<u></u>		DGSQGFKQRR
6202	2	426	INADRAAVASSLLSRPTRKMAPQKDRKPKRSTWRFNLDLTHPVE
1	1		DGIFDSGNFEQFLREKVKVNGKTGNLGNVVHIERFKNKITVVSE
1			KQFSKRYLKYLTKKYLKKNNLRDWLRVVASDKETYELRYFQISQ
			DEDESESED
6203	419	2550	RCPRPPATAGAAASRPDRSPPSGISGSEAAAGAGAAAPASQHPA
	1		TGTGAVQTEAMKQILGVIDKKLRNLEKKKGKLDDYOERMNKGER
İ			LNQDQLDAVSKYQEVTNNLEFAKELQRSFMALSQDIOKTIKKTA
}			RREQLMREEAEQKRLKTVLELOYVLDKLGDDEVRTDLKOGINGV
}			PILSEEELSLLDEFYKLVDPERDMSLRLNEOYEHASIHLWDLLE
	1		GKEKPVCGTTYKVLKEIVERVFQSNYFDSTHNHONGLCEEEEAA
-			SAPAVEDQVPEAEPEPAEEYTEOSEVESTEYVNROFMAETOFTS
1	}		GEKEQVDEWTVETVEVVNSLQQQPQAASPSVPEPHSLTPVAQAD
1	1		PLVRRQRVQDIMAQMQGPYNFIQDSMLDFENQTLDPAIVSAQPM
1	1		NPTQNMDMPQLVCPPVHSESRLAQPNQVPVQPEATQVPLVSSTS
i	ļ.		EGYTASQPLYQPSHATEQRPQKEPIDQIQATISLNTDQTTASSS
	1		LPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNMNAPVP
1	1 1		PVNEPETLKQQNQYQASYNQSFSSQPHQVEQTELQQEQLQTVVG
			TYHGSPDQSHQVTGNHQQPPQQNTGFPRSNQPYYNSRGVSRGGS
		1	RGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTQSQFSAP
1	!		RDYSGYQRDGYQQNFKRGSGQSGPRGAPRGRGGPPRPNRGMPQM NTOOVN
6204	2933	787	
		, . ,	CTHNLISLIGGRALIHFNRFLNLKIQEGEAHNIFCPAYDCFQLV
			PGDIIKSVVSKEMDKRYLQFDIKAFVENNPAIKWCPTPGCDRAV RLTKQGSNTSGSDTLSFPLLRAPAVDCGKGHLFCWECLGEAHEP
			CDCQTWKNWLQKITEMKPEELVGVSEAYEDAANCLWLLTNSKPC
1			ANCKSPIQKNEGCNHMQCAKCKYDFCWICLEEWKKHSFVHWEVI
1 1		i	YRCTRYEVIQHVEEQSKEMTVEAEKKHKRFQELDRFMHYYTRFK
]			NHEHSYQLEQRLLKTAKEKMEQLSRALKETEGGCPDTTFIEDAV
]			HVLLKTRILKCSYPYGFFLEPKSTKKEIFELMQTDLEMVTEDL
1			AQKVNRPYLRTPRHKIIKAACLVQQKRQEFLASVARGVAPADSP
1 1	1	1	EAPRRSFAGGTWDWEYLGFASPEEYAEFQYRRHRQRRRGDVHS
			LLSNPPDPDEPSESTLDIPEGGSSSRRPGTSVVSSASMSVLHSS
1 1	İ		SLRDYTPASRSENQDSLQALSSLDEDDPNILLAIQLSLQESGLA
1		1	LDEETROFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSE
]]	ļ		LLELGDSLMRLGAENDPFSTDTLSSHPLSEARSDFCPSSSDPDS
1 1	[AGQDPNINDNLLGNIMAWFHDMNPQSIALIPPATTEISADSQLP
1 1	ł		CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEENI
}]		PGGGKQHPQAW
6205	1	1200	RAHRGKMALEVGDMEDGOLSDSDSDMTVAPSDRPLQLPKVLGGD
			SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR
1 1			KRQKCFNPPPKPEPFQFGQSSQKPPVAGGKKINNIWGAVLQEQN
		1	QDAVATELGILGMEGTIDRSRQSETYNYLLAKKLRKESQEHTKD
		· · · · · · · · · · · · · · · · · · ·	LDKELDEYMHGGKKMGSKEEENGQGHLKRKRPVKDRLGNRPEMN
			The state of the s

		· · · · · · · · · · · · · · · · · · ·		
	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
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		location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1		amino acid	sequence	Codon, /=possible nucleotide deletion,
١	·	sequence		\=pcssible nucleotide insertion)
ı				YKGRYEITAEDSQEKVADBISFRLQEPKKDLIARVVRIIGNKKA
١				IELLMETAEVEQNGGLFIMNGSRRRTPGGVFLNLLKNTPSISEE
ı				QIKDIFYIENQKEYENKKAARKRRTQVLGKKMKQAIKSLNFQED
-				DDTSRETFASDTNEALASLDESQEGHAEAKLEAEEAIEVDHSHD
- [•	LDIF
ſ	6206	10	1442	IISERRERSCLHLVCIRCSCDVVEMGSVLGLCSMASWIPCLCGS
١				APCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQ
- 1				LNKIPGFCENEKGVVPCNILVGYKAVYRLCFGLAMFYLLLSLLM
-1	[IKVKSSSDPRAAVHNGFWFFKFAAAIAIIIGAFFIPEGTFTTVW
-				FYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKMEEGNSRCWYA
-1				ALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLC
١				VGASVMSILPKIQESQPRSGLLQSSVITVYTMYLTWSAMTNEPE
- [[TNCNPSLLSIIGYNTTSTVPKEGQSVQWWHAQGIIGLILFLLCV
1	ı			FYSSIRTSMNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
1	ł			RAVDNERDGVTYSYSFFHFMLFLASLYIMMTLTNWYRYEPSREM
1	i	i		KSQWTAVWVKISSSWIGIVLYVWTLVAPLVLTNRDFD
Г	6207	2924	1471	TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG
1	İ			GGGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSPY
	j			SVVCKYFQRGYCIYGDRCRYEHSKPLKQEEATATELTTKSSLAA
1	ľ			SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEDWVNAIEPVP
1				GQPYCGRTAPSCTEAPLQGSVTKEESEKEQTAVETKKQLCPYAA
ł	.			VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA
1		1		HEKDMEL SERVORSKERINGOT ON THE HEKDMELSER VAN THE HEKDWELSER VAN THE HEKDWELSER VAN THE H
ı	j	1		HEKDMELSFAVQRSKDMVCGICMEVVYEKANPSERRFGILSNCN
	1	İ		HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWVEE
1	J	1		KEEKQKLILKYKEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD
	ľ	l		GRRESPOROKVGTSSRYRAQRRNHFWELIEERENSNPFDNDEEE
H	6208	2924	1471	VVTFELGEMLLMLLAAGGDDELTDSEDEWDLFHDELEDFYDLDL
1	1		14/1	TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG
l	- 1			GGGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSPY
				SVVCKYFQRGYCIYGDRCRYEHSKPLKQEEATATELTTKSSLAA
L	1	ļ		SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEDWVNAIEFVP
1	į.			GOPYCGRTAPSCTEAPLQGSVTKEESEKEQTAVETKKQLCPYAA
ı	1			VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA
1	1			HEKDMELSFAVQRSKDMVCGICMEVVYEKANPSERRFGILSNCN
1	1	f	İ	HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWVEE
	į]	KEEKQKLILKYKEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD
	1			GRREEPQRQKVGTSSRYRAQRRNHFWELIEERENSNPFDNDEEE
H	6209	1758	920	VVTFELGEMLLMLLAAGGDDELTDSEDEWDLFHDELEDFYDLDL
l		1.30	829	ERLCFPCMQSKIYSYMSPNKCSGMRFPLQEBNSVTHHEVKCQGK
1				PLAGIYRKREEKRNAGNAVRSAMKSEEQKIKDARKGPLVPFPNQ
		İ		KSBAAEPPKTPPSSCDSTNAAIAKQALKKPIKGKQAPRKKAQGK
l				TQQNRKLTDFYPVRRSSRKSKAELQSEERKRIDELIESGKEEGM
1				KIDLIDGKGRGVIATKQFSRGDFVVEYHGDLIEITDAKKREALY
1	1		j	AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ
	1	1		TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL
┢	6210	3761	387	KH
		2.01	30/	IFGMSKLRMVLLBDSGSADFRRHFVNLSPFTITVVLLLSACFVT
١.		·		SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV
			٠. ا	SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD
	}	1	l	CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE
		1		IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG
				SGPIWFDDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKG
	1	ļ	f	ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK
	J			QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWOCKHHE
	-	ļ	1	WGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVETORI.
_				LGKVCDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWL

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ı	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			FLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLV
	!		GGDIPCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVV
			SILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSH
	<u>'</u>		SRDVGVVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD
1	J.	[IEDAHVLCQQLKCGVALSTPGGARFGKGNGQIWRHMFHCTGTEQ
			HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT
1			RPTIPEESAVACIESGQLRLVNGGGRCAGRVEIYHEGSWGTICD
	1		DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEMKCN
İ			GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE
1	İ		ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGKINP
			ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET
ŀ			WITCDNKIRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAQV
ł			VCQQLGCGPALKAFKEAEFGQGTGPIWLNEVKCKGNESSLWDCP
1			ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIA
1			VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR
			EMNSCLNADDLDLMNSSGGHSEPH
6211	3761	387	IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT
			SSLGGTDKELRLVDGENKCSGRVEVKVOREWGTVCNNGWGMPAT
			SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHV9CRGNEGALWD
			CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCGGDTF
			IKFQGRWGTVCDDNFNIDHASVICROLECGSAVSESGSSNEGEG
			SGPIWFDDLICNGNESALWNCKHOGWGKHNCDHAEDAGVICSKG
			ADLSLRLVDGVTECSGRLEVRFOGEWGTICDDGWDSVDAAVACV
1 1			QLGCPTAVTAIGRVNASKGFGHIWLDSVSCOGHEDAVWOCKUUB
1 1	1		WGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVETOR
1			LGKVCDRGWGLKEADVVCROLGCGSALKTSYOVYSKTOATNTWIL
			FLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLV
1 1	ı		GGDIPCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVV
]			SILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSH
}			SRDVGVVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD
1 1			IEDAHVLCQQLKCGVALSTPGGARFGKGNGQIWRHMFHCTGTEQ
1	ł		HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT
1			RPTIPEESAVACIESGOLRLVNGGGRCAGRVBIYHEGSWGTICD DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEMKCN
l f			GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE
1 1	i		ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGKINP
		1	ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET
1 1	i	i	WITCDNKIRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAQV
[1	Ì	VCQQLGCGPALKAFKEAEFGQGTGPIWLNEVKCKGNESSLWDCP
1 1	1	j	ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIA
			VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR
 			EMNSCLNADDLDLMNSSGGHSEPH
6212	1	1134	LKWELRPGGAVWGTGRGAGTGAPRSCCCOTNPGPPSSLRRAFRE
		[RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL
1			GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE
	İ	1	QKNNCVMPEDVKNFYLMINGFHMTWSVKLDEHIIPLGSMAINSI
			SKLTQLTQSSMYSLPNAPTLADLEDDTHRASDDOPEKPHFDSPS
		;	VIFELDS CNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFI.T
		1	DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY
}	Ì		NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK
			GPSGPSGPSTSSTSKSSSGSGNPTRK
6213	1	1134	LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR
1		1	RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEREASSPGI.
	•	- I	GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE
i	j	1 '	QKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMATNST
			SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS
•			SACULTURA SACULT

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1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first		L=Leucine, M=Methionine, N=Asparagine,
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- 1	residue of	1	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion -
	sequence	<u> </u>	\=possible nucleotide insertion)
			VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHET.T
1			DTFTAYYRLLITHLGLPQWQYAFTSYGISPOAKORVSMYKDTTV
ı			NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGOK
			GPSGPSGPSTSSTSKSSSGSGNPTRK
6214	2	460	HELAPSAIRRAARLGLGPARWQSRAAAFYFVRGFRTGWSFVGWV
· I		Į.	VLGTSAKRTRLFFFLSKMAASSRAOVLALYRAMLRESKRESAVN
ļ	1	ĺ	YRTYAVRRIRDAFRENKNVKDPVEIQTLVNKAKRDLGVIRRQVH
			IGQLYSTDKLIIENRDMPRT
6215	2	1849	FVAGGPRGSGSAAETMPEIRVTPLGAGQDVGRSCILVSIAGKNV
1	J]	MLDCGMHMGFNDDRRFPDFSYITONGRLTDFLDCVIISHFHLDH
1	1		CGALPYFSEMVGYDGPIYMTHPTQAICPILLEDYRKIAVDKKGE
1			ANFFTSQMIKDCMKKVVAVHLHQTVQVDDELEIKAYYAGHVLGA
1			AMFQIKVGSESVVYTGDYNMTPDRHLGAAWIDKCRPNLLITEST
			YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGRAQELC
1			ILLETFWERMNLKVPIYFSTGLTEKANHYYKLFIPWTNQKIRKT
1	i .		FVQRNMFEFKHIKAFDRAFADNPGPMVVFATPGMLHAGQSLQIF
	ļ		RKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRQVLEVK
			MOVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKMEFLKQ
i l	1		KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKREMAQGL
			LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEHQLRFTC
			RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSVTVESVL
			LQXXXPSEDPGTKVLLVSWTYQDEELGSFLTSLLKKGLPQAPS
6216	11	393	QTTRPEPRNSALRQSRSKMAVVGVSSVSRLLGRSRPQLGRPMSS
1 1			GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHHGEHERPE
			FIAYPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYEDE
6217	9	1178	TRVGRGESGLKMEVKPPPGRPQPDSGRRRRRGEEGHDPKEPEQ
1 1	İ		LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQTKRSRG
1 1			FGFVTYSCVEBVDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA
1 1	1	i	HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEDRQSGK
1			KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSKQEMQS
1 1			AGSQRGRGGGSGNFMGRGGNFGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
1	Į.		GGSRGSYGGGDGGYNGFGGDGGNYGGGPGYSSRGGYGGGGPGYG
i 1	i		NQGGGYGGGGYDGYNEGGNFGGGNYGGGGNYNDFGNYSGQQQS
L	1		NYGPMKGGSFGGRSSGSPYGGGYGSGGGGGGGGGGRRF
6218	1305	906	SCERRGFIMADDLKRFLYKKLPSVEGLHAIVVSDRDGVPVIKVA
			NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV
L		i	VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELRQVVEVS
6219	2	890	AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPEADRPHORPFL
1		-	IGVSGGTASGKSTVCEKIMELLGQNEVEQRQRKVVILSQDRFYK
1			VLTABQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP
			TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF
1 1	1	İ	VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEEFCLP
1 1	f		TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG
		1	RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH
6220	227	764	EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN
Į į	1		KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ
1 1			ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK
1 1	J	1	LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ
	1	ļ	NAH
6221	98		RWIWDLNPVSDGLBLRPKYNGILHCLTTIWKLDGLRGLYQGVTP
ı - F		1	NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG
		,	AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK
			ABCONG ANGUING BOUGHOUS ANGUING INCOME DIPOKIAK
. ,			
' '		1.	YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AOLSTVEYISVAALSKIFAVAATYDYONWAADLODOUMEYGGUY
		[]	AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI
			AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL LDLREKRK

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide		Managarine, Catysteine, Dalamarkia haid a
""	location	location	Grande Acid, F=Phenylalanine G_clicate
ı	corresponding	corresponding	n=nistidine, I=Isoleucine, K=Tweine
İ	toffesponding	to first	L=Leucine, M=Methionine, N=Asparagine
- }	to first	amino acid	P=Proline, Q=Glutamine R=Arginine
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ĺ	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	-	\=possible nucleotide insertion)
6222	2	2116	MADELPALLINGER PROFESSION
1	1		MARELRALLWGRRLRPLLRAPALAAVPGGKPILCPRRTTAQLG
ŀ	ł	1	PRRNPAWSLQAGRLFSTQTAEDKEEPLHSIISSTESVQGSTSKH
		j	LEVALTRELDIVARSLYSEKEVFIRELISMA STALEVI TITTI
			SUGUAL PEMETHLOTNAEKGTITIODTGIGMTOPPINGNIGHTA
i		ļ	RSGSKAFLDALQNQAEASSKIIGOFGVGFVSA FMIA DDIIBINGD
]		ĺ	SAAPGSLGYQWLSDGSGVFEIAEASGVRTCTKTTTHI.VETCVES
1	1		SSEARVRDVVTKYSNFVSFPLYLNGRRMNTI.OATUMMDDVDVDE
ĺ	1	Į.	WQHEEFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPDMKPSM
j		1	FDVSRELGSSVALYSRKVLIQTKATDILPKWLRFIRGVVDSEDI
	1	i	PLNLSRELLQESALIRKLRDVLQQRLIKFFIDQSKKDAEKYAKF
	1	i	FEDYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTSLS
1			FYASHMACTINITYYLGADYREDIAKLLRYESSALPSGQLTSLS
Í			EYASRMRAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLFCF
1	1		EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPAAE
i	1		CLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLEMG
- 1	1		AARHFLRMQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLRAS
6223	3	716	LEGUMQULVDQIYENAMIAAGLVDDPRAMVGRINET.T.VKAT EDU
	-	715	DAWARTMAGMVDFODEEOVKSFIENMEVECNVUCVUDVDDOGGV
Į	1		KLVDILEGIRKNFDEAAKVLKFNCEFNOHSDSCVVI.GA VVXIIIGI
[1		GGLTQDLKAAARCFLMACEKPGKKSIAACHNVGLLAUDGOMED
i	1		GOPDLGKARDYYTRACDGGYTSSCFNT.SAMFI.OGADGEDVDWDT
1			ACKISMKACDLGHIWACANASRMYKLGDGVDKVEAKAEVIKNRA
6224	1		QQVHKEQQKGVQPLTFG
6225		133	LRTISSMAWGPLLLTLLAHCTGSWAQSVLTQPPSVSGARIPHEK
0223	3259	938	LLSCHRLAICKLPFSVESRKTVMGPOGARROAFLAEGDVENDER
1	1 1		QKEWRLLSPAQRALYREVTLENYSHIVSLGTIJJSKDBLIDDIBO
	ļ.		GEV PWGEERRRRPGPCAGIYAEHVI.RPKNT.GLAHODOOOT OROD
l l	1		QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES
i	i i		SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH
i			KKAHSRQKLFTCRECHQGFRDESALLLHQNTHTGEKSYVCSVCG
1	{		RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH
1]]		TGEKPYECQECGRRFNDKSSYNKHLXAHSGEKPFVCKECGRGYT
1	i i		NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK
	!	ı	PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST
1	i i	ļ	LVYHORTHSGEVOETGPROGGETOVATT
	i	i	LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEK>FVC
1			KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH
1 1	·		LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE
1 1	1		KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH
			SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN
1		i	WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE
1 1		ŀ	RPFVCQECKRGYTSKSDLTVHERIHTGERPVECORCGPKEENVC
6226	29		YYSKHLKRHLREKRFCTGSVGEASS
	23	266	TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS
6227			IMEGGGQSLRVSTGLSWLLSLPWRAORIRAGRSYA
1 022/	2581	890	MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP
}	!		NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS
			YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS
1 1	1	1	AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL
]]	1	ľ	NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI
·	ľ	[-	VASNSI DDATIADDVDASUADIA GVDAVIGORIVA
1		1	VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL
1	į	1.	PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG
			QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQQAAQPTRWV
}	1	1:	APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN
	i	1	NYNPRDFDWNLKHGRVFIIKSYSEDDIHRSIKVNIWCSTRUCHV
1		1 1	RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDVNTCAG
		1.7	VWSQDKWKGRFDVRWIFVKDVPNSOLRHIRIENWENKDVTNCDD
		1.7	VWSQDKWKGRFDVRWIFVKDVPNSQLRHIRLENNENKPVTNSRD FQEVPLEKAKQVLKIIASYKHTTSIPDDFSHYEKRQ

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
No:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
i	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
i	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
6228	47	1978	\=possible nucleotide insertion)
	1	1370	GRRCRRGAVMELAQEARELGCWAVEEMGVPVAARAPESTLRRL
	ł	<u>'</u>	CLGQGADIWAYILQHVHSQRTVKKIRGNLLWYGHQDSPQVRRKL
	1		ELEAAVTRLRAEIQELDQSLELMERDTEAQDTAMEQARQHTQDT
1	į.		QRRALLLRAQAGAMRRQQHTLRDPMQRLQNQLRRLQDMERKAKV
			DVTFGSLTSAALGLEPVVLRDVRTACTLRAQFLQNLLLPQAKRG
		Į	SLPTPHDDHFGTSYQQWLSSVETLLTNHPPGHVLAALEHLAAER
İ	l .		EAEIRSLCSGDGLGDTEISRPQAPDQSDSSQTLPSMVHLIQEGW
1			RTVGVLVSQRSTLLKERQVLTQRLQGLVEEVERRVLGSSERQVL
1			ILGLRRCCLWTELKALHDQSQELQDAAGHRQLLLRELQAKQQRI
1	1		LHWRQLVEETQEQVRLLIKGNSASKTRLCRSPGEVLALVQRKVV
			PTFEAVAPQSRELLRCLEEEVRHLPHILLGTLLRHRPGELKPLP
			TVLPSIHQLHPASPRGSSFIALSHKLGLPPGKASELLLPAAASL
1	1		RQDLLLLQDQRSLWCWDLLHMKTSLPPGLPTQELLQIQASQEKQ
}	1		QKENLGQALKRLEKLLKQALERIPELQGIVGDWWEQPGQAALSE
6229	1571	560	ELCQGLSLPQWRLRWVQAQGALQKLCS
]	560	GPSLLGTRGTPNPARTLQIFFLIIGRRLTGRMAAVDDLQFEEFG
l	1		NAATSLTANPDATTVNIEDPGETPKHQPGSPRGSGREEDDELLG
	l i		NDDSDKTELLAGQKKSSPFWTFEYYQTFFDVDTYQVFDRIKGSL
1]		LPIPGKNFVRLYIRSNPDLYGPFWICATLVFAIAISGNLSNFLI
I	1 1		HLGEKTYHYVPEFRKVSIAATIIYAYAWLVPLALWGFLMWRNSK
ĺ	! !		VMNIVSYSFLEIVCVYGYSLFIYIPTAILWIIPHKAVRWILVMI
	Į į		ALGISGSLLAMTFWPAVREDNRRVALATIVTIVLLHMLLSVGCL
6230	1723	600	AYFFDAPEMDHLPTTTATPNQTVAAAKSS
	-/20	800	SKMSGRSGKKKMSKLSRSARAGVIFPVGRLMRYLKKGTFKYRIS
	1		VGAPVYMAAVIEYLAAEILELAGNAARDNKKARIAPRHILLAVA
	1		NDEELNQLLKGVTIASGGVLPRIHPELLAKKRGTKGKSETILSP
			PPEKRGRKATSGKKGGKKSKAAKPRTSKKSKPKDSDKEGTSNST
			SEDGPGDGFTILSSKSLVLGQKLSLTQSDISHIGSMRVEGIVHP
	1		TTAEIDLKEDIGKALEKAGGKEFLETVKELRKSQGPLEVAEAAV
			SQSSGLAAKFVIHCHIPOWGSDKCEEQLEETIKNCLSAAEDKKL
			KSVAFPPFPSGRNCFPKQTAAQVTLKAISAHFDDSSASSLKNVY FLLFDSESIGIYVQEMAKLDAK
6231	149	870	LIFECCTMDDGIDVILLINGSGD
		0,0	LIFSSSTMDRSLRNVLVVSFGFLLLFTAYGGLQSLQSSLYSEEG
-	1		LGVTALSTLYGGMLLSSMFLPPLLIERLGCKGTIILSMCGYVAF SVGNFFASWYTLIPTSILLGLGAAD WCACGOWY
1	1		SVGNFFASWYTLIPTSILLGLGAAPLWSAQCTYLTITGNTHAEK AGKRGKDMVNOYEGIEFLIFOSSGUNGNI TOOLUGU
ļ	ļ. <u>j</u> .	ł	AGKRGKDMVNQYFGIFFLIFQSSGVWGNLISSLVFGQTPSQETL PEBOLTSCGASDCLMATTTTNSTQRPSQQLVYTLLGIYTGSGVL
			AVLMIAAFLQPIRDVQRESE
6232	3679	1476	FVAGTTMAGFWVGTAPLVAAGRRGRWPPQQLMLSAALRTLKHVL
Į	ļ.		YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC
ĺ		}	KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA
}			IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA
		J	IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY
	1	İ	PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL
1		ł	LIEKFIDNPRHIEIQVLGDKHGNALWLNERECSIQRRNQKVVEE
i	`	ľ	APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY
		į	FLEMNTRLQVBHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR
			INGWAVECRYYAEDPYKSFGLPSIGRLSQYQEPLHLPGVRVDSG
ł	ļ		TOPGSDISTYVDPMICKLTTVGGDDDD23
	1		IQPGSDISIYYDPMISKLITYGSDRTEALKRMADALDNYVIRGV THNIALLREVIINSRFVKGDISTKPLSDVYPDGFKGHMLTKSEK
1			NOLLA LASSI FVA FOLDA OU FORMORIO DE LA LASSI FOLDA OU FORMORIO DE LA LASSI FVA FOLDA OU FORMORIO DE LA LASSI FOLDA OU FORMORIO DE LA LASSI FO
		1	NOLLAIASSLFVAFQLRAQHFQENSRMPVIKPDIANWELSVKLH
		1	DKVHTVVASNNGSVFSVEVDGSKLNVTSTWNLASPLLSVSVDGT
	. 1	I	ORTVOCLSREAGGNMSIQFLGTVYKVNILTRLAAELNKFMLEKV TEDTSSVLRSDMBGWWWANGWYDGDNAADGOELGNKFMLEKV
	1		TEDTSSVLRSPMPGVVVAVSVKPGDAVAEGQEICVIEAMKMQNS MTAGKTGTVKSVHCQAGDTVGEGDLLVELE
6233	1	2654	HSTRENLNAGNFNFPSEGHLVRSTGPGGSFAKHMVAQCVSFKGP
	 		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	_	\=possible nucleotide insertion)
			LACSRTYFFGATHVPYLGGDSKLPKKTEQIRLLSQIYAAVIEAV
ı	1		LAGIACYAYTESI TYAYEYA BOTTI GOGT DOOD TO
į			LAGIACYAKTSSLTKAKEVAEQTLGSGLDSFELIPFKAALRSKM
1			TFHIHAVNNOGRIVPLDSEDSLSFVKTACMAVYDIPDLLGGNGC
1		,	LGSVVFSESFLTSQILVKEKDGTVTTETSSVVLTAAVPRFCSWL
	i		VEDNEVKLSEKTHQAVRGDESFLGTYLTGGEGAYLYSSNLQSWP
	1		EEGNVHFFSSGLLFSHCRHGSIIISKDHMNSISFYDGDSTSTVA
1	1		ALLIDFKSSLLPHLPVHFHGSSNFLMIALFPKSKIYQAFYSEVF
	1		SLWKQQDNSGISLKVIQEDGLSVEQKRLHSSAQKLFSALSQPAG
}			EKRSSLKLLSAKLPELDWFLQHFAISSISQEPVMRTHLPVLLQQ
İ	l i		AEINTTHRIESDKVIISIVTGLPGCHASELCAFLVTLHKECGRW
			MVYRQIMDSSECFHAAHFQRYLSSALEAQQNRSARQSAYIRKKT
ŀ]		RLLVVLQGYTDVIDVVQALQTHPDSNVKASFTIGAITACVEPMS
	[CYMEHRFLFPKCLDQCSQGLVSNVVFTSHTTEQRHPLLVQLQSL
ł	1 1		IRAANPAAAFILAENGIVTRNEDIELILSENSFSSPEMLRSRYL
1	}		MYPGWYEGKLNAGSVYPLMVQICVWFGRPLEKTRFVAKCKAIQS
1	1		SIKPSPFSGNIYHILGKVKFSDSERTMEVCYNTLANSLSIMPVL
	i i		EGPTPPPDSKSVSQDSSGQQECYLVFIGCSLKEDSIKDWLRQSA
1	i		KQKPQRKALKTRGMLTQQEIRSIHVKRHLEPLPAGYFYNGTQFV
			NFFGDKTDFHPLMDQFMNDYVEEANREIBKYNQELEQQEYHDLF
6234	1731	400	ELKP
1 0254	1/31	404	PRVREDMDHKSPGNKGSLVYAGIKSIVKSSLGMVESSRHNWSGL
			DKQSDIQNLNEERILALQLCGWIKKGTDVDVGPFLNSLVQEGEW
1			ERAAAVALFNLDIRRAIQILNEGASSEKGDLNLNVVAMALSGYT
1			DEKNSLWRENCSTLRLQLNNPYLCVMFAFLTSETGSYDGVLYEN
l i	1 1		KVAVRDRVAFACKFLSDTQLNRYIEKLTNEMKEAGNLEGILLTG
1			LTKDGVDLMESYVDRTGDVQTASYCMIQGSPLDVLKDERVQYWI
1			ENYRNLLDAWRFWHKRAEFDIHRSKLDPSSKPLAQVFVSCNFCG
	İ		KSISYSCSAVPHQGRGFSQYGVSGSPTKSKVTSCPGCRKPLPRC
ŀ			ALCLINMGTPVSSCPGGTKSDEKVDLSKDKKLAQFNNWFTWCHN
i i	· .		CRHGGHAGHMLSWFRDHAECPVSACTCKCMQLDTTGNLVPAETV
6235	1		QP
1 0233	·	571	EKRDHRLPSWPRAALKVPGRGGRVGTTPELAAGGIMATRNPPPQ
İ			DYESDDDSYEVLDLTEYARRHQWWNRVFGHSSGPMVEKYSVATQ
	ł		IVMGGVTGWCAGFLFQKVGKLAATAVGGGFLLLQIASHSGYVQI
1			DWKRVEKDVNKAKRQIKKRANKAAPEINNLIEEATEFIKQNIVI
6236	-		SSGFVGGFLLGLAS
0230	1	703	WDQNKGAAAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF
[]		,	NLKFAAKELSRSAKKCDKEEKAEKAKIKKAIOKGNMEVARIHAE
[NAIRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVK
			SMDATLKTMNLEKISALMDKFEHQFETLDVQTQOMEDTMSSTTT
		ļ	LTTPQNQVDMLLQEMADEAGLDLNMELPQGQTGSVGTSVASAEQ
			DELSQRLARLRDQV
6237	312	720	PTAMAEEGIAAGGVMDVNTALQBVLKTALIHDGLARGIREAAKA
	i		LDKRQAHLCVLASNCDEPMYVKLVEALCABHQINLIKVDDNKKL
1	1		GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEEYFK
			CKK
6238	2	4666	EKVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI
. 1			CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLF
I			YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE
ľ	1		TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP
1			KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNNSSL
ľ			INLHCQLELEVHYYNEMFGVWEPLLEPLEIDQTEDFRPWNLGIK
		Ì	MKKKAKMAIVESDPEEENYKVPEYKTVISFHSKDQLNITLSKCG
	1	1	LVMLNNLVKAFTEAATGSSADFVKDLAPFMILNSLGLTISVSPS
- 1	ļ	ŀ	DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK
	1	1	LFFILLTPVNHSTADKIPLTKVGRRLYTVRHRESGVERSIVCQI
 -			TOO TO THE TAXOUR THE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
!	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ı			DTVEGSKKVTIRSPVQIRNHFSVPLSVYEGDTLLGTASPENEFN
	j		IPLGSYRSFIFLKPEDENYQMCEGIDFEEIIKNDGALLKKKCRS
			KNPSKESFLINIVPEKDNLTSLSVYSEDGNDLPYIMHLWPPILL
			RNLLPYKIAYYIEGIENSVFTLSEGHSAQICTAQLGKARLHLKL
j	}		LDYLNHDWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHMT
	i		YNTGQTVVAFHSPYWMVNKTGRMLQYKADGIHRKHPPNYKKPVL
			FSFQPNHFFNNNKVQLMVTDSELSNQFSIDTVGSHGAVKCKGLK
	i		MDYQVGVTIDLSSFNITRIVTFTPFYMIKNKSKYHISVAEEGND
			KWLSLDLEQCIPFWPEYASSKLLIQVERSEDPPKRIYFNKQENC
			ILLRLDNELGGIIAEVNLAEHSTVITFLDYHDGAATFLLINHTK
İ			NELVQYNQSSLSEIEDSLPPGKAVFYTWADPVGSRRLKWRCRKS
1			HGEVTQKDDMMMPIDLGEKTIYLVSFFEGLQRIILFTEDPRVFK VTYESEKAELAEQEIAVALQDVGISLVNNYTKQEVAYIGITSSD
			VVWETKPKKKARWKPMSVKHTEKLEREFKBYTESSPSEDKVIOL
			DTNVPVRLTPTGHNMKILQPHVIALRRNYLPALKVEYNTSAHQS
			SFRIQIYRIQIQNQIHGAVFPFVFYPVKPPKSVTMDSAPKPFTD
			VSIVMRSAGHSQISRIKYFKVLIQEMDLRLDLGFIYALTDLMTE
1			AEVTENTEVELFHKDIEAFKEEYKTASLVDQSQVSLYEYFHISP
1 1			IKLHLSVSLSSGREEAKDSKQNGGLIPVHSLNLLLKSIGATLTD
			VQDVVFKLAFFELNYQFHTTSDLQSEVIRHYSKQAIKQMYVLIL
1			GLDVLGNPFGLIREFSEGVEAFFYEPYQGAIQGPEEFVEGMALG
1			LKALVGGAVGCLACAASKITGAMAKGVAAMTMDEDYOOKRREAM
			NKQPAGFREGITRGGKGLVSGFVSGITGIVTKPIKGAOKGGAAG
1			FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR
1			PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD
6239	2108	674	DDDDDDDDESDLNH
0233	2100	634	KPGMAGKGSSGRRPLLLGLLVAVATVHLV1CPYTKVEESFNLQA
1 }			THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVLAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM
1	İ		FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI
1		i	WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG
1 1	İ		ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL
1 1	Į.		WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL
{	1		PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI
1			GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI
1	•		DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA
1 1		İ	PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL
6240	2262		ERLPRPS
1 0240	2202	1176	HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF
			DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ
	·		TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL
; [.	}	AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL
	1		LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP
		1	LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS
			ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV
6241	3	1341	RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT
[[-		RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR
· 1	į.	į	EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ
]		[KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV
}	ļ	l	FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP
	ĺ		TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM
	į)	WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC
	f	f	LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD
1		1	TERVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDOLOLE
			GLKYIERNEQKMKKVAKILSQEKTTLQKINDWIKLKTDMYEGLP

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ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			FFSKL
6242	198	1310	QHFLPGAETWSPGAAVCTARRFPGRSLAAFPRPAAPRRAVEMGE
1	Į	į	SSEDIDOMFSTLLGEMDLLTQSLGVDTLPPPDPNPPRAEFNYSV
			GFKDLNESLNALEDQDLDALMADLVADISEAEQRTIQAQKESLQ
1		1	NOHHSASLQASIFSGAASLGYGTNVAATGISQYEDDLPPPPADP
ĺ		i .	VLDLPLPPPPPPEPLSQEEEEAQAKADKIKLALEKLKEAKVKKLV
			VKVHMNDNSTKSLMVDERQLARDVLDNLFRKTHCDCNVDWCLVE
i			IYPELQIERFFEDHENVVEVLSDWTRDTENKILFIEKEEKVAUR
			KNPQNFYLDNRGKKESKETNEKMNAKNKESLLEVRLILQSGRKE
			KDVCSIFKSFASENNGKI
6243	1509	614	RSASRFSGCWSRDSTCCCCPSTCWSRSSASCPRARWPPSSAPAT
			TSRASSRRLACGPQTRAGAETRSTAMIRANSAARDTRRATCRCA
ļ.	1		AGTPSPTTMTCLTDVPTGCAAVEPTARLPAAAWASTITTGCCPA
1			MGQAGAGPAGRKGSEAGGGPGRAHHAHPSPLPREPRVPTGPDAU
1			SPTPGSIDPSPELSWGSAGVTQESPLLDPVDFLLFRTRAVDPLR
[RVFFFFYQHLTFFSIQPQPPPCHAFHPRDPPAGTKROLTLYDLK
6244	2119	3745	GPPILAPILSLTPILSRWSCYFPRSRIAQGWHLS
1	2113	1745	FEHAYASQFGTFLGNNESERCKLKLQQKTMSLWSWVNQPSELSK
1	i		FTNPLFEANNLVIWPSVAPQSLPLWEGIFLRWNRSSKYLDEAYE
6245	81	1148	EMVNIIEYNKELQAKVNILRRQLAELETEDGMQESP
}		****	LSLRNAKYSFPOELISLFSMTDLNDNICKRYIKMITNIVILSLI
			ICISLAFWIISMTASTYYGNLRPISPWRWLFSVVVPVLIVSNGL KKKSLDHSGALGGLVVGFILTIANFSFFTSLLMFFLSSSKLTKW
			KGEVKKRLDSEYKEGGQRNWVQVFCNGAVPTELALLYMIENGPG
1			EIPVDFSKQYSASWMCLSLLAALACSAGDTWASKVGPVLSKSSP
1			RLITTWEKVPVGTNGGVTVVGLVSSLLGGTFVGIAYFLTQLIFV
1 1			NDLDISAPQWPIIAFGGLAGLLGSIVDSYLGATMQYTGLDESTG
i i			MVVNSPTNKARHIAGKPILDNNAVNLFSSVLIALLLPTAAWGFW
			PRG
6246	1177	359	SLWPWILMDDSLMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV
	ŀ	·	QATHRGAVSNSLMLCILKLASOMPLENTTVOOMVFMLT.SNLAT.S
1 1			HDCKGVIQKSNFLQNFLSLALPKGGNKHLSNLTILWLKLLLNTS
1 1			SGEDGQQMILRLDGCLDLLTEMSKYKHKSSPLLPLLIFHNVCFS
1 1			PANKPKILANEKVITVLAACLESENONAORIGAAALWALTYNVO
1 1	I		KAKTALKSPSVKRRVDEAYSLAKKTFPNSEANPLNAYYLKCLEN
6247	3		LVQLLNSS
0277	,	1678	NSRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP
			PGPGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFGSSFL
1 1			YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV
	i		SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS
1 1	ŀ	ĺ	LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG
	ĺ		QVTAIFICIGVFTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL
1		i	LSLPFLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQEVREVL
] }		Į.	AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA
1	[1	IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI
			IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNPAVG
} }	ļ)	LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI
			SQAFSKRNKAYPPEEKIDSAVTDGKINGRP
6248	56	1773	VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI
		L L	AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL
		• [ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP
]		1	SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII
[].		1	LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLOEVARIOPMD
1		1	YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKT.F
L			LINEQSPRASEETLLGISKKAKOMKINVONNVDLGQPVKNKRVP

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ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- [amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			KEESSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
		i	VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCRSKKLKAQAI
-			FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
ł			TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
			ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
			HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
6249	56	1773	VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI
1			AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL
1	Ì		ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENOPLTTKVCVVP
1	1		SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLOFFII
1			LNLVMVGLVSRLWVLYKGVLKRLILLYBPLFGLLOEVARIOPMP
			YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF
			LINEQSPRASEETLLGISKKAKQMKINVQNNVDLGOPVKNKRVF
			KEESSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
j	j		VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCRSKKLKAQAI
}			FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
			TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
1			ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
6250	232	1200	HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
1 3333	232	1306	LAALHIMALPFRKDLEKYKDLDEDELLGNLSETELKQLETVLDD
			LDPENALLPAGFRQKNQTSKSTTGPFDREHLLSYLEKEALEHKD
1 1	į		REDYVPYTGEKKGKIFIPKQKPVQTFTEEKVSLDPELBEALTSA
1 1			SDTELCDLAAILGMHNLITNTKFCNIMGSSNGVDQEHFSNVVKG
1 1			EKILPVFDEPPNPTNVEESLKRTKENDAHLVEVNLNNIKNIPIP
			TLKDFAKALETNTHVKCFSLAATRSNDPVATAFAEMLKVNKTLK SLNVESNFITGVGILALIDALRDNETLAELKIDNQRQQLGTAVE
			LEMAKMLEENTNILKFGYQFTQQGPRTRAANAITKNNDLVRKRR
1 1			VEGDHO
6251	62	972	TPGSGPMSAWAAASLSRAAARCLLARGPGVRAAPPRDPRPSHPE
1 1	Ĭ		PRGCGAAPGRTLHFTAAVPAGHNKWSKVRHIKGPKDVERSRIFS
1 1			KLCLNIRLAVKEGGPNPEHNSNLANILEVCRSKHMPKSTIETAL
1 1			KMBKSKDTYLLYEGRGPGGSSLLIEALSNSSHKCQADIRHILNK
1 1	į		NGGVMAVGARHSFDKKGVIVVEVEDREKKAVNLERALEMAIEAG
1 1	1		AEDVKETEDEEERNVFKFICDASSLHQVRKKLDSLGLCSVSCAL
			EFIPNSKVQLAEPDLEQAAHLIQALSNHEDVIHVYDNIR
6252	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE
t i	ł	i	ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPOV
		ĺ	PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR
1 1			KLPHSKAKTRSRLEVARABEEETSIKAARSELLLAEEPGFLEGE
1		ŀ	DGEDTAKICQADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG
			RHLAFGGRRGHVAALDWVTKKLMCBINVMEAVRDIRFLHSEALL
1		ĺ	AVAQNRWLHIYDNQGIELHCIRRCDRVTRLEFLPFHFLLATASE
			TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG
1 . 1	1		TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL KIEDLEGTYODI STETT BUGACHI ABGORGI LVAGGGGAN
		1	KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA
1		1	GQGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPAELIC
	1	i	LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR
į į	İ	ľ	SSTASLVKRKKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS
	İ	Į.	ALDREVR
6253	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE
		'	ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV
	ł	i	PKKPREWKNPESQRGLSGAQDPPPGPAPVPVEVVQKFCRIDKSR
1		ļ	KLPHSKAKTRSRLEVAEABEEETSIKAARSELLLAEEPGPLEGE
İ		İ	DGEDTAKI CQADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG
			RHLAFGGRRGHVAALDWVTKKLMCEINVMEAVRDIRFLHSEALL

SEO	Predicted	Predicted end	I Amino poid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion, \-possible nucleotide insertion)
	•		AVAQNRWLHIYDNQGIELHCIRRCDRVTRLEFLPFHFLLATASE
		j	TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG
			TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL
			KIFDLRGTYQPLSTRTLPHGAGHLAFSORGLLVAGMGDVVNTWA
1		ļ	GQGKASPPSLEQPYLTHRLSGPVHGLOFCPFEDVLGVGHTGGIT
			SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPAELIC
1	1		LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR
1	İ		SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS ALDRFVR
6254	155	1139	HALGREGGSQELSAAACGCFALRLEAPGSGRPALAPGAAAFAGL
		. 1135	GGAPRFPPRGSAAGRTMLLKEYRICMPLTVDEYKIGQLYMISKH
			SHEQSDRGEGVEVVQNEPFEDPHHGNGQPTEKRVYLNSKLPSWA
			RAVVPKIFYVTEKAWNYYPYTITEYTCSPLPKFSIHIETKYEDN
1			KGSNDTIFDNEAKDVEREVCFIDIACDEIPERYYKESEDPKHFK
I			SEKTGRGQLREGWRDSHQPIMCSYKLVTVKFEVWGLOTRVEOFV
l			HKVVRDILLIGHRQAFAWVDEWYDMTMDDVREYEKNMHEQTNIK
6255	1	1444	VCNQHSSPVDDIESHAQTST
	_	7444	PTRPQQELLVSLATVIFVASQKALSVESKAVIKQQLESVSNGWT VYRIARQASRMGNHDMAKELYQSLLTQVASKHFYFWLNSLKEFS
			HAEQCLTGLQEENYSSALSCIAESLKFYHKGIASLTAASTPLNP
1			LSFQCEFVKLRIDLLQAFSQLICTCNSLKTSPPPAIATTIAMTL
1 .			GNDLQRCGRISNQMKQSMEEFRSLASRYGDLYOASFDADSATIR
1 1			NVELQQQSCLLISHAIEALILDPESASFQEYGSTGTAHADSEYE
			RRMMSVYNHVLEEVESLNGKYTPVSYMHTACLCNAIIALLKVPI.
i			SFQRYFFQKLQSTSIKLALSPSPRNPAEPIAVQNNQQLALKVEG
			VVQHGSKPGLFRKIQSVCLNVSSTLQSKSGQDYKIPIDNMTNEM
}			EQRVEPHNDYFSTQFLLNFAILGTHNITVESSVKDANGIVWKTG PRTTIFVKSLEDPYSQQIRLQQQQAQQPLQQQQRNAYTRF
6256	1	1542	CRGAGAEPAANPRSPRSLVPSLESTSTSVPPAPGTMATDSWALA
			VDEQEAAAESLSNLHLKEEKIKPDTNGAVVKTNANAEKTDEEEK
			EDRAAQSLLNKLIRSNLVDNTNQVEVLORDPNSPLYSVKSFERI.
1	j		RLKPQLLQGVYAMGFNRPSKIQENALPLMLAEPPONLIAOSOSG
			TGKTAAFVLAMLSQVEPANKYPQCLCLSPTYELALQTGKVIEQM
i i			GKFYPELKLAYAVRGNKLERGQKISEQIVIGTPGTVLDWCSKLK
			FIDPKKIKVFVLDEADVNIATQGHQDQSIRIQRMLPRNCQMLLF
			SATFEDSVWKFAQKVVPDPNVIKLKREBETLDTIKQYYVLCSSR DEKFQALCNLYGAITIAQAMIFCHTRKTASWLAAELSKEGHQVA
	•		LLSGEMMVEQRAAVIERFREGKEKVLVTTNVCARGIDVEQVSVV
		i	INFDLPVDKDGNPDNETYLHRIGRTGRFGKRGLAVNMVDSKHSM
			NILNRIQEHFNKKIERLDTDDLDEIEKIAN
6257	210	615	AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGROKLEAOLTE
	1		NNIVKEELALLDGSNVVFKLLGPVLVKOELGEARATVGKRI,DYT
			TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG
6258	210	615	KA
		۷ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ ـ	AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI
			TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG
			KY KY
6259	2	1540	ILEKGFPSQCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV
1		}	SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII
1			SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDOKRNAI
		[NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNKRSQIGETVCK
1		l	YNECGRTFIESLKLNISORPHLEMEPYGCSICGKSFCMNLRFGH
1		1	QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD
	1		KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTQLRRAHT
I_			GEKTFECGECGKTFWEKSNLTQHQRTHTGEKPYECTECGKAFCQ

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ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	B .	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence		\=possible nucleotide insertion)
			VPVV myviopmvmorvov
	į.		KPHLTNHQRTHTGEKPYECKQCGKTFCVKSNLTEHQRTHTGEKP
	1		YECNACGKSFCHRSALTVHQRTHTGEKPFICNECGKSFCVKSNL
ł	1	i	IVHQRTHTGEKPYKCNECGKTFCEKSALTKHQRTHTGEKPYECN
			ACGKTFSQRSVLTKHQRIHTRVKALSTS
6260	2081	1436	GTGPEIHACAHASARAPGSRAMALRELKVCLLGDTGVGKSSIVW
J			RFVEDSFDPNINPTIGASFMTKTVQYQNELHKFLIWDTAGQERF
1	Í		RALAPMYYRGSAAAIIVYDITKEETFSTLKNWVKELRQHGPPNI
-{	1		VVAIAGNKCDLIDVREVMERDAKDYADSIHAIFVETSAKNAINI
i			NELFIEISRRIPSTDANLPSGGKGFKLRRQPSEPKRSCC
6261	3	1188	TWYPT CROSS TO AND PSGGKGFKLRRQPSEPKRSCC
	1	1100	FWYRLGPGTRSRWPRRGSWAASLVPRGPSPAALVTSPCPPDPLR
	i i		SPACEPCRPDFAPRPALLLRSGPRSAPAVTGKPALKGQPGPWPG
			MAEVSIDQSKLPGVKEVCRDFAVLEDHTLAHSLQEQEIEHHLAS
•	1		NVQRNRLVQHDLQVAKQLQEEDLKAQAQLQKRYKDLEOODCEIA
1			QEIQEKLA1EAERRRIQEKKDEDIARLLQEKELQEEKKRKKHFP
1	j i		EFPATRAYADSYYYEDGGMKPRVMKEAVSTPSRMAHRDQEWYDA
			EIARKLQEBELLATQVDMRAAQVAQDEEIARLLMAEEKKAYKKA
ľ	į (KEREKSSLDKRKQDPEWKPKTAKAANSKSKESDEPHHSKNERPA
ļ]		RPPPPIMTDGEDADYTHFTNQQSSTRHFSKSESSHKGFHYKH
6262	2	1759	DECHEOGL CENTEDCRICO DE PROCESSES DE CONTROL DE CHEOGLE CENTEDCRICO DE PROCESSES DE CONTROL DE CONT
İ] -	2,00	PECHSOGLCSVHRPGKVPQARMSGLVLGQRDEPAGHRLSQEEIL
ŀ	l i		GSTRLVSQGLEALRSEHQAVLQSISQTIECLQQGGHEEGLVHEK
	l l		ARQLRRSMENIELGLSEAQVMLALASHLSTVESEKQKLRAQVRR
			LCQENQWLRDELAGTQQRLQRSEQAVAQLEEEKKHLEFLGQLRQ
1	ľ		YDEDGHTSBEKEGDATKDSLDDLFPNEEEEDPSNGLSRGOGATA
1 1	i i		AQQGGYEIPARLRTLHNLVIQYAAQGRYEVAVPLCKOALEDLER
			TSGRGHPDVATMLNILALVYRDQNKYKEAAHLLNDALSIRESTL
	1		GPDHPAVAATLNNLAVLYGKRGKYKEAEPLCQRALEIREKVLGT
i :	l [NHPDVAKQLNNLALLCQNQGKYEAVERYYQRALAIYEGQLGPDN
1	i .		PNVARTKNNLASCYLKQGKYAEAETLYKEILTRAHVQEFGSVDD
			DHKPIWMHAEEREEMSKSRHHEGGTPYAEYGGWYKACKVSSPTV
	1		NTTI DNI CAL VEDOCAT EN APPRE ECAL DODDOCTOR
1 1	1	1	NTTLRNLGALYRRQGKLEAAETLEECALRSRRQGTDPISQTKVA
1	i l	l	ELLGESDGRRTSQEGPGDSVKFEGGEDASVAVEWSGDGSGTLQR
6263	1		SGSLGKIRDVLRR
""	- 1	2408	RELDSLADLPERIKPPYANGLSTSHLRSSSVEDVKLIISEGRPT
1 1			IEVRRCSMPSVICEHTKQFQTISEESNQGSLLTVPGDTSPSPKP
1 . 1			EVFSNVPERDLSNVSNIHSSFATSPTGASNSKYVSADRNI.IKNT
1	1		APVNTVMDSPVHLEPSSQVGVIQNKSWEMPVDRLETLSTRDFIC
1 1		ł	PNSNIPDQESSLQSFCNSENKVLKENADFLSLRQTELPGNSCAO
1			DPASFMPPQQPCSFPSQSLSDABSISKHMSLSYVANQEPGILQQ
1 1	•		KNAVQIISSALDTDNESTKDTENTFVLGDVQKTDAFVPVYSDST
1			IQEASPNFEKAYTLPVLPSEKDFNGSDASTQLNTHYAFSKLTYK
1 1		l	SSSGHEVENSTTDTQVISHEKENKLESLVLTHLSRCDSDLCEMN
[ļ	j	AGMPKGNLNEQDPKHCPESEKCLLSIEDEESQQSILSSLENHSQ
	1]	OSTODEWRKAGOTAKAISI BENYESIASI BENYESIASI BENYESIASI BENYESIASI PROPERTIES TENESONOSI PROPERTIES AND PROPERTIES
1	l	İ	QSTQPEMHKYGQLVKVELEENAEDDKTENQIPQRMTRNKANTMA
† I	Į.	1	NQSKQILASCTLLSEKDSESSSPRGRIRLTEDDDPQIHHPRKRK
	ĺ		VSRVPQPVQVSPSLLQAKEKTQQSLAAIVDSLKLDEIQPYSSER
] [ļ	ANPYFEYLHIRKKIEEKRKLLCSVIPQAPQYYDEYVTFNGSYLL
1	1	ì	DGNPLSKICIPTITPPPSLSDPLKELFRQQEVVRMKLRLOHSIE
	İ		REKLIVSNEQEVLRVHYRAARTLANQTLPFSACTVLLDAEVYNV
1			PLDSQSDDSKTSVRDRFNARQFMSWLQDVDDKFDKLKTCLLMRQ
1	İ		QHEAAALNAVQRLEWQLKLQELDPATYKSISIYEIQEFYVPLVD
1 1	}	ľ	VNDDFELTPI
6264	143		KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILSAI
1 1			PODUNDAD THOS APPROVAL AND A STATE OF THE ST
		1	TQPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI
			WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL
j		i	SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS
LL			ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	In-Institutine, reisoleucine, kelysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
-	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	sequence	sequence	Codon, /=possible nucleotide deletion,
ļ	Doduciico		\=possible nucleotide insertion)
			SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDE
			ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY
	1		INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQ
	ĺ		LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFQKKLAAQL
1			DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG
			YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAIL
J			QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK
1			EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER
6265	143	1960	CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI
]	1960	KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILSAI
Ī			TQPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI
	1		WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL
	[SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS
			ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT
1	1 1		SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDE
1] }		ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQ
i			LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFQKKLAAQL
1			DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG
1			YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAIL
i .			QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK
			EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER
			CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI
6266	276	1421	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE
·			GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD
			ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF
			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR
			GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN
			SINLGSPEQMPSEREVGTEAKMLLLAREDKKLOCLGLOSROLVF
i i	i		LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVOVIH
1 1	·		RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD
h			PVYKVATWEKQIYTCCRDGLVRRYQLSDL
6267	3	622	LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK
1 1	İ		NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCBELRKSKS
i I	i		RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA
			ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA
6268	762		VASTSTSDGMLTLDLIQEEDPSPEEPTSLC
0200	160	1368	HRELCONLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV
<u> </u>		1	DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA
]			PNSDIPEEBPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV
]		İ	LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE
		1	SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ
]		Į.	KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK
1 1	1		1FRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS
j l		1	GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ
			SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR
6269	2886	1449	KKKQPTS
}		1117	HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL
	İ		TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT
]	. [GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN
	1		FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR
	1	1	IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKEALSINP
1			TDAWSVHTVAHIHEMKAEIKDGLEFMQHSETLWKDSDMLACHNY
		1	WHWALYLIEKGEYEAALTIYDTHILPSLQANDAMLDVVDSCSML YRLQMEGVSVGQRWQDVLPVARKHSRDHILLFNDAHFLMASLGA
		1	HDPQTTQELLTTLRDASESPGENCQHLLARDVGLPLCQALVEAE

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	corresponding	to first	H-Histidine, I-Isoleucine, K-Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
j	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	1	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
		 	DGNPDPVLFLLLDIPVPTVOY CCCV
		}	DGNPDRVLELLLPIRYRIVQLGGSNAQRDVFNQLLIHAALNCTS
6270	23	2086	SVHKNVARSLLMERDALKPNSPLTERLIRKAATVHLMQ
1	í		SVTVTLGSEGDGRPPTYHLEEMEQEPQNGEPAEIKIIREAYKKA
			FLFVNKGLNTDELGQKEEAKNYYKQGIGHLLRGISISSKESEHT
	1		GPGWESARQMQQKMKETLQNVRTRLEILEKGLATSLQNDLQEVP
[1		KLYPEFPPKDMCEKLPEPQSFSSAPQHAEVNGNTSTPSAGAVAA
1	į		PASLSLPSQSCPAEAPPAYTPQAAEGHYTVSYGTDSGEFSSVGE
1	1		EFYRNHSQPPPLETLGLDADELILLIPNGVQIFFVNPAGEVSAPS
			YPGYLRIVRFLDNSLDTVLNRPPGFLQVCDWLYPLVPDRSPVLK
	}		CTAGAYMFPDTMLQAAGCFVGVVLSSELPEDDRELFEDLLRQMS
1	j i		DLRLQANWNRAEEENEFQIPGRTRPSSDQLKEASGTDVKQLDQG
1			NKDVRHKGKRGKRAKDTSSEEVNLSHIVPCEPVPEEKPKELPEW
1	ĺ		SEKVAHNILSGASWVSWGLVKGAEITGKAIQKGASKLRERIQPE
1	l		EKPVEVSPAVTKGLYIAKQATGGAAKVSQFLVDGVCTVANCVGK
			ELAPHVKKHGSKLVPESLKKDKDGKSPLDGAMVVAASSVQGFST
			VWQGLECAAKCIVNNVSAETVQTVRYKYGYNAGEATHHAVDSAV
L I			NVGVTAYNINNIGIKAMVKKTATQTGHTLLEDYQIVDNSQRENQ EGAANVNVRGEKDEQTKEVKEAKKKDK
6271	32	1058	GCGVERCHICERUS
1 :			GCGVKTAGMVGREKELSIHFVFGSCRLVEEEVNIPNRRVLVTGA
1 !	1		TGLLGRAVHKEFQQNNWHAVGCGFRRARPKFEQVNLLDSNAVHH
			IIHDFQPHVIVHCAAERRPDVVENQPDAASQLNVDASGNLAKEA
1	1		AAVGAFLIYISSDYVFDGTNPPYREEDIPAPLNLYGKTKLDGEK
	- 1		AVLENNLGAAVLRIPILYGEVEKLEESAVTVMFDKVQFSNKSAN
			MDHWQQRFPTHVKDVATVCRQLAEKRMLDPSIKGTFHWSGNEQM
L i			TKYEMACAIADAFNLPSSHLRPITDSPVLGAQRPRNAQLDCSKL
6272	1136	528	ETLGIGQRTPFRIGIKESLWPFLIDKRWRQTVFH
1			GAVMEDAAAPGRTEGVLERQGAPPAAGQGGALVELTPTPGGLAL
ľ			VSPYHTHRAGDPLDLVALAEQVQKADEFIRANATNKLTVIAEQI
			QHLQEQARKVLEDAHRDANLHHVACNIVKKPGNIYYLYKRESGQ
	}		QYFSIISPKEWGTSCPHDFLGAYKLQHDLSWTPYEDIEKQDAKI SMMDTLLSQSVALPPCTEPNFQGLTH
6273	256	843	SCOPPEDE COOLUMN PROPERTY OF THE SCOPPED COOLUMN PROPERTY OF T
	i		SCPRVSPECRSLGCQVMFSLPLNCSPDHIRRGSCWGRPQDLKIA
- 1			SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV
f		Į	HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS
			ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT
6274	56	1142	AAAAMAAAACCGACAAAACCAAAACCAAAAA
			AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEFDPGTPGSERTEALYYTDDTAMARALVQSL
j		1	LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCR
- 1		1	DVFEPARAQFIGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS
	1	1	AOLTHASSI GVICA II CALAYIN AL COMPANION AND AND AND AND AND AND AND AND AND AN
- 1	1	į	AQLTHASSLGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS
1		l	ELGNGIAAFESVPTATYCELDCMEDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
]	ĺ		ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI SLGGDTDTIATMAGATAGAYYCMIYYDDIYYDG
			SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA QSLHRVFQKS
6275	20		
			SRRGRARCLARGSRRPVPRPAKTMAFMVKTMVGGQLKNLTGSLG
i		1	GGEDKGDGDKSAAEAQGMSREEYEEYQKQLVEEKMERDAQFTQR
1		1	KAERATLRSHFRDKYRLPKNETDESQIQMAGGDVELPRELAKMI
	Ĭ	1	EEDTEEEEEKASVLGQLASLPGLNLGSLKDKAQATLGDLKQSAE
6276	797		
ł	1		TLLPLPPLPDTEGMILLNTGLEGTVAENPVPIVHTPSGNILTLE
ı		1 ;	SCLQQLATHPGHWGIHLQIAEPAALRPSLALLARLSSLGLLHWP
			VWVGAKISHGSFSVPGHVAGRELLTAVAEVFPHVTVAPGWPEEV
Į.		4 1	MASSAY MEDIT TOMERT GOOT MODIZOROMOS AT TORROWS
-	j	1:	LGSGYREQLLTDMLELCQGLWQPVSFQMQAMLLGHSTAGAIGRL
	ļ	į,	LASSPRATVTVEHNPAGGDYASVRTALLAARAVDRTRVYYRLPQ

Si	Q Predicted	Predicted end	Amino acid segment containing signal peptide
I	D beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NC	o: nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
62	77 4600	2744	MAFRTEMGLYYSYFKTIVEAPSFLNGVWMIMNDKLTEYPLVINT
1		1	LKRFNLYPEVILASWYRIYTKIMDLIGIQTKICWTVTIGEGLSP
1	1	İ	TESCEGLGDPACFYVAVIFILNGLMMALFFIYGTYLSGSRLGGI
1	1		VTVLCFFFNHGECTRVMWTPPLRESFSYPFLVLOMLLVTHILRA
			TKLYRGSLIALCISNVFFMLPWQFAQFVLLTQIASLFAVYVVGY
			IDICKLRKIIYIHMISLALCFVLMFGNSMLLTSYYASSLVIIWG
ļ	ł		ILAMKPHFLKINVSELSLWVIQGCFWLFGTVILKYLTSKIFGIA
1			NDAHIGNLLTSKFFSYKDFDTLLYTCAAEFDFMEKETPLRYTKT
1	ļ		LLLPVVLVGFVAIVRKIISDMWGVLAKQQTHVRKHQFDHGELVY
1	i		HALQLLAYTALGILIMRLKLFLTPHMCVMASLICSRQLFGWLFC
1	[1	KVHPGAIVFAILAAMSIQGSANLQTQWNIVGEFSNLPQEELIEW
		1	IKYSTKPDAVFAGAMPTMASVKLSALRPIVNHPHYEDAGLRART
1			KIVYSMYSRKAAEEVKRELIKLKVNYYILEESWCVRRSKPGCSM
			PEIWDVEDPANAGKTPLCNLLVKDSKPHFTTVFQNSVYKVLEVV KE
627	8 3	823	ILFRLVLLSLVYLLNSVATEERKPAEVLIVEGQQYAVVGTVLLL
!	i	i	IRIILEYCQGVDNIPSVTTDMLTRLSDLLKYFNSRSCQLVLGAG
1		ļ	ALQVVGLKTITTKNLALSSRCLQLIVHYIPVIRAHFEARLPPKQ
i			YSMLRHFDHITKDYHDHIAEISAKLVAIMDSLFDKLLSKYEVKA
	1		PVPSACFRNICKOMTKMHEAIFDLLPEEQTOMLFLRINASYKLH
			LKKQLSHLNVINDGGPQNGLVTADVAFYTGNLQALKGLKDLDLN
627	9 127		MAEIWEQKR
1 02,	3 12/	1687	GGAMASDGARKQFWKRSNSKLPGSIQHVYGAQHPPFDPLLHGTL
}			LRSTAKMPTTPVKAKRVSTFQEFESNTSDAWDAGEDDDELLAMA
			AESLNSEVVMETANRVLRNHSQRQGRPTLQEGPGLQQKPRPEAE
			PPSPPSGDLRLVKSVSESHTSCPAESASDAAPLQRSQSLPHSAT
1			VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELRR LSWSGIPKPVRPMTWKLLSGYLPANVDRRPATLQRKQKEYFAFI
1			EHYYDSRNDEVHQDTYRQIHIDIPRMSPEALILQPKVTEIFER:
			LFIWAIRHPASGYVQGINDLVTPFFVVFICEYIRAEEVDTVDVS
1	1		GVPAEVLCNIEADTYWCMSKLLDGIQDNYTFAQPGIQMKVKMLE
			ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNNLLMREVPLRCTIR
l	1 !		LWDTYQSEPDGFSHFHLYVCAAFLVRWRKEILEEKDFOELLLFL
L-05			QNLPTAHWDDEDISLLLAEAYRLKFAFADAPNHYKK
6280	857	2515	ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE
			DVDLAQVLAYLLRRGQVRLVQGGGAANLOFIOALLDSEEENDRA
1			WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA
1			QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPMDLGFTDS
			YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA
ļ			RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD
Ì			LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ
1		1	IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK
		1	PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR RGMEASPOAATOONUDYPWOOYPYYAYPYIVI PCDGGIMTYS
]	I	EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK
	- 1	İ	LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM
	1		PESEECASAPAPVPQSSTPFSSPQ
6281	857	2515	ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEBEEEDE
		İ	DVDLAQVLAYLLRGQVRLVQGGGAANLQFIQALLDSEEENDRA
		ļ	WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA
	1		QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS
			YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA
		ì	RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD
			LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREONRRTLO
	1 1	i	IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK
			PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR
			· · · · · · · · · · · · · · · · · · ·

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	IM-ALGUIDE, CECVSCEINE DEAchartin x-11 -
ŀ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine V=V=line
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Gc
- 1	amino acid sequence	sequence	COGON, /=possible nucleofide dolardon
<u> </u>	sedgeuce		\=possible nucleotide insertion\
ŀ			EGMEASRQAATQQNWDYRWOOVPKKAWRKI,KI,DCDCCI MITTEROX
i		l.	GVDATLIRCRFSPIHSTGOOFTVSGCSTGVARAUDT I COUTTY
1			LINKACVRDVSWHPFEEKIVSSSWDGNT.PLWOVDONEVEODDA
6282	125	906	PESEECASAPAPVPQSSTPFSSPQ
i		1	RMAACRALKAVLVDLSGTLHIEDAAVPGAQEALKRLRGASVIIR
1			FVTNTTKESKQDLLERLRKLEFDISEDETFTSLTARSLLERKQ VRPMLLVDDRALPDFKGIQTSDPNAVVMGLAPEHFHYQTLMQAF
1			RLLLDGAPLIAIHKARYYKRKDGLALGPGPFVTALEYATDTKAT
İ			VVGKPEKTFFLEALRGTGCEPEEAVMIGDDCRDDVGGAQDVGML
6283			GILVRIGRYRASDEEKINPPPYLTCESFPHAVDHILOUIT
6283	140	1043	LSLFGIHVMNPFWSMSTSSVRKRSEGEEKTLTGDVVTGDDDTDD
1	1		KKQLPSIPKNALPITKPTSPAPAAOSTNGTHA SYGDEVI EVELT
1	1		AEFTLVVKQKLPGVYVOPSYRSALMWFGVTFTPHGLVODGVEVF
1	1		TVIIPDNYPDGDCPRLVFDIPVFHPLVDPTSGELDUKPA PAVUP
İ]		RNHNHIWQVLMYARRVFYKIDTASPLNPEAAULVEVDIOLEVOV
!			VVDSVKVCTARLFDQPKIEDPYAISFSPWNDSJUDEADEVIKI TO
6284	1	2879	KKKPEEQHNKSVHVAGLSWVKPGSVQPFSKEEKTVAT
f		2075	RSVIPGSTISSRWPGLSRPRFMAAHEWDWFQREELIGQISDIRV
			QNLQVERENVQKRTFTRWINLHLEKCNPPLEVKDLFVDIQDGKI
I			LMALLEVLSGRNLLHEYKSSSHRIFRLINNIAKALKFLEDSNVKL VSIDAAEIADGNPSLVLGLIWNIILFFQIKELTGNLSRNSPSSS
1			LAPGSGGTDSDSSFPPTPTAERSVAISVKDQRKAIKALLAWVQR
ļ	j		KTRKYGVAVQDFAGSWRSGLAFLAVIKAIDPSLVDMKQALENST
1	İ		RENLEKAPSIAQDALHIPRLLEPEDIMVDTDDTQCIMTVVA QUI
1			ERFPELEAEDIFDSDKEVPIESTFVRIKETPSEOESVIPHT TEN
[GERTYTVNHETSHPPPSKVFVCDKPESMKPPDI.DCVCCUAT CDC
l i			STEFMHQIIDQVLQGGPGKTSDISEPSPESSIT.GCPVPNCBGNC
1 1			DELKATVALEADTYKDPFCSKNLSLCFFGSDDVAKDSI DODGURI
1 1	İ		LAVEVAEEKEQKQESSKIPESSSDKVAGDIFLVEGTNNNSQSSS
[]	1		CNGALESTARHDEESHSLSPPGENTVMADSFQIKVNLMTVEALE
			EGDYFEAIPLKASKFNSDLIDFASTSQAFNKVPSPHETKPDEDA EAFENHAEKLGKRSIKSAHKKKDSPEPQVKMDKHEPHQDSGEEA
1	Í		EGCPSAPEETPVDKKPEVHEKAKRKSTRPHYEEEGEDDDLQGVG
	1		LELSSSPPSSCVSLETLGSHSEEGI,DFKpgppt,gvvcvrpvprp
1			I FPHYEVPLAAVLEAYVEDPEDLKNEEMDLEEPEGVMDDY DCDE
ł			EEADGSQSSSSSSVPGESLPSASDOVT,VI,SPGGVGTTDAGEDAD
			APPREDRUQUETKENDPMDSHOSORSPNIENTANDLEDNIEUDO
1	1		1 100 KKKKKKKHVDHVESSLFVAPGSVOSSDDLFFDSSDVCTDSD
6285	2157	1331	TSHSDSSIYLRRHTHRSSESDHFSLCSVEERSRSG
	1		SCKTENLLEMWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHH IDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATIYVRYKQVH
1	!	İ	ALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVS
- 1			GAVLTFGMGSLYMFVQTILSYQMQPKIHGKQVFWIRLLLVIWCG
1	ļ		VSALSMLTCSSVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAA
			EWSMSFSFFGFFLTYIRDFQKISLRVEANLHGLTLYDTAPCPIN
6286			REKTRILISKOI
0200	1619	276	KAGASCCGSANPYVSVGKSCVLLAMAQLQTRFYTDNKKYAVDDV
1		į	PFSIPAASEIADLSNI INKLLKDKNEFHKHVEFDFLIKGOELDM
l		1	PHUKEMENISSBEVVEIEYVEKYTAPODEOCMEHDDWICCIW
-]	İ	GAZEWILIGSYDKTSRIWSLEGKSIMTIVGHTDVVKDVAKUVVD
	ſ	!	SISCIDESASMOQTILLWEWNVERNKVKALHCCRCHAGGIOGIA
ſ	1		VIGSGTRFCSGSWDKMLKIWSTVPTDEEDEMEESTNPDPKKOVT
		ſ	EQUICETRIPIVILSGHMEAVSSVLWSDAREICSASWDUTTDIMD
1	į	i i	VASGSLASTLTGNKVFNCISYSPLCKRLASGSTDRHTRLADDRE
			KDGSLVSLSLTSHTGWVTSVKWSPTHEQQLISGSLDNIVKLWDT
			RSCKAPLYDLAAHEDKVLSVDWTDTGLLLSGGADNKLYSYRYSP

SEQ	Predicted	Predicted end	l having a second
σι	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
-	amino acid	residue of	S=Serine, T=Threonine, V=Valine
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-ct
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
6287	278	1400	TTSHVGA
""	2/8	1482	MQFFFNFQIGLRSTSGKEKYSGDAGFLGDALQLFLQCLALDEDF
l	1	İ	APAKLQVQKILCDLLLPENLKEGLKESSWSSLPCTKNRPFDFHS
ŀ			VMEESQSLNEPSPKQSEEIPEVTSEPVKGSLNRAQSAQSINSTE
1	1		MPAREDCLKRVSSEPVLSVQEKGVLLKRKLSLLEQDVIVNEDGR
	Í		NKLKKQGETPNEVCMFSLAYGDIPEELIDVSDFECSLCMRLFFE
			PVTTPCGHSFCKNCLERCLDHAPYCPLCKESLKEYLADRRYCVT OLLEELIVKYLPDELSERKKIYDEBTAELSHLTKNVPIFVCTMA
1			YPTVPCPLHVFEPRYRLMIRRSIQTGTKQFGMCVSDTQNSFADY
			GCMLQIRNVHFLPDGRSVVDTVGGKRFRVLKRGMKDGYCTADIE
			YLEDV
6288	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
1			MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM
İ			HMMVSKPEQWVKPMAVAGANOYTFHI.EATENPGALTKDTDENGM
1	i i		KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGOKFMRDMM
1			PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMTVGGGATM
6289	1	743	RSEDPRSVINLLRNVCSEAAOKRSLDR
****	. .	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
1	ĺ		MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM
ł			HMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGM
			KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM
			PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM RSEDPRSVINLLRNVCSEAAQKRSLDR
6290	3	1856	TLGRWLLGVYETVAPTLACLPRPRLRRRRRRRRRRRRRRMISRYTRKA
1			VPQSLELKGITKHALNHHPPPEKLEEISPTSDSHEKDTSSQSKS
1 1	Ì		DITRESSFTSADTGNSLSAFPSYTGAGISTEGSSDFSWGVGFLD
1	_		QNATERVQTMFTAIDELLYEOKLSVHTKSLOFECOOWTAGEDUT
	·		RILGRQIITPSEGYRLYPRSPSAVSASYETTLSOFRDSTIFGTP
	l	ì	GKKLHFSSYAHKASSIAKSSSFCSMERDERDSITUSEGITERV
}			LAPDHIDIEEGFHGKKSEAATEKOKLGYPPIAPFYCMKEDYIAV
	1		VFDSVWCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESSCV
1 1			LSELHPLVLPRVPQSKVLYITSNPMSLCQASRHQPNVNDLLVHG
			MPLQPRNLSLMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS
[1		TSSLSYTVQSTRRRNPPPRTLHPISTSHSCAETPRSVEEILRGA RVFVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK
f 1		i	PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPRPNTTQSFLLDT
]		J	QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG
(2)			P
6291	1732	602	LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSRKRIES
			PFAKYNRLGQLSCALCNTPVKSELLWOTHVLGKOHREKVAELKG
ŀ		ļ	AKEASQGSSASSAPQSVKRKAPDADDODVKRAKATI.VPOVODET
		j	SAWITNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEERCD
İ		1	GERKRGDASKPLSDAQGKEHSVSSSREVTSSVI,PNDFRSTNDDV
[·	ſ	APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDDRYDADY
			RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ
	[!	IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKBEEN ADSDDEGELQDLLSQDWRVKGALL
6292	1835	1142	TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV
- 1	İ	1	LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI
İ	ŀ		LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN
1	j] ;	SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY
- 1		[:	LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA
6202	03.06		AKEPPPPYVSA
6293	2382	1035	FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL
		1.	VGSRTLPVDFHIKMVESMKYPFROGMRLEVVDKSOVSRTPMAVV
			DTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIK

SEC		Predicted end	Amino acid gogment
ID	1 3	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			MSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVVTRCGWEERCMV
	1		LEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCV
	`	1	HASSHAIFPATFCQKNDIELTPPKGYEAOTFNWENYLEKTYCKA
	1	ł	APSRLFNMDCPNHGFKVGMKLEAVDLMEPRI,TCVATVKPVATVLDI
1	ļ	İ	LSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYOLOPPVARE
1	Ì		ATPLKAKEATKKKKKQFGKKRKRIPPTKTRPLROGSKKPLLEDD
			PQGARKISSEPVPGEIIAVRVKEEHLDVASPDKASSPELDVSVF
6294	251		NIKQETDD
0294	354	1814	AQLTTRGRTVAGGVRWIPSPFPDLELYSCCLGTDRGFPELSHHC
			KNVIATASDYDMAEITNIRPSFDVSPVVAGI,TGASVI,VVCVCVCV
,	}		VFVWSCCHQQAEKKHKNPPYKFIHMLKGTSTVDFTTSNYWYTTV
ł		•	VRRDKDGPGREGGRRNLLVDAAEAGLLSRDKDPRGPSSGSCTDO
1	.		LPIKMDYGEELRSPITSLTPGESKTTSPSSPEEDVMLGST.TEST
İ	1		DYNFPKKALVVTIQEAHGLPVMDDQTQGSDPYIKMTILPDKRHR
	1 .		VKTRVLRKTLDPVFDETFTFYGIPYSQLQDLVLHFLVLSFDRFS
1	1		RDDVIGEVMVPLAGVDPSTGKVQLTRDIIKRNIQKCISRGELQV
1			SLSYQPVAQRMTVVVLKARHLQKMDIAGLSGNPYVKVNVYYGRK
-	ł		RIAKKKTHVKKCTLNPIFNESFIYDIPTDLLPDISIEFLVIDFD
1	ŀ		RTTKNEVVGRLILGAHSVTASGAEHWREVCESPRKPVAKWHSLS
6295	2795	617	VSSALLTGATSGSDAAKSEGASASPLSCTNAVAMDRPDEGPPAK
}	1		TRRLSSSESPQRDPPPPPPPPPPLLRLPLPPPQQRPRLQEETEAA
			QVLADMRGVGLGPALPPPPPYVILEEGGIRAYFTLGAECPGWDS
	1		TIESGYGEAPPPTESLEALPTPHASGGSLEIDFQVVQSSSFGGE
	1		GALETCSAVGWAPQRLVDPKSKBEAIIIVEDEDEDERESMRSSR
1	1		RRRRRRRKQRKVKRESRERNAERMESILQALEDIQLDLEAVNI
1	1		KAGKAFLRLKRKFIQMRRPFLERRDLIIQHIPGFWVKAFLNHPR
l			ISILINRRDEDIFRYLTNLOVODLRHISMGYKMKI.YFOTNDVFT
	1		NMVIVKEFQRNRSGRLVSHSTPIRWHRGOEPOAPPHGNODAGUG
			FFSWFSNHSLPEADRIAEIIKNDLWVNPI,PVVI,PEDGGDTVDVV
l	1		QEMKKRKTRGRCEVVIMEDAPDYYAVEDIFSEISDIDETIUDIV
			ISDFMETTDYFETTDNEITDINENICDSENDDHNEUDANETTDNI
}	1		NESADDHETTONNESADDNNENPEDNNKNTDDNEENPNNNENTY
ł	1		GNNFFKGGFWGSHGNNQDSSDSDNEADEASDDEDNDGNEGDNEG
	1		SDDGNEGDNEGSDDDDRDIEYYEKVIEDFDKDQADYEDVIEII
			SDESVEEEGIEEGIQQDEDIYEEGNYEEEGSEDVWEEGEDSDDS DLEDVLQVPNGWANPGKRGKTG
6296	727	1199	RHCGCDAQGACDSLPPTGTSSPVTARNAIPEARCCVWLLDGTTV
	1	-	EAVRPARERLARKELRQKRMQQFSRDSAYSSNKDSTCLLTERDT
	1		LGTSLQFPSPFSGTISFGSFSDSGIFPLGSQCCLGFQQFSISGK
			KWALIHKRVRLSVFGARWGRIYFGK
6297	1	922	QRAAAASPSSCGPRGAEYGALMAMEGYWRFLALLGSALLUGFLS
	1		VIFALVWVLHYREGLGWDGSALEFNWHPVIMVTGEVETOGIATI
		ļ	VYRLPWTWKCSKLLMKSIHAGLNAVAAILAIISVVAVFENHNUM
		ļ	NIANMYSLHSWVGLIAVICYLLOLLSGFSVFLLDWAPI,SI,DAFI
			MPIHVYSGIVIFGTVIATALMGLTEKLIFSLRDPAYSTFPDFGV
	1	i	FVNTLGLLILVFGALIFWIVTRPQWKRPKEPNSTILHPNGGTEO
6298	ļ		GARGSMPAYSGNNMDKSDSBLNNEVAARKRNLALDEAGORSTM
0230	3	985	SVPLRRLSLSGTLQGAGTTTKMAVARLAAVAAWVPCRSWGWAAV
		i	PFGPHRGLSVLLARI PQRAPRWLPACROKTSLSFLNRPDI.PNT.D
		1	YKKLKGKSPGIIFIPGYLSYMNGTKALAIEEFCKSLGHACIDED
	[Į.	YSGVGSSDGNSEESTLGKWRKDVLSIIDDLADGPOILVGSSLGG
	[l	WLMLHAAIARPEKVVALIGVATAADTLVTKFNOLPVRLKKEVEM
			KGVWSMPSKYSEEGVYNVQYSFIKEAEHHCLLHSPIPVNCPTRI.
i			LHGMKDDIVPWHTSMQVADRVLSTDVDVILRKHSDHRMREKADI
			QLLVYTIDDLIDKLSTIVN

Deginning	SEQ	Predicted	Predicted end	Amino acid gomest
No:	ID			Amino acid segment containing signal peptide
corresponding to first anino acid amino acid amino acid amino acid amino acid amino acid amino acid asequence sequen	NO:		•	Glutamia Baid B Phanel
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence social expension of acid sequence social expension of acid sequence soc				White Acid, Fernenylatanine, GeGlycine,
be first amino acid residue of seidue of seidue of seidue of sanio acid amino acid sequence sequence sequence code, the sequence	ı		, -	Lalousine, Marking, Kalysine,
amino acid residue of amino acid sequence should be an acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be amino acid sequence should be acid be amino acid sequence should be acid	l l			B-Droline, M=Methionine, N=Asparagine,
maino acid sequence 6299 512 814 FEDERORIA TO TOPOSSINE X-UNCHOWN, "Stop COOTS / POSSINE NUCLEAR SECTION COOTS / POSSINE NUCL	1			F=Flotine, Q=Glutamine, R=Arginine,
amino acid sequence Cooling				S=Serine, T=Inreonine, V=Valine,
Sequence Sposible nucleotide distor.	İ			w=Tryptopnan, Y=Tyrosine, X=Unknown, *=Stop
6300 121 692 ARPSCHOEGINENVTISUSLITUSSICATURS SIDAMODISAFSGYKE PRITPLESYNLCYTISQUEUPILIGYQ MERCEVULRING ARPSCHORGROUPARGTPESPELLVSRAAABSAGDRAMRQGRA ARPSCHORGROUPARGTPESPELLVSRAAABSAGDRAMRQGRA ARPSCHORGROUPARGTPESPELLVSRAAABSAGDRAMRQGRA ARSSSTYRORGROUPARGTPESPELLVSRAAABSAGDRAMRQGRA ARSSSTYNCHORGROUPARGTPESPELLVSRAAABSAGDRAMRQGRA ARSSSTTHIKKORSGSBUMUSDENSESPEDGGGGRAPUGGSPGEPED LUIGSLEARLSPHMFGGYKCPVCSEFYSSDEMDLHLUMCLTUPR TYMEDVISKOMGGAILLEELQQODTIARLDCLITYRGCIDE MEEVNSCOERPED 6301 616 284 GKFYPVNMEPPPPPPFFFFYLRCYRCLLETELGCLIGSDICLTP ARSSCTITHIKKORSGSBUMWSDCRSKEQMSDCSNTRTSPVSGFW TSGYCFLDFOUNDPORRCLITY ARSSCTITHIKKORSGSBUMWSDCRSKEQMSDCSNTRTSPVSGFW TSGYCFLDFOUNDPORRCLITY ARSSCTITHIKKORSGSBUMWSDCRSKEQMSDCSNTRTSPVSGFW TSGYCFLDFOUNDPORRCLITY ARSSCTITHIKKORSGSBUMWSDCRSKEQMSDCSNTATSPVSGFW TSGYCFLDFOUNDPORRCLITY ARSSCTITHIKKORSGSBUMWSDCSSEVALHSDPCLLS PVLLNCLAGGURGUPPLDELYARGKAVTRATSELDHALMDMTSL TYMEYGGGLLMGSWCREFFGGALSSEPWNFPTTKERMEGHTSDF TSGYCFLDFOUNDPORRCLITY TSKYCHALLORGROUPENDFOUNDFOUNDFOUNDFOUNDFOUNDFOUNDFOUNDFOU	J		sequence	Codon, /=possible nucleotide deletion,
6300 121 692 AAPSCHOUGHEN AND AND AND AND AND AND AND AND AND AN	6299		034	\=possible nucleotide insertion)
6300 121 692 AAPSCMSGGVPAAGTPSSPRLLVSRAAAFSAGPRGARRAGGRAR AQSFSTPMSSSVPYGSGDSVPSSPEDGGGGRAPRVGGSFGDRR LUGSLEAGH AQSFSTPMSSSVPYGSGDSVPSSPEDGGGGRAPRVGGSFGDRR LUGSLEAGH LUGSLEAGH SPENTGGFCVCKSKVSSBEDGHLKUMCLTKPR TTYMEDULS KDAGECA ICLEELQGGDTTARLPCLCTYHKGCTDE WEEVINSCOPERPSON AGSSCTTHIKKINSSGDWUNGCKEKQMSDCSNTRTSPYGSFW TENDULS KDAGECA ICLEELQGGDTTARLPCLCTYHKGCTDE WEEVINSCOPERPSON AGSSCTHIKKINSSGDWUNGCHEKCQMSDCSNTRTSPYGSFW TENDULS KOMEN AG AGSSCTHIKKINSSGDWUNGCHEKCQMSDCSNTRTSPYGSFW TENDULS AG AGSSCTHAMENSSGDWUNGCHEKCQMSDCSNTRTSPYGSFW TENDULS AG AG AG AND AND AND AND AND AND AND AND AND AND	1 4222	1 312	014	ECDLEGIMPNVTISLSLPTNGSPLQDILVHPCVTSLDSAILTSS
6300 121 692 AAPSCMGGRUPAACTPSSPELLVSBAADSAADPSAADPSAGRARA ASPSTSINSSSVPYSGOBUVESSPEDGGGRORPVGGROPGOR LUTGSLPAILSPINFGGPKCPVCSRFVSSIEDDILLIMMCLTKPR TYMEPULSKUNGSCAI CLEELQGGDTTARLPCLCTYHRGCIDE WEFWARSCEHPSD 6301 616 284 GKFVPVNWEPFQPLFFFYLRCYRCLLETKELGGLIGSDICLTP AGSSCITLIKKINSSGSDWWSDCRSKEQMSDCSNTRTSPVSGFV 1FSQYCFLDFCNDPCNRGLYTP 1FSCYCFLDFCNDPCNRGLYTP 1FSCYCFLDFCNDPCNRGLYTP 1FSCYCFLDFCNDPCNRGLYTP 1FSCYCFLDFCNDPCNRGLYTP 1FSCYCFLDFCNDPCNRGLYTP 1FSCYCFLDFCNDPCNRGLYTP 1FSCYCFLDFCNDPCNRGLYTP 1FSCNCFLDFCNDPCNRGLYTTLSAFLDFCNDFCNDFCNDFCNDFCNDFCNDFCNDFCNDFCNDFCN		ŀ		SIDAMDCSAFSGPYKFPFTPPLESFNLCFYTSQVPVPPILGFYQ
AGSPSTINSSENVYGGGSVERSSPEDGGGGDRPVGGSFGPPB LVIGSLPAILSPRINGGPKCPVCSEFVSSBEDLHLUMCLTYPR LTYNEDVJS.NOAGGCAICLEGLGQGDTTABLCLCTYHKGCIDE WEEVINSCCERPSD 6301 616 284 GEFVPVINEPPPDIPFPRYLRCYRCLLEFKELGCLLSSICLTP AGSSCITLHKKINSSCSDWWSDCRSKEGMSDCSNTRTSPVSGFW FISCYCFLDFONDPGNGLIVTP AGSSCITLHKKINSSCSDWWSDCRSKEGMSDCSNTRTSPVSGFW IFSCYCFLDFONDPGNGLIVTP AGSSCITLHKKINSSCSDWWSDCRSKEGMSDCSNTRTSPVSGFW IFSCYCFLDFONDPGNGLIVTP AGSSCITLHKKINSSCSDWWSDCRSKEGMSDCSNTRTSPVSGFW IFSCYCFLDFONDPGNGLIVTP BULLINCLADGUREDLEVLYAGKYKYAT SEBELHALINDWTSL VANEYGGGLLGGSNGERFGCALSSEPNFFFTYKEREGOFYSGL VANEYGGGLLGGSNGERFGCALSSEPNFFFTYKEREGOFYSGL VANEYGGGLLGGSNGERFGCALSSEPNFFFTYKEREGOFYSGL VANEYGGGLLGGSNGERFGCALSSEPNFFFTYKEREGOFYSGL VANEYLGGGVAREAGGGFTDANDFTSKRUDDIBKKM VAPILASPLASSCSTANDHSSTADHBSTNATHSTRATEADIBKKM VAPILASPLASSCSTANDHSSGCTDTYTSKEREGOFYSGL VAPILASPLASSCSTANDHSSGCTDTYTSKEREGOFYSGL VAPILASPLASSCSTANDHSSGCTDTOTSKEREGOFYSGL VAPILASPLASSCSTANDHSSGCTDTOTSKEREGOFYSGL VAPILASPLASSCSTANDHSSGCTDTOTSKEREGOFYSGL VAPILASPLASSCSTANDHSSGCTDTOTSKEREGOFYSGL VAPILASPLASSCANDHSSGCTANSCCALSSCSGANDERSNG SGATNTOTDPARDSGCALSSEPNFFTYSKEREGOFYSGL VAPILASSCANDHSSGCTANDHSSGCTANGGCALGGGGSSGCANDERSNG VAPILASSCANDHSSGCTANDHSSGCTANGGCALGGGGSSCANDHSSSSGCSANDHSSSNG VAPILASSCANDHSSGCTANDHSSGCTANGGCANGGCANGGANDHSSSNG VAPILASVERVELASSCANDHSRADELASSCANDHSSSSGCANTESVELLASSCLADHSSSSGCANDHSSANDHSSSSGCANTESVELLASSCLADHSSSSGCANTESVELLASSCLADHSSAND	6300	121		
DVIOSEPALLSPHNFGGFKCPVCSKFVSSDEMDLHLWCLTYPKEGIDE	1	1 -2-1	054	AAPSCWSQRGVPAAGTPSSPRLLVSRAAAPSAGPWGAWRQGARA
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SGNTNTDPAEDS(KSSGANTSKDPPHASCTDGDEBEEDPPEN FSKKKRSHELD IDENPASS PDDGGSLLGFKYGSGQXYGGIPNFS HRQWRYLEKNVKLKSKYLDMRRQIKMKNKHIFFTKESEKFFKKK SKILSKVEKFLTWVKKMBDEBASGESSLIGHTKYGGIPNFS HRQWRYLEKNVKLKSKYLDMRRQIKMKNKHIFFTKESEKFFKKK SKILSKVEKFLTWVKKMBDEBASGESSJENOHDASTSCDSEQ DMSVKKGDDLLETINNEPBEKCOSVSSAGELETIN YEROBLLATV PDEGDCVTQBVPDSRQAETEABVKKKKKKKKKKKKUGLPPELAA VPELAKYWAQRYRLFSSFDGIKLDREGMFSVYPERLAHIAGR VSQSFKCDVVDAFCGVGGNTIQFALTGMRVIAIDIDPVKIALA RNNAEVYGIADKIEFICGDFLLLASFIKADVVFLSPPGGDPA TAASTFDIRTIMSPDGFEIFRLSKKTYNNIVYFLPRNADIDQVAS LAGPGGQVEIGONFLANKLKTITAYFGDLIRRPASET TAASTFDIRTIMSSPGGEIFRLSKKTYNNIVYFLPRNADIDQVAS LAGPGGQVEIGONFLANKLKTITAYFGDLIRRPASET DEVGDPTKDLGHPQHGSPIQETQSEVVTLVSPLPGSDMAALPA WRATSGLTLWPHTABGROLLGAENRALITGQQAEDPTLASGAYQ WPGSVEKLQGSVWCDAETLLSSSRTGQAPPWLTDHDVQMIRLL AQGEVVDKARVPAHGGVLQVGFSTERALQDLSSPRLSGLCSGGL CGLIKAPGDLPBVLSFHVDRVLLARSLPAVARRFHSPLLPYRY TDGGARPVIWWAPDVQHLSDPDDQNSLALGWLQYQALLAHSCN WPGQAPCPGIHHTBWARLALFDFLLQVURDLDRYCCGFEPPPSD PCVEERLBEKCHNPASELIVHLUVRSDPSHLVYIDMAGNIQHP EDKLMFRLLEGIDGFPESAVKVLAGGCLQNMLLKSLQMDPVFWE SQGAQGLKQVJUCTUEQRGQVLLGHIQKHNILTJFBDDP EDKLMFRLLEGIDGFPESAVKVLAGGCLQNMLLKSLQMDPVFWE SQGAQGLKQVJUCTUEQRGQVLLGHIQKHNILTJFBDDP SRDAGQREEDQGAAETQVPDLEADLQELSQSKTGDECGDGPD VQGKLITKSBGPKWPEGR 6306 1 1874 PTREPSKYKPHFRLSYTRPTVCQACKKLLKGLFRQGLQCKDC KFNCHKCATRVPNDCLGBALINGDVWEBEATDFSEADKSALMD SESDSGVI PGSHSNALHASEEGGGGKAAQSSLGYIPLMRVVQ SVRHTTRKSSTTLREGWVHYSNKDTLKRHYWRLDCKCTTLFQ NNTTMRYYKEI PLESE LITVESAQMPSLVPMPGTPHCFEIVTANA TYFVGEMPGGTPGGPSGQGAEAARGWETAIRQALMFVILQARS APGHAPHRQASLSISVSNSQIQENVDLATYQIFPDSVLGSGQF GVYGGKRKKTGRVDAVKUIDKLRFFFYKGSSGLRNEVALLQSLR HRGIVNLECMFETFEKVVVWEKLHGDMLEMILSSEKGRLPERL TKFLITTIQLIKARHFKRIVAKHLIGSLKR HRGIVNLECKFETFEKVVTWEKLHGDMLEMILSSEKGRLPERL TKFLITTIQLIKARHFKRIVALLGSLR HRGIVNLECKFETFEKVVTPAYLAPEVLLLAGANDSFPQVLCL DFGFARIIGEKSFFRSVVGTPAYLAPEVLLAGADPFPQVKLC DFGFARIIGEKSFFRSVVGTPAYLAPEVLLNGGYNRSLDMWSVG VIMYVSLSGTFPFNEDEDINDQIQNAAAFMYPASPWSHISAGAID LINLLQVWKRKGWER		ĺ		KVDLVSFLSSPIMGDNDSSGTSDKDHSEILDGISNIKLNSEEVT
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HRQVRYLEKNVLKIKSYLDMRRQIKMKNRHIFFTKESERFPFKK SKILSKVEKFLTWNINKPMDEREAGESSSHDNGHDASTSCDSEEQ DMSVKKGDDLLETNNPEPEKCQSVSSAGELETENYERDSLLATV PDEGDCVTQEVPDBRQAETEAEVKKKNKKKNKUNGLPPEIDA VPELAKYWAGRYRLFSRFDDGIKLDREGMFSVTPEKLAEHIAGR VSQSFKCDVVVDAPCGVGGNTIQFALTGMRVIAIDIDPVKIALA RNNAEVYGIADKIEFICGDFLLIKDFEMFSSTPEKLABHIAGR ARNAEVYGIADKIEFICGDFLLIKHTMIVYFLENRADIDQVAS LAGFGGQVEIEQNFLNNKLKTITAYFGDLIRRPASET HRARVDRSRESFGGDLRHFGRVRRDITLSGHFRLSTQHVVLLRE DEVGDPGTKDLGHPQHGSPIQETQSEVVTLVSPLPGSDMAALPA WRATSGITLMPHTAEGRDLLGAENRALTGGQQABDPTLASGAYQ WPSSVEKLQGSVWCDABTLISSSRTGGQAPPWLTDHDVQMLRLL AQGEVVDKARVPAHGQVLQVGFSTEAALQDLSSFRLSQLCGQGL CGLIKRPGDLPEVLSTHVDRVLGLRRSLPAVARFHSPLLPYRY TDGGARPVILWAPDVQHLSSSRTGQAPPWLTDHDVQALLAHSCN WPGQAPCPGIHTEWARLALFDFLLQVHDRLDRYCCGFEPEPSD PCVEERLREKCRNPABLRLVHILVRSDPSHLVYIDNAGNIQHP EKKLMFRLLEGIGFFESAVKVLASGCLQMMLLKSLQMDPVFWE SGGGAQGLKQVLQTLBQRGQVLIGHIQKHRLTLFRDEDP MINTMGRSTYRPRFRSVPPPELIGFMLEFGDEEPQGEEPPTES RPPARGQEREEDQGAAETQVPDLEADLGELSQSKTGDECGDGPD VGGKLITKSSQPKMPBGR 6306 1 1874 PTPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC KFNCHKCATRVPNDCLGBALINGDVPMEEATDFSRDKSALMD ESEDSGVIPGSHSENALHASEEEEGGGKAQSSLGVIPJMRVVQ SVRHTTRKSSTTLREGWVHYSKKDTLRKRHYWRLDCKCITLFQ NNTTNRYYKEIPLSSILTVESAQNFSLVPPGTNPHCFEIVTANA TTFVCEMPGGTTGGFSGCGARAARGMETAIRQALMFVILQDAPS APGHAPHRQASISISVSNSQIQENDVILATRQBLRWVILQDAPS APGHAPHRQASISISVSNSQIQENDVILASADPPDFVUKIC GVYYGGKRRKTGRDVAVKVIDKLRFPTKGESGLRNEVALLQSLR HPGIVNLECMFFSTERKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLITGILVALRHLHFKNICLLECPRLIAARDYNGLSGKGPPDQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVG VIMYVSLSGTFPFREDEDINDQIQMAAMYPARSPHSHISAGAID LINNLLQVKMRKRYSVDKSLSHPMLQEXQTWULLKERGMGER	1 1			SGNTNTDPPAEDSQKSSGANTSKDRPHASGTDGDESEEDPPEHK
SKILSKVEKFLITWVNKPMDERASGESSHDNGHDASTSCDEEEQ DMSVKKGDLLETNNPPEPEKCOSVSAGELETENYERDSLATV PDEODCVTQEVPDSRQAETEAEVKKKKNKKKKKUKKUGLPPEIAA VPELAKYWAGRYSHISERFDDGIKLDREGMFSVTTEKIAEHIAGR VSGSFKCDVVVDAFCGVGGGNTIQFALTGMRVIADIDPVKIALA RNNAEVYGIADKIEFICGDFLLLASFLKADVVPLSPPWGGPDYA TARTFDIRTMSPDGFEIFRLSKKITNNIVYFLPRNADIDQVAS LAGPGGQVETEQNFLNKKKITITAYFGDLIRRPASET LAGPGGQVETEQNFLNKKKITITAYFGDLIRRPASET DEVGPGTKUGHPGHOSPOTTLGSGHPRISTOHVVLLRE DEVGPGTKUGHPGHOSPOTTLGSGHPRISTOHVVLLRE DEVGPGTKUGHPGHOSPOTTLGSGHPRISTOHVVLLRE WRSSVEKLQGSVWCDAETLLSSSRTGQQAPPWILDHDVQMIRLL AQGEVVDKARVPAHGQVLQVGFSTEAALQDLSSPRLSGCLCSQGL CGLIKRPGDLPEVLSFHVDRVLGLRRSLPAVARRFHSPLLPYRY TDGGARPVIWWAPDVQHLSDPBEDQNSLALGWLQVQALLAHSCN WPSQAPCPGTHHTENARLALFDFLLQVHDRLDRYCCGFEPPSD PCVEERLREKCRNPASLRLVHILVRSSDPSHLVYIDMAGNLQHD EKKLNPRLLEGIGFPSAVKVLASGCLQNMLLKSLQMDPVFWE SQGGAGGLKQVLQTTLEQRGQVLLGHLQKHNLTLFRDEDP 6305 99 420 NMIWRGSTYRPPRRSVPPPELIGPMLEFGDEEPQGEEPPTES RDPAPGQRBEEDQGAAETQVLGHLQKINLTLFRDEDP VGGKILTKSEQFKMPEGR 6306 1 1874 PTRPSKVKYPHTFLHSYTRPTVCQACKKLLKGLFRGGLQCKDC KPNCHKCATRVPNDCLGRALINGDVPMEEATDFSEABKSALMD ESSDSGVIPGSHSENALHASEEEEGEGGKAQSSLGYIPLMRVVQ SVRHTTRKSSTTLREGWVVHYSNKDTLRRHTWRLDCKCTTLFQ NNTTNRYYKEIPLSSILTVESAQNPSLVPPGTNPHCFETVTANA TYFVGEMPGGTFGGPSGQGARAARGMETAIRQALMPVILQDAPS APGHAPHRQASLSISVSNSQIQENVOLATRVQFTNPHCETTVTANA TYFVGEMPGGTFGGPSGQGARAARGMETAIRQALMPVILQDAPS APGHAPHRQASLSISVSNSQIQENVOLATRVQISFDEVLGSGGF GVVYGGKHRKTGRDVAKVIDKLRFPTKGESGLRNEVALIGSLR HPGIVNLECMFSTPSKVFVVMEKKHGDMLEMILSSEKGRLPERL TKFLITGILVALRHHFKNUCDLKCPRNVLLASADPPDQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVG VVMXSLSGTFPFFMEDEDINDQIQMAAPMYPASPMSHISAGAID LINNLLQVKMRRYSVDNSLEHPMLQCHCYMULLASADPPDQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVG VIMYNSLGSTFPFFMEDEDINDQIQMAAPMYPASPMSHISAGAID	}			PSKLKRSHELDIDENPASDFDDSGSLLGFKYGSGQKYGGIPNFS
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VSOSFKCDVVDAFCGVGGNTIQFALTGMRVIAIDIDDVKIALA RNNAEVYGIADKIEFICGDFLLLASFIKADVVFLSPPWGGFDYA TAETFDIRTMMSPDGFEIFRLSKKITNNIVYFLPRNADIDQVAS LAGPGGQVEIEONFLNNKLKTITAYFGDLIRRPASET 6304 1 1438 HRARVDRSRESPGGDLRHPGRVRRDITLSGHPRLSTQHVVLLRE DEVGDPGTKDLGHPQHGSFIQETQSEVVTLVSPLPGSDMAALPA WRATSGITLWPHTAEGRDLLGERNRALTGGQQAEDPTLASGAYQ WPGSVEKLQGSVWCDAETLLSSRTGGQAPPWLTDHDVQMIRLL AQGEVVDKARVPAHGQVLQVGFSTEAALQDLSSPLUSQLCSQGL CGLIKRPGDLPSVLSPHVDRVLGLRRSLPAVARRFHSPLLPYRY TDGGARPVIWWAPDVQHLSDPDDQNSLALGWLQYQALLAHSCN WPGQAPCPGTHHTEWARLALFDFLLQVHDRLDRYCGFFEPEPSD PCVEERLREKCRNPAELRLVHILVRSSDPSHLVYIDNAGNLQHP EDKLNFRLLEGIDGFFESAVVLASGCLQMMLKSLQMDPVFWE SQGGAQGIKQVLQTHGQRGQVLIGHIQKHNLTLFADEDD SQGGAQGIKQVLQTHGQRGQVLIGHIQKHNLTLFADEDD SQGGAQGIKQVLQTHGQRGQVLIGHIQKHNLTLFADEDD VQGKLTLKSSQFKWFEGR 6306 1 1874 PTRPSKVKVPHTFLHSYTRPTVCQACKKLLKGLFRQGIQCKDC KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD ESSDSGVIPGSHSENALHASEEEEGEGGKAQSSLGYIPLMRVVQ SVRHTTRKSSTTLREGWVHYSNKDTLRRHYWRLDCKCITLFQ NNTTMRYYKEIPLSEILTVESAQNFSLVPPGTNHCFEIVTANA TYFVGEMPGGTPGGPSGGABAARGWETAIRQALMPVILQDAFS APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF GVYGGKHRKTGRDVAVKVIDKLRFPTKQBSQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMLEMLISSERGRLPERL TKFLITQILVALRHLHFKNIVHCDLKPERNVLLASADPFPQVKLC DFGFARIIGEKSFRRSVVGTFAYLAPEVLLNQGYNRSLDMWSVC VIMYVSLSGTFFNEDEDINNQIQNAARMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPMLQEYQTWLLDRELGKMGRER	1 1			WEEL A KYWA OR VELEBER DOTTYL DE TOURGUER DE TAA
RRNAEVYGIADKIEFICGDFLLLASFLKADVVPLSPPWGGPDYA TAETFDIRTMMSPDGFEIFRLSKKITNNIVYFLPRAADIDQVAS LAGPGGQVEIEDNFLNNKLKTITAYFGDLIRRPASET HRARVDRSRESPGGDLRHPGRVRRDITLSGHPRLSTQHVVLLRE DEVGDPGTKUDLGHPGGSPIGCTGSEVVTLVSPLPGSDMAALPA WRATSGITLWPHTASGRDLLGAENRALTGGQQAEDPTLASGAYQ WPGSVEKLQGSVWCDAETLLSSRTGGQAPPWLTHDUQMLRLL AQSEVVDKARVPAHGQVLQVGFSTEAALQDLSSPRLSQLCSQGL CGLIKRPGDLFBVLSPHVDRVLGLRRSLPAVARRPHSPLLPYRY TDGGARPVIWWAPDVQHLSDPDEDQNSLALGWLQVQALLAHSCN WPGQAPCPGIHHTEWARLALFPELQVHDRLDRYCCGFEPPESD PCVEERLREKCRNPAELRUVHLVRSSDPSHLVYIDNAGNLQHP EDKLNFRLLEGIDGFPESAVKVLASGCLQMMLLKSLQMDPVFWE SGGGAQGLKQVLQTLEQRGQVLLGHIQKHNLTLFRDEDP 6305 99 420 MNIWGRSTYRPRPRRSVPPFELIGPMLEFGDEEFQGEEPPTES RPDAPGQEREDQGAAETQVPDLEADLQELSQSKTGDECGDGPD VQGKILTKSEQFKMPEGR 6306 1 1874 PTRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSBANKSALMD ESEDSGVIPGSHENALHASEEEEGRGKAQSSLGYIPLMRVVQ SVRHTTRKSSTTLREGWVHYSNKDTLRKRHYWRLDCKCITLFQ NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA TYFVCEMPGGTPGGPSGGGARAARGMETAIRQALMPVILQDAFS APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF GVVYGGKHRKTGRDVAVKVIDKIRFFTKOESQLFMEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMILEMILSSEKGRLPERL TKFLITQILVALRHLHFKNIVHCDLKPERVLLASADPFPQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVC VIMYVSLSGTFFFNEDEDINGQVANAFMYPASPWSHLSAGAID LINNLLQVKMRKRYSVDKSLSHPHLQEYQTWLDLLEELGKMGER] [1		VENDER I MAGRICULUS RECOVERS TO THE RESERVE OF THE
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TDGGARPVIWMAPDVQHLSDPDEDQNSLALGWLQYQALLAHSCN WPGQAPCPGIHHTEWARLALFDFLLQVHDRLDRYCGFFPEPSD PCVEERLREKCRNPAELRLVHILVRSSDPSHLVYIDNAGNIQHP EDKINFRLLEGIDGF PESAVKVLASGCLQMMLLKSLQMDPVFWE SQGGAQGLKQVLQTLEQRGQVLLGHIQKHNLTLFRDEDP SQGGAQGLKQVLQTLEQRGQVLLGHIQKHNLTLFRDEDP MMIWRGRSTYRPRPRRSVPPPELIGPMLEPGDEEPQQEEPPTES RDPAPGQEREEDQGAAETQVPDLEADLQELSQSKTGDECGDGPD VQGKILTKSEQFKMPEGR 1 1874 PTRPSKVVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD ESEDSGVIPGSHSENALHASEEEGEGGKAQSSLGYIPLMRVVQ SVRHTTRKSSTTLREGWVHYSNKDTLRKRHYWRLDCKCITLFQ NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA TYFVGEMPGGTPGGPSGQGAEAARGWETAIRQALMFVILQDAPS APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF GVVYGGKHRKTGRDVAVKVIDKLRFPTKCESQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVILNQGYMRSLDMWSVC VIMYYSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRRRYSVDKSLSHPWLQEXQTVULDRELEGKMGER		1		CGLIKRPGDLPEVLSFHVDRVLGLRRSLPAVARREHSPLLDVDV
#PGQAPCPGTHHTEWARLALFDFLLQVHDRLDRYCCGFEPEPSD PCVEERLREKCRNPAELRLVHILVRSSDPSHLVYIDNAGRIQHP EDKLNFRLLEGIDGFPESAVKVLASGCLQNMLLKSLQMDPVFWE SQGGAQGLKQVLQTLEGRGQVLLGHIQKHNLTLFRDEDP MMIWRGRSTYRPRPRRSVPPPELIGPMLEPGDEEPQQEEPPTES RDPAPGQEREEDQGAAETQVPDLEADLQELSQSKTGDECGDGPD VQGKILTKSEQFKMFEGR 1 1874 PTRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD ESEDSGVIPGSHSENALHASEEEGEGGKAQSSLGYIPLMRVVQ SVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFQ NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA TYFVGEMPGGTPPGGPSQQGAEAARGWETAIRQALMFVILQDAPS APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSQQF GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLLTQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRSVVGTPAYLAPEVILNQSYRSLDMWSVC VIMYYSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRRRYSVDKSLSHPWLQEYQTVULDRELEGKMGER				TDGGARPVIWWAPDVOHLSDPDEDONSLALGWLOVOALLAHSCN
PCVEERLREKCRNPAELRUVHILVRSSDPSHLVYIDNAGNLQHP EDKLNFRLLEGIDGFPESAVKVLASGCLQNMLLKSLQMDPVFWE SQGAQGLQVLQVLEQRGQVLLGHIQKHNLTLFRDEDP 6305 99 420 NMIWRGRSTYRPRPRRSVPFPELIGPMLEPGDEEPQGEEPPTES RDPAPGQEREEDQGAAETQVPDLEADLQELSQSKTGDECGDGPD VQGKILTKSEQFKMPEGR PTRPSKVKVFHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD ESEDSGVI PGSHSENALHASEEEEGGGKAQSSLGYI PLMRVVQ SVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFQ NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA TYFVGEMPGGTPGGPSGQGAAARGWETAIRQALMEVILQDAPS APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF GVVYGGKHRKTGRDVAVKVIDKLRFFTKQESQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLTTQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRSVVGTPAYLAPEVILNQGYMRSLDMWSVC VIMYYSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRRRYSVDKSLSHPWLQEYOTWLDLRELEGKMGER	1 1	1	}	WPGQAPCPGIHHTEWARLALFDFLLOVHDRLDRYCCGFEPERSD
EDKINFRLIEGIDGF PESAVKVLASGCLQNMLLKSLQMDPVFWE SQGAQGLKQVLQTLEQRGQVLLGHIQKHNLTLFRDEDP MMIWRGRSTYRPRPRRSVPPPELIGPMLEPGDEEPQDEEPPTES RDPAPGQEREEDQGAAETQVPDLEADLQELSQSKTGDECGDGPD VQGKILTKSBQFKMPEGR 1 1874 PTRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD ESEDSGVI PGSHSENALHASEEEEGEGGKAQSSLGYI PLMRVVQ SVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFQ NNTTNRYYKE IPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA TYFVGEMPGGTPGGPSGQGAEAARGWETAIRQALMPVILQDAPS APGHAPHRQASLGISVSNSQLQENVDIATVYQI FPDEVLGSGQF GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLITQILVALHHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVILNQGYNRSLDMWSVC VIMYYSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRRRYSVDKSLSHPWLQESYOTWLDLRELEGKMGER	i		ļ	PCVEERLREKCRNPAELRLVHILVRSSDPSHLVYIDNAGNLOHD
SQGGQGLKQVLQTLEQRGQVLLGHIQKHNLTLFRDEDP 8051 8052 805306 8052 80520626252778787878787878787878787805052579755 805206262577878787878787878787878787878787878787				EDKLNFRLLEGIDGF?ESAVKVLASGCLQNMLLKSLOMDPVFWF
MIWRGRSTYRPRPRRSVPPPELIGPMLEPGDEEPQQEEPPTES RDPAPPGQEREEDQGAAETQVPDLEADLQELSQSKTGDECGDGPD VQGKILTKSEQFKMPEGR 1 1874 PTRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD ESEDSGVIPGSHSENALHASEEEGEGGKAQSSLGYIPLMRVVQ SVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFQ NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA TYFVGEMPGGTPGGPSGQGAEAARGWETAIRQALMFVILQDAPS APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVILNQGYNSLDMWSVC VIMYYSLSGTFPFNEDEDINDQIQNAAPMYPASPWSHISAGAID LINNLLQVKMRRRYSVDKSLSHPWLQEYQTWLDLRELEGKMGER	L 5305			SQGGAQGLKQVLQTLEQRGQVLLGHIOKHNLTLFRDEDP
RDPAPGQEREDQGAAETQVPDLEADLQELSQSKTGDECGDGPD VQGKILTKSEQFKMPEGR 1 1874 PTRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD ESEDSGVIPGSHSENALHASEEEEGEGGKAQSSLGYIPLMRVVQ SVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFQ NNTTNRYYKEIPLSEILTVESAQNFSLVPFGTNPHCFEIVTANA TYFVGEMPGGTPFGGPSGQGAEAARGWETAIRQALMFVILQDAPS APGHAPHRQASLGISVSNSQIQENVDIATVYQIFPDEVLGSGQF GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLLTQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRSVVGTPAYLAPEVILNQGYMRSLDMWSVC VIMYYSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRRRYSVDKSLSHPWLQEYQTWLDLRELEGKMGER	6303	99	420	NMIWRGRSTYRPRPRRSVPPPELIGPMLEPGDEEPOOFEPPTES
VQGKILTKSBQFKMPEGR PTRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSBADKSALMD ESEDSGVI PGSHSENALHASEEEEGEGGKAQSSLGYI PLMRVVQ SVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFQ MNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA TYFVGEMPGGTPGGPSGQGARAARGWETAIRQALMEVILQDAPS APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF GVVYGGKHRKTGRDVAVKVIDKLRFPTKQBSQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLLTQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRSVVGTPAYLAPEVLLNQGYMRSLDMWSVC VIMYYSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLQEYOTWLDLRELEGKMGER			i	RDPAPGQEREEDQGAAETQVPDLEADLQELSQSKTGDECGDGPD
FIRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD ESEDSGVJPGSHSENALHASEEEEGGGKAQSSLGYJPLMRVVQ SVRHTTRKSSTTLREGWVVHYSNKDTLRKHYWRLDCKCITLFQ MNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA TYFVGEMPGGTPGGPSGQGEAARGWETAIRQALMEVILQDAPS APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF GVVYGGKHRKTGGRVVAVKVIDKLRFPTKQBSQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRSVVGTPAYLAPEVLLNQGYMRSLDMWSVC VIMYYSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLQEYOTWLDLRELEGKMGER	6305		·	VQGKILTKSEQFKMPEGR
KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD ESEDSGVI PGSHSENALHASEEEGEGGKAQSSLGYI PLMRVVQ SVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFQ NNTTNRYKEI PLSEILTVESAQNFSLVPPGTNPHCFEIVTANA TYFVGEMPGGTPGGPSGQGARAARGWETAIRQALMFVILQDAPS APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLITQILVALHHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVC VIMYYSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRRRYSVDKSLSHPWLQEYOTWLDLRELEGKMGER	3,78	+	1874	PTRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC
SVRHTTRKSSTTLREGWVHYSNKDTLRKRHYWRLDCKCITLFQ NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA TYFVGEMPGGTPGGPSQQGABAARGWETAIRQALMFVILQDAPS APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSQQP GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVILNQGYMRSLDMWSVC VIMYYSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRRRYSVDKSLSHPWLQEYOTWLDLRELEGKMGER		1		KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD
NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA TYFVGEMPGGTPGGPSGQGARARGWETAIRQALMFVILQDAPS APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF GVVYGGKHRKTGRDVAVKVIDKLRFPTKQBSQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRSVVGTPAYLAPEVLLNQGYNRSLDMWSVC VIMYYSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLQBYQTWLDLRELEGKMGER	1	ļ		ESEDSGVIPGSHSENALHASEEEEGEGGKAQSSLGYIPLMRVVQ
TYFVGEMPGGTPGGPSGQGABAARGWETAIRQALMPVILQDAPS APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF GVVYGGKHRKTGRDVAVKVIDKLRFPTKQBSQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMIEMILSSEKGRLPERL TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVG VIMYVSLSGTFFFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLQBYQTWLDLRELEGKMGER				SVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFQ
APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDNIEMILSSEKGRLPERL TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQKKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVC VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLQEYQTWLDLRELEGKMGER			İ	NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA
GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDNLEMILSSEKGRLPERL TKFLITQILVALRHLHFKNIVHCDLKPENVILASADPFPQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVILNQGYNRSLDMWSVC VIMYYSLSGTFPRNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLQEYQTWLDLRELEGKMGER				TYPVGEMPGGTPGGPSGQGAKAARGWETAIRQALMPVILQDAPS
HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVC VIMYYSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRRRYSVDKSLSHPWLQEYQTWLDLRELEGKMGER	ŀ			AFGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF
TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVILNQGYNRSLDMWSVG VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLQEYQTWLDLRELEGKMGER				GVVIGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR
DFGFARIIGEKSFRRSVVGTPAYLAPEVILNQGYNRSLDMWSVG VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLQEYQTWLDLRELEGKMGER	I		1	HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL
VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLQEYQTWLDLRELEGKMGER	ŀ	ļ	i	TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC
LINNLLQVKMRKRYSVDKSLSHPWLQEYQTWLDLRELEGKMGER	- 1		1.	DIGFARTIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVG
LINNLLQVKMRKRYSVDKSLSHPWLQEYQTWLDLRELEGKMGER YITHESDDARWEQFAAEHPLPGSGLPTDRDLGGACPPQDHDMQG	!		1	VIMY VSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID
YITHESDDARWEQFAAEHPLPGSGLPTDRDLGGACPPQDHDMQG	1			LINNLLQVKMRKRYSVDKSLSHPWLQEYQTWLDLRELEGKMGER
	J			11THESDUARWEQFAAEHPLPGSGLPTDRDLGGACPPQDHDMQG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W-Triotophan V-Triotophan V-Triotophan V-Triotophan V-Triotophan
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
			LAERISVL
6307	2136	589	
		303	CFLLPRGRDPEPPEAGAAPCAPGAPDMSFRKVVRQSKFRHVFG
1	İ		QPVKNDQCYEDIRVSRVTWDSTFCAVNPKFLAVIVEASGGGAFL
ł	1		VLPLSKTGRIDKAYPTVCGHTGPVLDIDWCPHNDEVIASGSEDC
1	Ī		TVMVWQIPENGLTSPLTEPVVVLEGHTKRVGIIAWHPTARNVLL
1			SAGCDNVVLIWNVGTAEELYRLDSLHPDLIYNVSWNHNGSLFCS ACKDKSVRIIDPRRGTLVAEREKAHEGARPMRAIFLADGKVFTT
1	i		GFSRMSERQLALWDPENLEEPMALQELDSSNGALLPFYDPDTSV
	j i		VYVCGKGDSSIRYFEITEEPPYIHFLNTFTSKEPQRGMGSMPKR
1			GLEVSKCEIARFYKLHERKCEPIVMTVPRKSDLFQDDLYPDTAG
			PEAALEAEEWVSGRDADPILISLREAYVPSKQRDLKISRRNVLS
	l i		DSRPAMAPGSSHLGAPASTTTAADATPSGSLARAGEAGKLEEVM
1			QELRALRALVKEQGDRICRLEEQLGRMENGDA
6308	. 2	1118	GRPTRPEKMLLSLVLHTYSMRYLLPSVVLLGTAPTYVLAWGVWR
l .			LLSAFLPARFYQALDDRLYCVYQSMVLFFFENYTGVQILLYGDL
			PKNKENIIYLANHQSTVDWIVADILAIRQNALGHVRYVLKEGLK
1 1			WLPLYGWYFAQHGGIYVKRSAKFNEKEMRNKLQSYVDAGTPMYL
]			VIFPEGTRYNPEQTKVLSASQAFAAQRGLAVLKHVLTPRIKATH
1 1	1		VAFDCMKNYLDAIYDVTVVYEGKDDGGQRRESPTMTEFLCKECP
1			KIHIHIDRIDKKDVPEEQEHMRRWLHERFEIKDKMLIEFYESPD
1			PERRKRPPGKSVNSKLSIKKTLPSMLILSGLTAGMLMTDAGRKL
1 1			YVNTWIYGTLLGCLWVTIKA
6309	220	563	LVAEVKEPCSLPMLSVDMENKENGSVGVKNSMENGRPPDPADWA
			VMDVVNYFRTVGFEEQASAFQEQEIDGKSLLLMTRNDVLTGLQL
L i	i		KLGPALKIYEYHVKPLQTKHLKNNSS
6310	36	979	GPRCWKFLILSSVNCETLRIGKAWPQSSGQERYWTPRTHSSASE
i l	j		AQRGSLAELNVAAAGLWADCDQPLYDCPMCGLICTNYHILQEHV
1 1	į		DLHLEENSFQQGMDRVQCSGDLQLAHQLQQEEDRKRRSEESRQE
1 1			IEEFQKLQRQYGLDNSGGYKQQQLRNMEIEVNRGRMPPSEFHRR
	1		KADMMESLALGFDDGKTKTSGIIEALHRYYQNAATDVRRVWLSS
] [i		VVDHFHSSLGDKGWGCGYRNFQMLLSSLLONDAYNDCLKGMLTP
1 1	1		CIPKIQSMIEDAWKEGFDPQGASQLIIRLQGTKAWIGACEVYIL
6311			LTSLRV
6311	1	675	PVWWNSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMLTL
1			ASKLKRDDGLKGSRTAATASDSTRRVSVRDKLLVKEVAELEANI.
	1		PCTCKVHFPDPNKLHCFQLTVTPDEGYYOGGKFOFETEVPDAYN
		}	MVPPKVKCLTKIWHPNITETGEICLSLLREHSIDGTGWAPTPTI.
' I			KDVVWGLNSLFTDLLNFDDPLNIEAABHHLRDKEDFRNKVDDYI
6312	213	1400	KRYAR
	-13	1400	GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW
		[GKTEEBAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT
1		ļ	RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN
l l		1	VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC
- 1		ļ	DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA
	}	-	IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV
ł	ĺ	[GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD
ĺ	ļ	Į.	VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL
6313	2	2071	YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL
]	-		QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL
- 1	ļ]	FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD
[1	ľ	RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF
1	·		TOEPLVEIEGVSKMAFRHLIEFTYTAKLMIOGEEEANDVWKAAE
1		1	FLOMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI
1	ŀ		TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK
- 1		1	YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK
			QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE

SEQ Predicted Predicted end Amino acid segment containing circu	
SEQ Predicted Predicted end Amino acid segment containing signs ID beginning nucleotide (A-Alanine, C-Cysteine, D-Aspartic	al peptide
NO: nucleotide location Glutamic Acid, F=Phenylalanine, G=G	Acid, E=
location corresponding H=Histidine, I=Isoleucine, K=Lysine	elycine,
corresponding to first L=Leucine, M=Methionine, N=Asparagi	2, }
to first amino acid P=Proline, Q=Glutamine, R=Arginine,	ine,
amino acid residue of S=Serine, T=Threonine, V=Valine,	
residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknown	
amino acid sequence Codon, /=possible nucleotide deleti	i, *=Stop
sequence \=possible nucleotide insertion)	on,
SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQ	Dankerring
QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERF	ADMORT NOT
LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKD	ARNSTLKCH
PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEE	AL CABADAO MOATUTODY
TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQ	AND ATTACK
QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVE	PLUVEDINO
MPVEVQTELLEADLDHVTPEIMNQEERESSQADAA	EVVDEURED
AEDLETKPTVDSEAEKAENEDRTAT.PVT.E	CARREDNED
6314 2 2071 QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFV	WEMPT CVT.
FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEF	DEMHKWILD
RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSK	FFYKFFOEF
TQBPLVEIEGVSKMAFRHLIEFTYTAKLMIOGEEE	ANDVWKAAE
FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKR	KIARTSNVT
TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEE	VASAKOSVK
YIQSTGSSDDSALALLADITSKYRQGDRKGOIKED	GCPSDPTSK
QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKI	EHMKSHSTE
SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKO	RTGKKTHVC
QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERF	ARNSTI.KCH
LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKD	HLVIHTGDK
PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEV	VLSVETRVQ
TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQV	VHPDLLQDS
QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVE	ELHVERVNQ
MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAF AEDLETKPTVDSEAEKAENEDRTALPVLE	EAAREDHED
6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGI	
IDGKQARRINSCSPLGELFDHGCDSLSTVFMAVGAS	FIYQSLDA
PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVT	STAARLGTY
VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGV	STOTADAT
HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIM	TVKKCVLD
VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYL	ODTVELCE
GLLFLDQYFNNFIDEYVVLWMAMVISSFDMVIYFSA	T.CT.OTSPH
LHLNIFKTACHQAPEQVOVLSSKSHONNMD	.SCDQIDAI
6316 1503 792 VSAGAGTGIMGGTTSTRRVTFEADENENITVVKGIR	LSENVIDE
MKESSPSGSKSQRYSGAYGASVSDEELKRRVAEBLA	LEOAKKES
EDQKRLKQAKELDRERAAANEQLTRAILRERICSEE	ERAKAKHI.
ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVT	TEOYOKAA
EEVEAKFKRYESHPVCADLQAKILQCYRENTHQTLK	CSALATOY
MHCVNHAKQSMLEKGG	
6317 102 839 PEAQTSAVLAREKGHLPTMRHEAPMQMASAQDARYG	QKDSSDQN
FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVST	VGIDFKVK (
TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGF	ILMYDITN
EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDE	RVISTERG
QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKI	MSESLETD
PAITAAKQNTRLKETPPPPQPNCAC	
PWHPDRIDPHHPHPRPPRAEGREGADSMSHLPGLE	LRREAPPL
LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPC	KAAGRMNI
LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCA	CQEHRTGT
VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKA	PIGVDPEM
ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQA	IIIVFNLN
DVASLEHTKOWLADALKENDPSSVLLFLVGSKKDLST	IPAQYALM
EKDALQVAQEMKAEYWAVSSLTGENVREFFFRVAALT	reanvla
6319 88 717 BATWELLOWER LOWER	
AAIMALNQNILLIGKKVVLVPYTSEHVPSRYHEWMKS	SEELQRLT
ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQ CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGT	PGATEES
I CMVGDVNLFLTDLEDLTLGETEIMT X DDCCDCVCT CO	
SYGVTTLGLTKFEAKIGQGNEPSIRMFQKLHFEQVAT	TEAVLAML

SEQ	Predicted	Predicted end	Lamino noid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
ļ	sequence		\=possible nucleotide insertion)
6320			TLRLTVSESEHQWLLEQTSHVEEKPYRDGSAEPC
0320	90	1111	RPRTGREKVAMAAVDSFYLLYREIARSCNCYMEALALVGAWYTA
1			RKSITVICDFYSLIRLHFIPRLGSRADLIKQYGRWAVVSGATDG
1			IGKAYAEELASRGLNIILISRNEEKLQVVAKDIADTYKVETDII
			VADFSSGREIYLPIREALKDKDVGILVNNVGVFYPYPQYFTQLS
			BDKLWDIINVNIAAASLMVHVVLPGMVERKKGAIVTISSGSCCK PTPQLAAFSASKAYLDHFSRALQYEYASKGIFVQSLIPFYVATS
ł	1		MTAPSNFLHRCSWLVPSPKVYAHHAVSTLGISKRTTGYWSHSIQ
			FLFAQYMPEWLWVWGANILNRSLRKEALSCTA
6321	1418	341	HRKAALGALMAGRILIGKALAAVSLSLALASVTIRSSRCRGIQAF
1			RNSFSSWFHLNTNVMSGSNGSKENSHNKARTSPYPGSKVERSQ
1		_	VPNEKVGWLVEWQDYKPVEYTAVSVLAGPRWADPQISESNFSPK
1			FNEKDGHVERKSKNGLYEIENGRPRNPAGRTGLVGRGLLGRWGP
1			NHAADPIITRWKRDSSGNKIMHPVSGKHILQFVAIKRKDCGEWA
1			IPGGMVDPGEKISATLKREFGEBALNSLOKTSAEKREIEEKLHK
			LFSQDHLVIYKGYVDDPRNTDNAWMETEAVNYHDETGBIMDNLM
1			LEAGDDAGKVKWVDINDKLKLYASHSQFIKLVAEKRDAHWSEDS
6322	2047		EADCHAL
6322	2047	1083	NQEILKNVESSRTVQPHFLEFLLSLGWSVDVGRHPGWTGHVSTS
j i			WSINCCDDGEGSQQEEVISSEDIGASIFNGQKKVLYYADALTEI
			AFVVPSPVESLTDSLESNISDQDSDSNMDLMPGILKQPSLTLEL
			FPNHTDNLNSSQRLSPSSRMRKLPQGRPVPPLGPETRVSVVWVE
			RYDDIENFPLSELMTEISTGVETTANSSTSLRSTTLEKEVPVIF IHPLNTGLFRIKIQGATGKFNMVIPLVDGMIVSRRALGFLVRQT
			VINICRRKRLESDSYSPPHVRRKQKITDIVNKYRNKQLEPEFYT
]			SLFQEVGLKNCSS
6323	1	656	PASTTDGAQEARVPLDGAFWIPRPPAGSPKGCFACVSKPPALQA
1 1			PAAPAPEPSASPPMAPTLFPMESKSSKTDSVRAAGAPPACKHLA
			EKKTMTNPTTVIEVYPDTTEVNDYYLWSIFNFVYLNFCCLGFIA
			LAYSLKVRDKKLLNDLNGAVEDAKTDRLINITRSGLAASCIMLW
6324			MALSVIATHRGLRSSASILVAEPHDWNTERPQVTFRERCPAL
0324	1	2061	EGAGMRRCPCRGSLNEAEAGALPAAARMGLEAPRGGRRRQPGQQ
1			RPGPGAGAPAGRPEGGGPWARTEGSSLHSEPERAGLGPAPGTES
1	ļ		PQAEFWTDGQTEPAAAGLGVETERPKQKTEPDRSSLRTHLEWSW
			SELGTTCLWTETGTDGLWTDPHRSDLQFQPEEASPWTQPGVHGP
	,		WTELETHGSQTQPERVKSWADNLWTHQNSSSLQTHPEGACPSKE PSADGSWKELYTDGSRTQQDIEGPWTEPYTDGSQKKQDTEAARK
İ			QPGTGGFQIQQDTDGSWTQPSTDGSQTAPGTDCLLGEPEDGPLE
			EPEPGELLTHLYSHLKCSPLCPVPRLIITPETPEPEAQPVGPPS
	İ		RVEGGSGGFSSASSFDESEDDVVAGGGGASDPEDRSGSKPWKKL
i	i		KTVLKYSPFVVSFRKHYPWVQLSGHAGNFQAGEDGRILKRFCQC
			EQRSLEQLMKDPLRPFVPAYYGMVLODGOTFNOMEDLLADFEGP
	Ţ		SIMDCKMGSRTYLEEELVKARERPRPRKDMYEKMVAVDPGAPTP
			EEHAQGAVTKPRYMQWRETMSSTSTLGFRIEGIKKADGTCNINF
1	1		KKTQALEQVTKVLEDFVDGDHVILQKYVACLEELREALEISPFF
}	1		KTHEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPDHOTLSHRLP
6325	366		WAEGNREDGYLWGLDNMICLLQGLAQS
0323	165	944	GLRDPFRRKRRLKPQVKMSNYVNDMWPGSPQEKDSPSTSRSGGS
	1		SRLSSRSRSFSRSSRSHSRVSSRFSSRSRRSKSRSRRRRHQ
	}	. 1	RKYRRYSRSYSRSRSRSRSRRYRERRYGFTRRYYRSPSRYRSRS
		į	RSRSRSRGRSYCGRAYAIARGORYYGFGRTVYPBEHSRWRDRSR
	ŀ	1	TRSRSRTPFRLSEKDRMELLEIAKTNAAKALGTTNIDLPASLRT
6326	238	680	VPSAKETSRGIGVSSNGAKPEVSILGLSEQNFQKANCQI
		660	GEPSPATQQKPSATGAGVLHQHFSSGHIYVLMGLLPPPWTISFT VQTTLQPPGGLPAAPVSGRMAFEPVGRDLARRMVPRAGKRTQTL
			GARRVAAQGARPLPEDRRPKSGERLHVTVAPCWEFVLPSVSLTA
			THE PROPERTY OF THE PROPERTY O

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ŀ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- [amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ı	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	7-4-0	\=possible nucleotide insertion)
	•		QAWGGVGQEASSGVP
6327	† <u> </u>	1337	SLARLAPAGGSVVMPTQQPAAPSTRAPKPSRSLSGSLCALFSDA
1		2557	DSGSGMKAELPPGPGAVGREMTKEEKLQLRKEKKQQKKKRKEEK
1			GAEPETGSAVSAAQCQGPTRELPESGIQLGTPREKVPAGRSKAE
i			LRAERRAKQEAERALKQARKGEQGGPPPKASPSTAGETPSGVKR
			LPEYPQVDDLLLRRLVKKPERQQVPTRKDYGSKVSLFSHLPQYS
	j i		RQNSLTQFMSIPSSVIHPAMVRLGLQYSQGLVRGSNARCIALLR
1			ALQQVIQDYTTPPNEELSRDLVNKLKPYMSFLTQCRPLSASMHN
1			AIKFLNKEITSVGSSKREEEAKSELRAAIDRYVQEKIVLAAQAI
	į i		SRFAYQKISNGDVILVYGCSSLVSRILQEAWTEGRRFRVVVVDS
1			RPWLEGRHTLRSLVHAGVPASYLLIPAASYVLPEVSTEEKDSKV
			GGEKV
6328	1030	276	HASAEVTTAAARGLGAMEEEMHTDAKIRAENGTGSSPRGPGCSL
1	J l		RHFACEQNLLSRPDGSASFLQGDTSVLAGVYGPAEVKVSKEIFN
			KATLEVILRPKIGLPGVAEKSRERLIRNTCEAVVLGTLHPRTST
			TVVLQVVSDAGSLLACCLNAACMALVDAGVPMRALFCGVACALD
			SDGTLVLDPTSKQEKEARAVLTFALDSVERKLLMSSTKGLVSDT
			ELQQCLAAAQAASQHVFRFYRESLQRRYSKS
6329	3	2016	SSEVAAGGGTRSAMAEGSGEVVTVSATGAANGLNNGAGGTSATT
			SNPLSRKLHKILETRLDNDKEMLEALKALSTFFVENSLRTRRNT.
1 .			RGDIERKSLAINEEFVSIFKEVKEELESISEDVOAMSNCCODMT
1			SRLQAAKEQTQDLIVKTTKLQSESOKLEIRAOVADAFLSKFOLT
1			SDEMSLLRGTREGPITEDFFKALGRVKOIHNDVKVLLRTNOOTA
1			GLEIMEQMALLQETAYERLYRWAQSECRTLTOESCDVSPVT.TOA
			MEALQDRPVLYKYTLDEFGTARRSTVVRGFIDALTRGGPGGTPP
			PIEMHSHDPLRYVGDMLAWLHQATASEKEHLEALLKHVTTQGVE
1 1			ENIQEVVGHITEGVCRPLKVRIEQVIVAEPGAVLLYKISNLLKF
1			YHHTISGIVGNSATALLTTIEEMHLLSKKIFFNSLSLHASKLMD
1			KVELPPPDLGPSSALNQTLMLLREVLASHDSSVVPLDARQADFV
1 1			QVLSCVLDPLLQMCTVSASNLGTADMATFMVNSLYMMKTTLALF
1	į		EFTDRRLEMLQFQIEAHLDTLINEQASYVLTRVGLSYIYNTVQQ
]	i		HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL
] [LSATVKEQIVKQSTELVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTLLS
6330	1151	333	
			FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR
1		İ	KFYERGDFPIALEHDSKGNKIAWKVEIBKLDYHHYLPLFFDGLC
, 1		ļ	EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN
	1		RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV
	1		NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP
[I			TYESCLIN
6331	3	495	QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL
		-	LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY
1	1		RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA
L l			IFGFMATFLCMASIWLSYKISCVTQSTDAAV
6332	1	878	.VTESNKFDLVSFIPLLRERIYSNNOYAROFITSWILMT.FSVODT
] [1	1	NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS
	1		SVKFAEMANILVIHCQTTDDLIQLTAMCWMREFIQLAGRVMLPY
	j	İ	SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD
			ELRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD
		İ	VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG
	_		KLSTMATHSQLVKTGTGLEPRQAVSSSH
6333	3	1467	TRTPSEAEAGGESPOSCVSAAHSDWTAGKPVSLLAPLIPPRSAG
	ł	1	QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGAERG
1	ļ		GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP
		j	MGQMPGMMSSVMPGMMMSHMSQASMQPALPPGVNSMDVAAGTAS
			- CONTROL OF THE POST OF THE P

SEQ	Predicted	Predicted end	Amino agid gooment
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ĺ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	i	\=possible nucleotide insertion)
			GAKSMWTEHKSPDGRTYYYNTETKQSTWEKPDDLKTPAEQLLSK
1			CPWKEYKSDSGKPYYYNSOTKESRWAKPKELEDLEGYONTTUAG
ľ			SLITKSNLHAMIKAEESSKOEECTTTSTAPVPTTETPTTMSTMA
		;	AAEAAAAVVAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
ı	1		EVTSIVATVVDNENTVTISTBEQAQLTSTPAIODOSVEVSSNTG
ſ	i i		EETSKQETVADFTPKKEEEESQPAKKTYTWNTKEEAKOAFKELL
1			KEKRVPSNASWEQAMKMI INDPRYSALAKLSEKKQAFNAYKVOT
6334			EKK
6334	. 17	644	GGNPSGRAAGFAAAAMPSSPLRVAVVCSSNQNRSMEAHN1LSKR
			GFSVRSFGTGTHVKLPGPAPDKPNVYDFKTTYDOMYNDLLRKDK
1	ł i		ELYTQNGILHMLDRNKRIKPRPERFONCKDLFDLILTCEERVYD
			QVVEDLNSREQETCQPVHVVNVDIQDNHERATLGAFLICELCQC
6335	00		IQHTEDMENEIDELLQEFEEKSGRTFLHTVCFY
0335	82	529	AARARPGVLCCRLLGAALGDQSRVEMSYIPGQPVTAVVQRVEIH
[·	KLRQGENLILGFSIGGGIDQDPSQNPFSEDKTDKGIYVTRVSEG
ļ			GPAEIAGLQIGDKIMQVNGWDMTMVTHDQARKRLTKRSEEVVRL
6336	1003		LVTRQSLQKAVQQSMLS
0330	1003	438	HEPASKGRAEVGNMRLSVAAAISHGRVFRRMGLGPESRIHLLRN
			LLTGLVRHERIEAPWARVDEMRGYAEKLIDYGKLGDTNERAMRM
			ADFWLTRKDLIPKLFQVLAPRYKDQTGGYTRMLQIPNRSLDRAK
[MAVIEYKGNCLPPLPLPRRDSHLTLLNQLLQGLRQDLRQSQEAS
6337	76	524	NHSSHTAQTPGI
1	,,,	524	EGIQMLSVQPDTKPKGCAGCNRKIKDRYLLKALDKYWHEDCLKC
1 1	1		ACCDCRLGEVGSTLYTKANLILCRRDYLRLFGVTGNCAACSKLI
1 1			PAFEMVMRAKDNVYHLDCFACQLCNQRFCVGDKFFLKNNMILCQ TDYBEGLMKEGYAPQVR
6338	66	1349	APNSESGTQGPLPTPANLFWTRRANPDPTTSMSATDRMGPKAVP
1 1		4347	GLRLALLLLLGLGTPKSGVQGQEGLDFPEYDGVDRVINVNAKNY
1			KNVFKKYEVLALLYHEPPEDDKASQRQFEMEBLILELAAQVLED
1			KGVGFGLVDSEKDAAVAKKLGLTEVDSMYVFKGDEVIEYDGEFS
1 1	i		ADTIVEFLLDVLEDPVELIEGERELQAFENIEDEIKLIGYFKSK
1	ļ		DSEHYKAFEDAAERFHPYIPFFATFDSKGAKKLTLKLNEIDFYE
1 1	Ī		AFMEEPVTIPDKPNSEEEIVNFVEEHRRSTLRKLKPESMYETWE
1 1			DDMDGIHIVAFAEEADPDGFEFLETLKAVAQDNTENPDLSIWI
1			DPDDFPLLVPYWEKTFDIDLSAPQIGVVNVTDADRLWMEMDDEE
			DLPSAEELEDWLEDVLEGEINTEDDDDDDDD
6339	246	1813	NRCDRGGGGQAERQAGQGCRTQGAGPGFGFGHSFFSOGAMKAFH
1			TFCVVLLVFGSVSEAKFDDFEDEEDIVEYDDNDFAEFEDVMEDS
	1	1	VTESPORVIITEDDEDETTVELEGODENOEGDFEDADTOEGDTE
1 1			SEPYDDEEFEGYEDKPDTSSSKNKDPITIVDVPAHLONSWESYY
1			LEILMVTGLLAYIMNYIIGKNKNSRLAQAWFNTHRELLESNFTI.
] [VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIOLRFI.
1 1			KRQDLLNVLARMMRPV3DQVQIKVTMNDEDMDTYVFAVGTRKAI.
1			VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM
1		j	DTKMVHFLTHYADKIESVHFSDQFSGPKIMQEEGQPLKLPDTKR
	1		TLLLTFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNRE
1		J	GKQKADKNRARVBENFLKLTHVQRQEAAQSRREEKKRAEKERIM
6340	2	E03	NEEDPEKQRRLEEAALRREQKKLEKKQMKMKQIKVKAM
	~	583	EACAHTLSCPAFARLGRARRRPWMSHRTSSTFRAERSFHSSSS
			SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF
		j	PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA
1 1		1	EKLAADGTVMNNFAHKCQLPEDVDPTSVTSALREDGSLTIRARR
6341	2	645	HPHTEHVQQTFRTEIKI
	-	043	KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ
i 1	1	ľ	PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA
			CCAVEMMHMAAPRYDMDRFGVVFRASPRQSDVMIVAGTLTNKMA

SEQ	Predicted		
ID	beginning	Predicted end	The second second containing as and second
NO:	nucleotide	nucleotide	In-Alenande, CattySteine, Dalenaveic hair m
1.0.	location	location	Grutamic Acid, F-Phenylalanine C-Clarette
1	corresponding	corresponding	n=nistidine, I=Isoleucine K-lacine
i	to first	to first	Labeucine, Mamethionine, Nahanaragine
1	amino acid	amino acid	Parcline, QaGlutamine, Rahrginine
i	residue of	residue of	S=Serine, T=Threonine, V=Valine
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine Y=Introdum 4 Ct
1	sequence	sequence	Codon, /=possible nucleotide deletion
	pedaence	<u> </u>	\=possible nucleotide insertion)
- 1			PALRKVYDQMPEPRYVVSMGSCANGGGYYHYSYSYAPCCDBTYD
6342			VDIIIPGCPPTAEALLYGILOLORKIKRERRI.OTWVDD
6342	2	1191	DPRVRAMLATLARVAALRKTCLFSGRGGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
	1		APPEGVKILDLTRVLAGPFATMNLGDIGARVIKVERDOAGDDDD
	1	1	TWGPPFVGTESTYYLSVNRNKKSIAVNIKDPKGVKIIKELAAVC
			DVFVENYVPGKLSAMGLGYEDIDEIAPHIIYCSITGYGQTGPIS
1	i	1	QRAGYDAVASAVSGLMHITGPEVACLSHIAANYLIGQKEAKRWG
ł			TAHGSIVPYQAFKTKDGYIVVGAGNNQQFATVCKILDLPELIDN
			SKYKTNHLRVHNRKELIKILSERFEEELTSKWLYLFEGSGVPYG
			PINNMKNVFAEPQVLHNGLVMEMEHPTVGKISVPGPAVRYSKFK
			MSEARPPPLLGQHTTHILKEVLRYDDRAIGELLSAGVVDQHETH
6343	2	936	GTAMVSDEDELNLLVIVVDANPIWWGKQALKESQFTLSKCIDAV
			MVLGNSHLFMNRSNKLAVIASHIQESRFLYPGKNGRLGDFFGDP
1			GNPPEFNPSGSKDGKYELLTSANEVIVEEIKDLMTKSDIKGQHT
			ETLLAGSLAKALCYIHRMNKEVKDNQEMKSRILVIKAAEDSALQ
i i			YMNFMNVIFAAQKQNILIDACVLDSDSGLLQQACDITGGLYLKV
1			PQMPSLLQYLLWVFLPDQDQRSQLILPPPVHVDYRAACFCHRNL
1 1	1		IEIGYVCSVCLSIFCNFSPICTTCETAFKISLPPVLKAKKKKLK
6344			I VSA
6344	2508	147	TMPTATIGNLRGYGMASPGLAAPSLTPPQLATPNLQQFFPQATR
ļ l			QSLLGPPPVGVPMNPSQFNLSGRNPQKQARTSSSTTPNRKDSSS
j f			QTMPVEDKSDPPEGSEEAAEPRMDTPEDQDLPPCPEDIAKEKRT
1	İ		PAPEPEPCEASELPAKRLRSSEEPTEKEPPGQLQVKAQPQARMT
1 1	.		VPKQTQTPDLLPEALEAQVLPRFQPRVLQVQAQVQSQTQPRIPS
1			TDTQVQPKLQKQAQTQTSPEHLVLQQKQVQPQLQQEAEPQKQVQ
1 1			PQVQPQAHSQGPRQVQLQQEAEPLKQVQPQVQPQAHSQPPRQVQ
1 1	i		LOLOKQVQTQTYPQVHTQAQPSVQPQEHPPAQVSVQPPEQTHEQ
1 1			PHTQPQVSLLAPEQTPVVVHVCGLEMPPDAVEAGGGMEKTLPEP
1			VGTQVSMEBIQNESACGLDVGECENRAREMPGVWGAGGSLKVTI
1 1	1		LQSSDSRAFSTVPLTPVPRPSDSVSSTPAATSTPSKQALQFFCY
1 1	1		ICKASCSSQQEFQDHMSEPQHQQRLGEIQHMSQACLLSLLPVPR
1 1			DVLETEDEEPPPRRWCNTCQLYYMGDLIQHRRTQDHKIAKQSLR
1	ļ		PFCTVCNRYFKTPRKFVEHVKSQGHKDKAKELKSLEKEIAGQDE
1 1	ļ	ĺ	DHFITVDAVGCFEGDEEEEEDDEDEEEIEVEEBLCKQVRSRDIS
			REEWKGSETYSPNTAYGVDFLVPVMGYICRICHKFYHSNSGAQL
			SHCKSLGHFENLQKYKAAKNPSPTTRPVSRRCAINARNALTALF
6345			TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT
6345	2	3483	PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMPEMTEOLOFICE
	1		HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK
	1	i	ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE
1		ļ	IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENEIELSLLQLR
1	ĺ	ĺ	EQUATDURSNIRDNVEMIKLHKOLVEKSNALSAMEGVETOLODI.
-	ł		QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER
			RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ
			QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNEKLVQENREL
1	j		QLQYLEQKQQLDBLKKRIKLYNQENDINADBLSEALLLIKAQKE
1	į	1	QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM
1		1	LIMOHKINKDYOMEVEAVTRKMENLOODYELKVEQYVHLLDIRA
1		1.	ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG
-		į '	ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV
	ļ		VRGLHPEYNFTSQYLVHVNDLFLQYIQKNTITLEVHQAYSTEYE
i	į	} ,	TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL
		J 1	RV3MDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL
ļ		1.7	SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA
1	- 1	i	DHDTALIPSSNDPQFDDHMYFPVPMNMDLDRYLKSESLSFYVFD
		l i	OSDTQENIYIGKVNVPLISLAHDRCISGIFELTDHQKHPAGTIH

SEQ	Predicted	Predicted end	Amino agid goggest gotte
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Wight ding T T-clevely attaine, G-Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	F-Floring, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	Sequence	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
	1		VILKWKFAYLPPSGSITTEDLGNFIRSEEPEVVQRLPPASSVST
İ	<u>}</u>		LVLAPRPKPRQRLTPVDKKVSFVDIMPHQSDVSQEGSVDEVKEN
	[1	TEKMQQGKDDVSLLSEGQLAEQSLASSEDETEITEDLEPEVEED
	1		MSASDSDDCIIPGPISKNIKQPSEKIRIEIIALSLNDSQVTMDD
	1		TIQRLFVECRFYSLPAEETPVSLPKPKSGQWYYYNYSNVIYVDK
	J		ENNKAKRDILKAILQKQEMPNRSLRFTVVSDPPEDEQDLECEDI GVAHVDLADMFQEGRDLIEQNIDVFDARADGEGIGKLRVTVEAL
ı			HALQSVYKQYRDDLEA
6346	2921	533	QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL
			AKYTQKEESAEQPEFYYDEFGFRVYKEEGDEPGSSLLANSPLME
1	j i		DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA
1	· .		GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
			QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC
Ì	1		QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ
ł			TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
1	[]		DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI
			FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL
1	! !		IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
			KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL
1	ł		PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH
			RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL
1			RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK
1	1		ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL
			CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAOMDVKLRSL
1 .			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVOIKC
1			ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW
6347	2921		DVDG
034/	2921	533	QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL
			AKYTQKEESAEQPEFYYDEFGFRVYKEEGDEPGSSLLANSPLME
			DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA
1 1			GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
]			QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ
] [1		TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
1		ĺ	DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI
1			FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL
1			IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
]]	J		KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL
į į			PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH
j [RRRAKALLDFERHDDDELGFRKNDIITIVSOKDEHCWVGELNGL
1 1	Ì		RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK
		i	ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL
1 1	}	Ī	CKTFRLDEDGKVLTPEELLYRAVOSVNVTHDAVHAOMDVKLRSI.
}	ļ	ļ	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVOIKC
[[ļ		ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW
6348			DVDG
0348	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE
		1	KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN
	İ		EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVOKLSPENDN
1		1	DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
		j	NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECODALN
1		Ĭ	ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPOLA
		1	EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
		i	ERQFKEBKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR
Ì		1	DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK
			LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE

WO 01/53312

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A-Alanine, C=Cysteine, D=Aspartic Acid, B=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion
ļ	sequence		\=possible nucleotide insertion)
ļ			ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
}			EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG
1			YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK
İ			KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
		ĺ	COPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR
1			ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
}			QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALBEKHVGFSLDVGEIE
i			KKGKGKKRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG
1			PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV
1			DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS
l	1		TPSGCLELTDSCQPYRSAFYILEOORVGLAVDMDETEKYOEVEE
		,	DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGO
			PYSSAVYSLEEQYLGLALDVDRIKKDOEEEEDOGPPCPRISPRI
	1		LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCOPYGSSFYALEEKH
1			VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDONPPCP
1			RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY
6349	3	3679	SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ
ŀ			AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEB KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN
			EIILQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN
1		-	DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
ĺ			NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
İ]		ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLEDOLA
	1		EKKQQFRNLKEKCFLTQLACFLANOONKYKYEECKDI.TKFMI.PN
1			ERQFKEEKLAEQLKQAEELROYKVLVHSOERELTOLBEKLDEGD
I			DASRSLNEHLQALLTPDEPDKSOGODLOEOLAEGCRI.AOHT.VOK
	i		LSPENDNDDDBDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE
ł			ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
			EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK
			KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
			CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR
			ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGOPYSSAVVSLEE
i			QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLOD
			SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGETE
	!		KKGKGKKRRGRRSKKERRRGRKEGEEDONPPCPRLSRELLDEKG
i. i]]	PEVLQDSLDRCYSTPSGCLBLTDSCQPYRSAFYILEQQRVGLAV
		į	DMDEIEKYQEVERDQDPSCPRLSGELLDEKEPEVLQESLDRCYS
	İ	1	TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE
		ļ	DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEROYLGLALDVDP LYVDGEREEDGGPRGDD
	Į	-	PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH
	1		VGFSLDVGEIEKKGKGKKRGRRSKKERRRGRKEGBEDQNPPCP
	1		RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY
			SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ
6350	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELOFKEE
		. 1	KLAEQLKQAEELRQYKVLVHSQERELTOLREKLREGRDASRSIN
		}	EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAOHLVOKLSPENDN
		i	DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
		i	NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECODALN
{	1	ł	ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
	ļ	į.	EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
i		1:	ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR
	'		DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic hold F
NO:	nucleotide	location	Glucamic Acid, F=Phenylalanine G-Glucine
	location	corresponding	A=HISTICINE, I=ISOleucine K-Lucine
	corresponding to first	to first	L=beucine, M=Methionine N-lenaragine
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
	residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
		 	\=possible nucleotide insertion)
	j	1	ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVER
			EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK
			KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
		İ	CQPYRSAFYVLBQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR
			ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
			QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD
			SEDRCYSTPSSCLEQPDSCOPYGSSFYALEEKHUGEGI.DUGETE
	İ		KKGKGKKRRGRRSKKERRRGRKEGEEDONPPCPPLSPPLLDPVC
			PEVLQDSLDRCYSTPSGCLELTDSCOPYRSAFYTLFOODUCT AND
	j i		DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEDEVLOEGI DBCVC
			TPSGCLELTDSCQPYRSAFYILEOORVGLAVDMDETEKVOEVER
			DQDPSCPRLSRELLDEKEPEVLODSLGRCYSTPSGVLELBDICO
			PYSSAVYSLEEQYLGLALDVDRIKKDORREEDOGDDCDDLCDDL
			LEVVEPEVLQDSLDRCYSTPSSCLEOPDSCQPYGSSFYALEEKH
	j		VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP
			RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY
6351	1291	319	SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ
			REARRTERSQLGRMLVVEVANGRSLVWGAEAVQALRERLGVGG RTVGALPRGPRQNSRLGLPLLLMPEEARLLAEIGAVTLVSAPRP
			DSRHHSLALTSFKRQQEESFQEQSALAAEARETRRQELLEKITE
į			GQAAKKQKLEQASGASSQEAGSSQAAKEDETSDGQASGEQEEA
- 1	j		GPSSSQAGPSNGVAPLPRSALLVQLATARPRPVKARPLDWRVQS
1	İ		KDWPHAGRPAHELRYSIYRDLWERGFFT-SAAGKECCDELWYDCD
	•		PLRFHAHYIAQCWAPEDTIPLQDLVAAGRLGTSVRKTLLLCSPQ
6352) PDGKVVYTSLQWASLQ
0332	235	923	WSEWLSPCHAAKCKGLSMLRITMKTRAISLAADATEFVQGRSAP
}	}		AMAKSLVHDTVFYCLSVYOVKISPTPOLGAASSARGHUGOGARG
ĺ			LMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQPPPEE
	j		PAQAAMEGPQPENMQPRTRRTKFTLLQVEELESVFRHTQYPDVP
[TRRELAENLGVTEDKVRVWFKNKRARCRRHQRELMLANELRADP
6353	65	672	RFAGAGAIPEARARPPDVQAAEEEKEMDLPDSASRVFCGRILSM
- 1	1		VNTDDVNAIILAQKNMLDRFEKTNEMLLNFNNLSSARLQQMSER
I	İ		FIRETRILVEMKRDLDSIFRRIRTLKGKLAPOHDER EGUIDER C
			FLEEEDEDPIPPSTTTTIATSEOSTGSCDTSPDTVSDSLSDGED
6354	2.55		DLSAVQPGSPAINGRSQTDDEEMTGE
0354	965	510	PSLRPMEPTRDCPLFGGAFSAILPMGAIDVSDLPDVDDVDDVDC
			HPVTDQSLIVELLELOAHVRGEAAARYHFEDVGGVOGADAINIR
	1		SVQPLSLENLALRGRCQEAWVLSGKOOIAKENOOVAKDVTI.HOA
6355	158	1665	LLKLPQYQTDLLLTFNOPP
	120	1662	RGSSAAFRGSGLRGAMIRRVLPHGMGRGLLTRRPGTRRGGFSLD
1	j	ļ	WDGKVSEIKKKIKSILPGRSCDLLODTSHLPPRHSDA/TVCCCV
		ſ	LGLSVAYWLKKLESRRGAIRVLVVERDHTYSOASTGLSVGGICO
		i	QFSLPENIQLSLFSASFLRNINEYLAVVDAPPLDLRFNPSGVII
			LASEKDAAAMESNVKVQRQEGAKVSLMSPDQLRNKFPWINTEGV
1	1		ALASYGMEDEGWFDPWCLLQGLRRKVQSLGVLFCQGEVTRFVSS
ĺ			SQRMLTTDDKAVVLKRIHEVHVKMDRSLEYQPVECAIVINAAGA
-	1]	WSAQIAALAGVGEGPPGTLQGTKLPVEPRKRYVYVWHCPQGPGL
[j	ETPLVADTSGAYFREGLGSNYLGGRSPTEQEEPDPANLEVDHD
l	ł	1	FFQDKVWPHLALRVPAFETLKVQSAWAGYYDYNTFDQNGVVGPH
		ļ	PLVVNMYFATGFSGHGLQQAPGIGRAVAEMVLKGRFQTIDLSPF LFTRFYLGEKIQENNII
6356	354	633	
			TGLTSSCLPLQVMMTKRTKDMGKFSSVTVSTIDEEEEEIEAREV ADSYAQNAKVIEKQLERKGMSKRRLQELABLEAKKAKMKGTLID
		J.	

SEQ Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence Sequence 6357 Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence 6357 2 915 GLEMMALLYURNQTSISQWVPVCSRLIPVSPTQQQ RTSQWPQMSQSQACGGSEQIPGIDIQLNRKYHTTRKLS QPVEEKVGAFTKIIEAMGFTGPLKYSKWKIKIAALRMY TDFEEFFLRCQMPDTFNSWFLITLLHWMCLVRMKQEG CRIIVHFMWEDVQQRGRVMGVNPYILKKNMILMTNHFY, DEGILSDDHGLAAALWRTFFNRKCEDPRHLELLVEYVRIDSMNGEDLLLTGEVSWRPLVEKNPQSILKPHSPTYNDEG ASDALHSLSSPSAARPATMTEQALSFAKDFLAGUE GOGVLSFWRGNLANVIRYFPTQALMFAFKDKYKQIFLGG GFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADWC	ESTOP GDRALS TTKDSP TSCVEK RSGKYM ANGLIGY KQIQYL GL AGGIAA IVRIPK GVEKHTE
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence 6357 2 915 GLIRMMALLVRVLRNQTSISQWVFVCSRLIFVSFTQQQ RTSQWPQMSQSQACGGSEQIPGIDIQLNRKYHTTRKLS QPVEEKVGAFTKLIEAMGFTGPLKYSKWKIKIAALRMY TDFEEFFLRCQMPDTFNSWFLITLLHVWMCLVRWKQEG CRIIVHFMWEDVQQRGRWMGVNPYILKKNMILMTNHFY DEGILSDDHGLAAALWRTFFNRKCEDPRHLELLVEYVR ASSKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDC: EQGVLSFWRGNLANVIRYFFTQALMFAFKDKYKGIVDC: EQGVLSFWRGNLANVIRYFTQALMFAFKDKYKGIVDC: EQGVLSFWRGNLANVIRYFTQALMFAFKDK	GDRALS TTKDSP TSCVEK RSGKYM AAILGY KAGIQYL GL AGGIAA IVRIPK GVDKHT
location corresponding to first amino acid residue of amino acid sequence 6357 2 915 GLERNMALLVRVLRNQTSISQWVPVCSRLIPVSPTQGQ RTSGWPQMSQSQACGGSEQLPGIDIQLNRKYHTTRKLS QPVEEKVGAFTKLIEAMGFTGPLKYSKWKIKIAALRMY TDFEEFFLRCQMPDTFNSWFLITLLHVWMCLVRMKQEG, CRIIVHFMWEDVQQRGRWMGVNPYILKKNMILMTNHFY, DEGILSDDHGLAAALWRTFFNRKCEDPRHLELLVEYVR DSMNGEDLLLTGEVSWRPLVEKNPQSILKPHSPTYNDEG ASDALHSLSPVLRLSSRSAARPARMTEQAISFAKOFL AISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDC: ECGVLSFWRGNLANVIRYFPTQALMFAFKDKYKGIFLGE GOGVLSFWGNLANVIRYFPTQALMFAFKDKYKGIFLGE GOGVLSFWGNLANVIRYFPTQALMFAFKDKYKGIFLGE GOGVLSFWGNLANVIRYFPTQALMFAFKDKYKGIFLGE GOGVLSFWGNLANVIRYFPTQALMFAFKDKYGIFLGE GOGVLSFWGNLANVIRYFPTQALMFAFKDKYGIFLGE GOGVLSFWGNLANVIRYFPTQALMFAFKDKYGIFLGE GOGVLSFWGNLAN	=Stop GDRALS TTKDSP TSCVEK RSGKYM AAILGY KQIQYL GL AGGIAA IVRIPK GVSGTT
corresponding to first amino acid residue of amino acid sequence 6357 2 915 GLERUMALLVRVLRNGTSISQWVPVCSRLIPVSPTQQQ RTSQWPQMSQSQACGGSEQIPGIDIQLNRKYHTTRKLS QPVEEKVGAFTKIJEAMGFTGPLKYSKWKIKIAALRMY TDFEEFFLRCQMPDTFNSWFLITLLHVWMCLVRMKQEG CRIIVHFMWEDVQQRGRVMGVNPYILKKNMILMTNHFY. DEGILSDDHGLAAALWRTFFNRKCEDPRHLELLVEYVRIDSMNGEDLLLTGEVSWRPLVEKNPQSILKPHSPTYNDE ASSALHSLSAPVLRLSSRSAARPATMTEQAISFAKDFLD EGGVLSFWRGNLANVIRYFFTOALNFAFKDKYKGIFLGG EGGVLSFWRGNLANVIRYFFTOALNFAFKDKYKGIFLGG	GDRALS TTKDSP TSCVEK RSGKYM KQIQYL GL AGGIAA IVRIPK GVEKHTE
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amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide insertion) 6357 2 915 GLRNMALLVRVLRNQTSISQWVPVCSRLIPVSPTQGQ RTSQMPQMSQSQACGGSEQIPGIDIQLNRKYHTTRKLS QPVEEKVGAFTKIIEAMGFTGPLKYSKWKIKIAALRMY TDFEEFFLRCQMPDTFNSWFLITLLHVWMCLVRMKQEG CRIIVHFMWEDVQQRGRVMGVNPYILKKNMILMTNHFY. DEGILSDDHGLAAALWRTFFNRKCEDPRHLELLVEYVR DSMNGEDLLLTGEVSWRPLVEKNPQSILKPHSPTYNDEG ASDALHSLSAPVLRLSSRSAARPATMTEQATSFAKDFL AISKTAVAPIERVKLLQVQHASKQIAADKQYKGIVDCC ECGVLSFWRGNLANVIRYFPTOALNFAFKDKYKGIFLGG	GDRALS TTKDSP TSCVEK RSGKYM AAILGY KQIQYL GL AGGIAA IVRIPK GVSGTT
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GPLEEAEEAPQLMRTKSDASCMSQRRPKCRAPGEAORIF INGHFYNHKTSVFTPAYGSVTNVRVNSTMTTLQVLTLLLI	RHRFS
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RLPYKVLSVPESTPFTAVLKFAAEEFKVPAATSAIITND	CICIN
PAQTAGNVFLKHGSELRIIPRDRVGSC	
158 RPGLGQLQHCALAPOAGNRRCRFHGRI.HAI TRETTURGED	MSTMO
FKDTLNTPLPDSSPVAVPLGAPIAVASTLSVEHNDGVET	CTWAC
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1 TIMOGSHSAALKLQQLPPTSSSSAVSEASFSVKENLTCh	LLAIF
GHLVVSIALNLQKYCHIRLAGSKDPRAYFKTKTWWLGLF	LMLLG
ELGVFASYAFAPLSLIVPLSAVSVIASAIIGIIFIKEKW	KPKDF
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PFLLYMLVEIILFCLLLYFYKEKNANNIVVILLLVALIGS	SMTVV
TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQA ASQMYDSSLIASVGYILSTTIAITAGAIFYLDPIGEDVL	AFLSQ
ALGCLIAFLGVFLITRNRKKPIPFEPYISMDAMPGMONME	IICMF
TVQPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSI	1DKGM
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DFHSSSEFEIVKAIKERACYLSINPOKDETLETEKAOYYL	פסחע.
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DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRG	T.T.S.T
RYPMEHGIVKDWNDMERIWQYVYSKDOLOTFSEEHPVI.T.T	RADI.
NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTG	AATD
SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLR	KEGY
DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYL	PDGS
TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSD	

ID beginning nucleotide location corresponding to first amino acid residue of amino acid sequence Sequ	•	nucleotide location	nucleotide location corresponding	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Clutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence P=Proline, Q=Glutamine, R=Arginine, P=Proline, Q=Glutamine, R=Arginine, R=Serine, T=Threonine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, R=Serine, T=Threonine, V=Valine, Codon, /=possible nucleotide deletion, N=Dosaible n	NO:	nucleotide location	corresponding	Clutamic Acid, F=Phenylalanine, G=Glycine,
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to first amino acid residue of residue of amino acid residue of amino acid sequence W=Tryptophan, Y=Tyrosine, X=Unknown, *=Sto codon, /=possible nucleotide deletion, =possible nucleotide insertion) RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF ASMGTLAFDEYGRPDLIKKDQDKKKENGGLEALKSHIMAAKA NTMRTSLGFNGLDKMWVDKDGDVTVTNDGATILSMMDVDHQI LMVELSKSQDDEIGDGTTGVVVLAGALLEEAEQLLDRGIHPI ADGYEQAARVAIEHLDKISDSVLVDIKDTEPLIQTAKTTLGG VNSCHRQMAEIAVNAVLTVADMERRDVDFELIKVEGKVGGRI TKLIKGVIVDKDFSHPQMFKKVEDAKIAILITCPFEPPEPEPK LDVTSVEDYKALQKYKKEKFEEMIQQIKETGANLAICQWGFI ANHLLLQNNLPAVRWQGFPEIELIAIATGGRIVPRFSELTAE GFAGLVQEISFGTTKDKMLVIEQCKNSRAVTIFIRGGNKMII AKRSLHDALCVIRNLIRNNRVVYGGGAAEISCALAVSQEADK TLEQYAMRAFADALEVIPMALSENSGMNPIQTMTEVRARQVK NPALGIDCLHKGTNDMKQQHVIETLIGKKQQISLATOMVRMI IDDIRKPGESEE GKEGAHSSTFWVLLSIYLGAVAMLCKEQGITVLGLNAVPDI IGKFNVLEIVQKVLHKDKSLENLGMLRNGGLLPRMTLLTSGG WLLLCPWLCFDWSMGCIPLIKSISDWRVIALAALWFCLIGI QALCSEDCHKRILITGLGFLVIFFLPASNLFFRYGFVVAER VLPSVGYCVLLTFGFGALSKHTKKKKLIAAVVLGILFINTIR VLPSVGYCVLLTFGFGALSKHTKKKKLIAAVVLGILFINTIR	4		l to first	L=Leucine, M=Methionine, N=Asparagine,
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, amino acid sequence Sequenc	1	to first	amino acid	
residue of amino acid sequence (Codon, /=possible nucleotide deletion, /=possible nucleotide insertion) RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF KKKSTASCAARAQAFGPSREREVKSTRSGCRRLGESNSGCC ASMCTLAFDEYGRPFLIIKDQDRKSRLMGLEALKSHIMAARY NTMRTSLGPNGLDKMMVDKDGDVTVTNDGATILSMMDVDHQI LMVELSKSQDDEIGDCTTGVVVLAGALLEEAEQLLDRGHHN ADGYEQAARVAIEHLDKISDSVLVDIKDTEPLIQTAKTTLGS VNSCHRQMABIAVNAVLTVADMERRDVDFELIKVEGKVGGRI TKLIKGVIVDKDFSHPQMPKKVEDAKIAILTCPFEPPKPKTK LDVTSVEDYKALQKYKKEKFEEMIQQIKETGANLAICQWGFT ANHLLLQNNLPAVRWVGGPEIELIAIATGGRIVPRFSELTAE GFAGLVQEISFGTTKDKMLVIEQCKNSRAVTIFIRGGNKMII AKRSLHDALCVIRNLIRDNRVVYGGGAAEISCALAVSQEADK TLEQYAMRAFADALEVIPMALSENSGMPPIQTMTEVRARQVK NPALGIDCHKGTNDMKQQHVIETLIGKKQQISLATQMVRMI IDDIRKPGESEE 6366 257 1898 GNKEGAHSSTFWVLLSIFLGAVAMLCKEQGITVLGLNAVFDI IGKFNVLEIVQKVLHKDKSLENLGMLRNGGLLFRMTLLTSGG MLYVRWRIMGTGPPAFTEVDNPASFADSMLVRAVNYNYYYSI WLLLCPWWLCFDWSMGCIPLIKSISDWRVIALAALWFCLIGL QALCSEDCHKRRILTLGLGFLVIFFLPSNLFFRVGFVVAER WLLLCPWWLCFDWSMGCIPLIKSISDWRVIALAALWFCLIGL QALCSEDCHKRRILTLGLGFLVIFFLPSNLFFRVGFVVAER LRSGEWRSEEQLFRSALSVCPLNAKVHVNIGKNLADKGNQTA	į.	amino acid	residue of	
amino acid sequence Codon, /=possible nucleotide deletion, -possible nucleotide insertion RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF ASMGTLAFDEYGRPFLIIKDQDRKSRLMGLEALKSHIMAAKA NTMRTSLGPNGLDKMWVDKDDVTVTNDGATILSMMDVDHQI LMVELSKSQDDEIGDGTTGVVVLAGALLEAREQLLDRGIHP ADGYEQAARVAIEHLDKISDSVLVDIKDTEPLIQTAKTTLGS VNSCHRQMAEIAVNAVLTVADMERRDVDFELIKYEGKVGGRI TKLIKGVIVDKDFSHPQMPKKVEDAKIAILTCPFEPPKPKTK LDVTSVEDYKALQKYFKEKFEEMIQQIKETGANLAICQWGFI ANHLLLQNNLPAVRWVGGFIELIATGGRIVPFFSELTA AKRSLHDALCVIRNLIRDNRVVYGGGAAEISCALAVSQEADK TLEQYAMRAFADALEVIPMALSENSGMNPIQTMTEVRARQVK NPALGIDCLHKGTNDMKQQHVIETLIGKKQQISLATQMVRMI IDDIRKPGESEE GNKEGAHSSTFWVLLSIFLGAVAMLCKEQGITVLGLNAVFDI IGKFNVLEIVQKVLHKDKSLENLGMLRNGGLLFRMTLLTSGG MLYVRWRIMGTGPPAFTEVDNPASFADSMLVRAVNYNYYYSI WLLLCPWWLCFDWSMGCIPLIKSISDWRVIALAALWFCLIGI QALCSEDGHKRRILTLGLGFLVIPPLPASNLFFRVGFVVAE VLPSVGYCVLLTFGFGALSKHTKKKKLIAAVVLGILFINTLR LRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNQTA	l .	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
=possible nucleotide insertion		amino acid	sequence	Codon, /=possible nucleotide deletion.
RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAE RLYSTWIGGS ILASLDTFKKMWYSKEYEEDGARSIHRKTF RLYSTWIGGS ILASLDTFKKMWYSKEYEEDGARSIHRKTF RLYSTWIGGS ILASLDTFKKMWYSKEYEEDGARSIHRKTF ASMGTLAFDEYGRPFLIIKDQDRKSRLMGLEALKSHIMAAKA NTMRTSLGPNGLDKMWUDKDGDVTVTNDGATILSMMDVDHQI LMVELSKSQDDEIGDGTTGVVVLAGALLERAEQLLDRGHPH ADGYEQAARVAIEHLDKISDSVLVDIKDTEPLIQTAKTTLGS VNSCHRQMAEIAVMAVLTVADMERRDVDFELIKVEGKVGGRI TKLIKGVIVDKDFSHPQMPKKVEDAKIAILTCPFEPPKPKTK LDVTSVEDYKALQKYFKEKFEEMIQQIKETGANLAICQWGFI ANHLLLQNNLPAVRWVGGPEIELIAIATGGRIVPRFSELTAE GFAGLVQEISFGTTKDKMLVIEQCKNSRAVTIFIRGGNKMII AKRSLHDALCVIRNLIRDNRVVYGGGAAEISCALAVSQEADK TLEGYAMRAFADALEVIPMALSENSGMNPIQTMTEVRARQVK NPALGIDCLHKGTNDMKQQHVIETLIGKKQQISLATOMVRMI IDDIRKPGESEE GNEGAHSSTFWVLLSIFLGAVAMLCKEQGITVLGLNAVFDI IGKFNVLEIVQKVLHKDKSLENLGMLRNGGLLFRMTLLTSGG MLYVRWRIMGTGPPAFTEVDNPASFADSMLVRAVNYNYYYSI WLLLCPWWLCFDWSMGCIPLIKSISDWRVIALAALWFCLIGI QALCSEDGHKRRILTLGLGFLVIFFLPASNLFFRVGFVVAER YLFSVGYCVLLTTGFGALSKUTKKKKLIAAVVLGILFINTLR LRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNQTA	ļ	sequence	1 -	
RLYSTWIGGS ILASLDTFKKMWVSKKBYEEDGARS IHRKTF 6365 234 1989 KHKSRASCAARAQAFGPSREREVHSRFRSGLRALGESNSGCO ASMGTLAFDEYGRPFLIIKDQDRKSRLMGLEALKSHIMAAKA NTMRTSLGPNGLDKMWVDKDGDVTVTNDGATILSMMDVDHQI LMVELSKSQDDE IGDGTTGVVVLAGALLERAEQLLDRG IHPI ADGYEQAARVAIEHLDKISDSVLVDIKDTEPLIQTAKTTLGS VNSCHRQMAEIAVNAVLTVADMERRDVDFELIKVEGKVGGRI TKLIKGVIVDKDFSHPQMPKKVUDAKIAILTCPFEPPKPKTK LDVTSVEDYKALQKYFKEKFEEMIQQIKETGANLAICQWGFI ANHLLLQNNLPAVRWVGGPEIELIAIATGGRIVPRFSELTAE GFAGLVQEISFGTTKDKMLVIEQCKNSRAVTIFIRGGNKMII AKRSLHDALCVIRNLIRDNRVVYGGGAAEISCALAVSQEADK TLEGYAMRAFADALEVIPMALSENSGMNPIQTMTEVRARQVK NPALGIDCHKGTNDMKQQHVIETLIGKKQQISLATQMVRMI IDDIRKPGESEE 6366 257 1898 GNEEGAHSSTFWVLLSIFLGAVAMLCKEQGITVLGLNAVPDI IGKFNVLEIVQKVLHKDKSLENLGMLRNGGLLFRMTLLTSGG MLYVRWRIMGTGPPAFTEVDNPASFADSMLVRAVNYNYYYSI WLLLCPWWLCFDWSMGCIPLIKSISDWRVIALAALWFCLIGL QALCSEDGHKRRILTLGLGFLVIFFLPASNLFFRVGFVVAER YLPSVGYCVLLTFGFGALSKHTKKKKLIAAVVLGILFINTLR LRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNQTA			†	
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				RYYREAVRLNPKYVHAMNNLGNILKERNELQEAEELLSLAVQIQ
PDFAAAWMNLGIVQNSLKRFEAAEQSYRTAIKHRRKYPDCYY		1		PDFAAAWMNLGIVQNSLKRFEAAEQSYRTAIKHRRKYPDCYYNL
GRLYADLNRHVDALNAWRNATVLKPEHSLAWNNMIILLDNTG				GRLYADLNRHVDALNAWRNATVLKPEHSLAWNNMIILLDNTGNL
AQAEAVGREALELIPNDHSLMFSLANVLGKSQKYKESEALFL				AQAEAVGREALELIPNDHSLMFSLANVLGKSQKYKESEALPLKA
IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTAS		1		IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT
KENYGLLRRKLBLMQKKAV				KENYGLLRRKLELMQKKAV
	6367	287	1934	SIGFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS
		1		QKNLYRDVMQETFKNLTSVGKTWKVQNIEDEYKNPRRNLSLMRE
		1		KLCESKESHHCGESFNQIADDMLNRKTLPGITPCESSVCGEVGT
		1		GHSSLNTHIRADTGHKSSEYQEYGENPYRNKECKKAFSYLDSFQ
				SHDKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKF
				CGKAFYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER
1 1				THTGVNADECKECGNAFSFPSEIRRHKRSHTGEKPYECKQCGKV
				FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG
		1		EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA
1 1				SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH
		1		ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR
				YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC
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Z ZZ KEVENARUNEKSWEKINGHUEUKEFEULWAVINDEVELEDEQI	0200	1	34/	RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE
1 1		1		DSTTYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK
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				PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET
				PKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG
				ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD
1 1 "		1		TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY
1 1				DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL
IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECI				I IHERIHTGVKPYKCKOCGKAFTRSTTLPVHERTHTGVNADECKE
l		1		
				CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM
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EKPHECKECGKVFKYFSSLRIHERTHTGEKPHECKQCGKAFR:				CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG

SEQ	Predicted	Predicted end	Amino agid coment contain
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
İ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
į	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	Dequence	Codon, /=possible nucleotide deletion,
		<u> </u>	\=possible nucleotide insertion)
1	ĺ		SSLHIHERTHTGDKPYECKVCGKAFTCSSSIRYHERTHTGEKPY
			ECKHCGKAFISNYIRYHERTHTGEKPYQCKQCGKAFIRASSCRE
6370	1711	329	HERTHTINR
02.0	1 2/11	329	FVLSEQRLRTERTWPRSPGLGRGAAAAGARTAGAGLLRLLLGCG
	i	}	ALVGGLRPVTMTTPANAQNASKTWELSLYELHRTPQEAIMDGTE
J			IAVSPRSLHSELMCPICLDMLKNTMTTKECLHRFCSDCIVTALR
1			SGNKECPTCRKKLVSKRSLRPDPNFDALISKIYPSREEYEAHQD
i			RVLIRLSRLHNQQALSSSIEEGLRMQAMHRAQRVRRPIPGSDQT
	1		TTMSGGEGEPGEGEGDGEDVSSDSAPDSAPGPAPKRPRGGGAGG
1			SSVGTGGGGTGGVGGGAGSEDSGDRGGTLGGGTLGPPSPPGAPS
1	f		PPEPGGEIELVFRPHPLLVEKGEYCQTRYVKTTGNATVDHLSKY
1			LALRIALERROQQEAGEPGGPGGGASDTGGPDGCGGEGGGAGGG
	1		DGPEEPALPSLEGVSEKQYTIYIAPGGGAFTTLNGSLTLELVNE
6371	3	288	KFWKVSRPLELCYAPTKDPK
		200	GVANMSTAMNFGTKSFQPRPPDKGSFPLDHLGECKSFKEKFMKC
j			LHNNNFENALCRKESKEYLECRMERKLMLQEPLEKLGFGDLTSG KSEAKK
6372	2141	625	
		023	RVSAIASEGKALERYKKLEDLLEKSFSLVKMPSLQPVVMCVMKH
			LPKVPEKKLKLVMADKELYRACAVEVRRQIWQDNQALFGDEVSP
	1		LLKQYILEKESALFSTELSVLHNFFSPSPKTRRQGEVVQRLTRM
1 1			VGKNVKLYDMVLQFLRTLFLRTRNVHYCTLRAELLMSLHDLDVG
1			EICTVDPCHKFTWCLDACIRERFVDSKRARBLQGFLDGVKKGQE QVLGDLSMILCDPFAINTLALSTVRHLQBLVGQETLPRDSPDLL
1 1			LLLRLLALGQGAWDMIDSQVFKEPKMEVELITRFLPMLMSFLVD
1			DYTFNVDQKLPAEEKAPVSYPNTLPESFTKFLQEQRMACEVGLY
			YVLHITKQRNKNALLRLLPGLVETFGDLAFGDIFLHLLTGNLAL
1 . 1			LADEFALEDFCSSLFDGFFLTASPRKENVHRHALRLLIHLHPRV
1			APSKLEALQKALEPTGQSGEAVKELYSQLGEKLEQLDHRKPSPA
			QAAETPALELPLPSVPAPAPL
6373	67	711	PSRAARASPARLPAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK
1 1	1		DIKEYVKWMMYWIIFALFTTAETFTDIFLCWFPFYYELKIAFVA
	İ		WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL
1 1	1		VHFGKRGLNVAATAAVMAASKGQGALSERLRSFSMQDLTTIRGD
			GAPAPSGPPPPGSGRASGKHGQPKMSRSASESASSGTA
6374	535	2105	HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS
1	į		CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRD
1	1		HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC
1 1	į.	j	CPAELQTEGSNGKKEVLSGFQVVLEDTVLFPEGGGQPDDRGTIN
1 1		j.	DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH
1	1	i	SGQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA
	I		IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR
1 1		•	VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL
]			SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKI,QNSTKIL
1 1	1		QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII
1 1	1		ANEIGSEETLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL
			EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE
6375	1	1535	AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT
	[į.	CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK
			PPGRACSNPSFLRFQLDFYQVYFLALAADWLOAPYLYKLYOHYY
.		•	FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY
	ļ	j	SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVRR
i 1		j	HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP
	ľ		FVAAIPLLALAGALALRNWGENYDRORAFSRTCAGGLRCLLSDR
			RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA
-	}	J	SLLGSSLYRIATSKRYHLOPMHLLSLAVLIVVFSLFMLTFSTSP
	<u> </u>		GQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPETEQAGVLN

ID	SEQ	Predicted	Predicted end	I Project on the second
No: nucleotide	ID			
corresponding to first anino acid acid acid acid acid acid acid acid	NO:			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid sequence sequen	İ			Glutamic Acid, F=Phenylalanine, G=Glycine,
to first a mino acid amino id acid sequence seq	ļ			M=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of anino acid acid sequence anino acid sequence acid sequence anino acid sequence anino acid sequence anino acid sequence acid sequence acid sequence anino acid sequence acid sequence acid sequence acid sequence anino acid sequence acid sequence acid sequence acid sequence anino acid sequence aci			1	L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence Magnopath Magnopat				P=Proline, O=Glutamine, P=Arginine
amino acid sequence Codon, /-possible nucleotide deletion (-possible nucleotide deletion) REPRYPHAISACIGALULUSBESENETYERMSEIGSAVMMALLAV VOLTTVYRIDAGUEVESTEEPYAPEL 1830 1837 ISTOIDHYRESFIUNSKUPPSKESSGRETNEAAVHKSKOEGKO QOLLIAALGMKLGSPKSSVTIMOPLKLFAVSGLTSLVRARHITKE ROCHTVYRIDAGUEVESSTEEPYAPEL COLVINGCSKWYPHOCKEPLKHVKVYSCOLTTLVRAHITKEN VUDMCIREISERGINSEGLINVSKGSSLLEDVRAHAPBENGERKA 15VNNYEDINIITGALKLYFRDLPFLITTDAYPKFIESRIMMA 25NLGIVVERCISKUPPTLIVISKAPHTKEYSTEEPKHAPEL 6377 23311 1845 SIKRESSERPEPEPFSFRERRERPPFTWPSEKFYFORRTFE QRVSDVRLIREQHPTLIVIIRVKGSKQLPVLDKTKKLVPDHV NSSLLIKIIRRIQINAQAFFLINMSHAWSYSTEEYYSSE KDEDGETHWAYASQUTFORMLSV GRYBERFFFFICHIKASSAPAASSESTIVGGVK NSSLLIKIIRRIQINAQAFFLINMSHAWSYSTEEYYSSE KDEDGETHWAYASQUTFORMLSV 6378 6378 606 191 GRIFREFFSERDESFRERRERPPFTYFFERFYFORRTFE QRVSDVRLIREQHPTLIVIIRVKGSKQLPVLDKTKKLUPDHV NSSLLIKIIRRIQINAQAFFLINMSHAWSYSTEYYSSE KDEDGETHWAYASQUTFORMLSV GRIFREFFSTARTSKAPPDAYARFFORGGSGGGRAYMAYA ALALIPDVIDISGGVFKVVLIRVHSAPRSQAPAASSKETYGGSGGRAY MEASHADITYDVAYAGQBTAGRARSHARAYARFFORGGGGGRAY LENSVANVQCAPABERVLLITGLHAVADIYCHNCKTTLGHKYHAA 6380 1414 462 PRACGGRAGPPTGRGGSANAAFFLIVVKHGETPFNERTIOMIGG GVDEPLSTGTGRAAAGIFLAVKHGETPFNERTIOMIGG LERSKECKOMTVKYDSKLERRERVOVVBGKLASELSRAMARABEEG CPVFTPGGTLICQVKHRIDIPFFFICQLLIKERAGUERGE GVDEPLSTGTGRAAAGIFLAVKHTHAFSDIGHAAVALVSHGAY MESIEPTYLTDLKGCLAAAGIFLAVKHTHAFSDIGHAAVALVSHGAY MESIEPTYLTDLKGCLAAAGIFLAVKHGETPFNERTIOMIGG LERSKECKOMTVKYDSKLERRERVOVVBGKLASELSRAMARABEEG CPVFTPGGTLICQVKHRDIDFFFICQLLIKERAGUERGE GVDEPLSTGTGRAAAGIFLAVKHTHAFSDIGHAAVALVSHGAY MESIEPTYLTOKTKORGUERGAGLAASGWSPORAHATITUTEEG CPVFTPGGTLICQVKHRDIDFFICQLIKETHAAMARABEEG CPVFTPGGTLICQVKHRDIDFFICQLIKETHAAMARABEEG CPVFTPGGTLICQVKHRDIDFFICQLIKETHAAMARABEEG PSNCLETSLAEIFTYLGNINGSKWISDSGIGLAASGWSPGGRAAAGIFLINFTTATATATATATATATATATATATATATATATATATAT		residue of		S=Serine, T=Threonine, V=Valine,
sequence	ı		j	w=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
G376 380 1437 ISSTUDIANCES PIERVINESICSAVMMALLAV VOLETVYRIDAELIKVES PIERVAREL WOLETVYRIDAELIKVES PIERVAREL G00L11AALGMIKURS PIERVAREL G00L11AALGMIKURS PIERVAREL G00L11AALGMIKURS PIERVAREL G00L11AALGMIKURS PIERVAREL G00L11AALGMIKURS PIERVAREL G00L11AALGMIKURS PIERVAREL G00L11AALGMIKURS PIERVAREL G00L11AALGMIKURS PIERVAREL G00L11AALGMIKURS PIERVAREL G00L11AALGMIKURS PIERVAREL G00L11AAGAMALANDI ANGEN PIERVAREL G00L11AAGAMALANDI	ŀ		sequence	Codon, /=possible nucleotide deletion
6376 1437 1437 15STDIDHYSPEKSSWSTKTRRAVHKSKOEGE OULLIALGENKLGSRESSVTIMOPLIK PAYSQLTSUKRAVHKSKOEGE OULLIALGENKLGSRESSVTIMOPLIK PAYSQLTSUKRATIKE NEOLISKUKSCERMYPHOCKPOLANPINGCLANPINGLIAQSVKCADE GLWYKKQCERMYPHOCKPOLANPINGCIAQSVKCADE GLWYKKQCERMYPHOCKPOLANPINGCIAQSVKCADE GLWYKKQCERMYPHOCKPOLANPINGSPOLAUTHKARTITERP VADAPHER SEGNINGGLIAVSVGSPOLLEUNKAPODEGEKAD I SVANNYDINIITGALKLYFROLDEIDLITVDAYPHETESJAKIND PPOLETILKERELMAN ENLGIVYGPTIMRSPELDAMAAINDITYQRIVVUELIKUKUSLIP GENEGILTEN SERIKESSER SER		- Dodgaratec		\=possible nucleotide insertion)
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1937 ISSTITUDHYRESPIUWSKAPSKSSKRITTRADVIKSKRGERS ODLITALAGUKKGSPKSSTVITMOPLIK-PAYSQITSLUVRAPILKE NEQIPEVTEKIHNFKVHTFROPHINGEVCANFFWGLIAQGVKCADC GLWNYKCGRWYDDCCPDLAVKVKYVSGLVIVKAHTTEKPH VUDMCIBETESRGINSGLYRVSGFSDLIEDVMAPDDEDGKAD ISVNYNYDINITTOALKUFFUDEPILTIVKAHTTKEPH VUDMCIBETESRGINSGLYRVSGFSDLIEDVMAPDDEDGKAD ISVNYNYDINITTOALKUFFUDEPILTIVKAHTKEVTHIBEERILMAA ENGIVERPTHIN PILDEPILTIVALELIKWATHTEKPH VUDMCIBETERSGINGGLYRVSGFSDLIEDVMAPPERSAKIND PDEQLETIKERAKLIPPAHCETLEYTHAHLKEVTHIBEERILMAA ENGIVERPTHINSPELIKAKINDEPILTIVALIKWALULIKWEDILIF BENGIVERPTHINSPELIKAKINDEPILTIVALIKWALULIKWEDILIF BENGIVERPTHINSPELIKURKYUPHVENERITYKORKYPE NEBORIYIKWALOROPYKYPLIRVESRGINGGOKKHHYVG NASLIKII RERLOLJANQAFFILMAGKSWYSTYTISEVYESS KUBGOPLYHVANSQETTOMINSV MASLIKII RERLOLJANQAFFILOVARGOPSGGSGRAMAVA DLALIEDVUIDSDCVKYVLIRVESAPBSGAPAASSKIVRGYK WARYHADI VIDAVSOMOKOGCOCCCIGGGISIGSGOKKHHYVG YSMAYGAQHAISTERIKAKYPYEVTANDOV YSMAYGAQHAISTERIKAKYPYEVTANDOV YSMAYGAQHAISTERIKAKYPYEVTANDOV YSMAYGAQHAISTERIKAKYPYEVTANDOV YSMAYGAGAGAPPTIRRSGNAPROPARARCRESFOGSGGRAY LENSVANVOCCOPABERVLITCHIAVADIYCENCKTTIGWKYEHA PESSOKYKEKYI IELAMIKKOKSON GUDEPISETGGKGAAAAGITANVYFTHARSGOKKHOPTROTMEDI LERSKECKOMTVKYDSHIRREKYGVVBCKALGELRAMAKAAREE CPVYPTPOGGETLOOVMAGICDFEPILCOLLIKADGKOGPOGGS PSNCLETSIABIPPICKSHIRSVINOSOGIPGIAASVILVYSHGAY WRSISPYHLTDIKCSILPATISCELMINISVENDELASVILVYSHGAY WRSISPYHLTDIKCSILPATISCELMINISVENDELASVILVYSHGAY KANTAGILVQWSLEOPENHCKILDGINGIINSADSHILLE AMYKAGILVQWSLEOPENHCKILDGINGIINSADSHILLE MYLASCVORTIVVRUDHTQILCITTTITOOTUGHIINSADSHILLE CRUKPYVGIICKOMULLIKUMPITOOTUGHIINSADSHILLE CRUKPYVGIICKOMULLIKUMPITANDVATAGRACOLGOHT TEPHRITIVVSLCTRSVYIKYPRACLQGIITTEDORVAMALARE RUCKYYVGIICKOMULLIKUMPITANDVATORGARANDOCLIAVWO TCLBYKILLISLOGRALLIKUMPITOOTUGHIINSADKOOPDADA CARACAAAANASSASSOCORMALIKUMOTAVIKSAGAKSPOGGHAA TCHBYKILLISLOGRALLIKUMPITOOTUGHIINSADKOOPDADA CARACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	6376	380	ļ	VGLFTVVRHDAELRVPSPTEEPYAPRI,
GUNLIKALGENKUSSKSSTITMOPILKIPANGGUTSLVARATIKE NEGIPKYEKIHPKYHTREPRIMCEYCANPHMCGUTALVARMALDAGUKCADA GUNYHKICERMYPHOCEYDLHIVKKVYSGULTILVKARTIKER NEGIPKYEKIHPKYHTREPRIMCEYCANPHMCGUTALVARMALDAGUKCADA GUNYHKICERSGUNSGULTUKARTIKERDINAS UVDMCIRE LESGGUNSGULYKYSGSDLITUKARTIKERDINAS 1 SVANNYBURNITTGALKUYFBLDIPLITYDAYPKFIESAKIMD PPEDLETILHERLKILPPALEKUKPSOFDLIEDUKMAPDDGEKAD ENLGIVYGPTIMRSPELDAMAAINDITYQRIVVELLIKNISULIF GARTA ENLGIVYGPTIMRSPELDAMAAINDITYQRIVVELLIKNISULIF GARTINITARA ENLGIVYGPTIMRSPELDAMAAINDITYQRIVVELLIKNISULIF GARTINITARA ENLGIVYGPTIMRSPELDAMAAINDITYQRIVVELLIKNISULIF GARTINITARA ENLGIVANDATIVARGULYTIGHKUSULIKKKYLVPDHV NNSELIKII TRRELQIANNADA FILVWGHSMYVSVTISVYISSE KDEDGPLYWVANSQUTGKKISV GAGPMEAFPEDGGERSERARIDYYKEPFGRVGGOGGRAN MAXHADI UNDKISODWOKQGCOCCICGGI SHQQOKKHIYG VSMAXQBAQHAISTERIKAKYDPSVVMANDAG LAILPUVISDOWCKYVULIRVHSAPRSGAPAASSKEVYGYK VSMAXQBAQHAISTERIKAKYDPSVVMANDAGOKKKTIGGKYKY VSMAXQBAQHAISTERIKAKYDPSVVMANDAG LERSKYNAGKYIIBLAMH KOMIGND GUNDELISTIGSKQAAAAAIFINNVKFTHARSSDIMRTKOTMIGI LERSKEKOMVVKYNSRILREKKYGVUKKALARAKAAREE CPYFTPOGGETLQVUKMGIDFFEFLCULLIKAADVLVUSHGAY MRSIFPYILTILKCSLAPATISRSELMSVTRYTGMSLEI INFEGE REVKPTYQCI CHNICHOMLOHIMGIATSNISIAINESSDILHTIC AMYKGRUVQWSLEOPBRHCLATTSNISIAINESSDILHTIC AMYKGRUVQWSLEOPBRHCLATTSNISIAINESSDILHTIC AMYKGRUVQWSLEOPBRHCLATTSNISIAINESSDILHTIC AMYKGRUVQWSLEOPBRHCLATTSNISIAINESSDILHTIC AMYKGRUVQWSLEOPBRHCLATTSNISIAINESSDILHTIC TEPHLRITUVSLCTRSVYIKYPRACLQGITTTDORVANIAER CHARLESSORYALARAKAAREE CHARLYVKRINITARSHAMISERVKINSSGI HARAPAKAAREE CHARLYVYMGHLORENGAGUKAREENDOLLA SYDGWRILLHVIVMMITEEGEPBAAINDERLOPBRHCLITATSHICHOMLAER CHARLYVANGUKUVANGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1	1 300	1437	ISSTDIDHYRFSFLVNSKMPSKESWSGRKTNRAAVHKSKQEGRQ
GLNVIKICESKMYNDRCKEDLKHYKKVYSTENDHARDKERGYGANGENGGGGGGGGNAVHORGENGKHYKUKYSTENDHARDKERKAN GLNVIKICESKGIANSEGLYRVSGFSDLIEDVMRPRODECKAD 1 SVNNYEDINITIGALKIYFRDLIPTJUTDAYPFFTESKAIMD PDEOLETIHRALKILIPPAHCETILRYLMAHLKRUTHKERDIMAN 6377 2311 1845 SKIRRRSSRRFREPPGFPRERERFPFFRWEFFFF KORRTFF GRENDGTURVYNSGDTTENDHARALINDIVKTRUPDHYV NISELIKITERHCHONANGAFFLINGHGWVSVSTPISEVYBSE KORDGPLYWYNSGDTTENKLSV 6378 686 191 GRENDRYNSGTROKGCOCKCLGGGGGGGIGHGNMAVA DLALIPDVDIDEDGVFKYULIRVISARRSGAPABESETVRGYK WARTHADITUKVSGDMKGCOCKCLGGGGGGGIGHGNGONKINY YSMAYGRAGHAISTEKKKAKYDDVEVVWANDGY SANGYGRAGHAISTEKKKAKYDDVEVVWANDGY SANGYGRAGHAISTEKKKAKYDDVEVVWANDGY FRAGSFFSERRALBRCRPGRSGAPRARGERFGGSGGGRAY LFRSVVNVGCGPABERVLLTGLHAVADITCENCKTTLGWKYEHA 6380 1414 462 PAVGGGRGAGPFURGSGMARFALTVVHGESTFFRERITIGGC GVDEPISFSGYKRAGKYITELAHNIKNOKOD FRAGSFFSERRALBRCRPGRSGAPRFURGKSTGGSGGRAY LFRSVNVNVGCGPABERVLLTGLHAVADITCENCKTTLGWKYEHA 6381 1668 218 AVVEAGGSGGFSGNAGFFLTVVHGGSTFFRERITIGGC CPYFTPDGGETLOCVWRIGHTFNIKGINLSKNINSGSTFGLAASVLVVSKGAY MRSLFTYFTLDKKSLPALSRSELMSVTFTTOMSHJFINNEGE CPYFTPDGGETLOCVWRIGHTPSFFLCOLILEADQUGGPSGGS PSNCLISTSLAEIFPLKKNINSSKNINSGSTFGLAASVLVVSKGAY MRSLFTYFTLDKKSLPALSRSELMSVTFTTOMSHJFINNEGE LERSKCKDMTVKYDSRLEERKYGVVEGKALSELRAMSLEVLVVSKGAY MRSLFTYFTLDKKSLFALSRSELMSVTFTTOMSHJFINNEGE LERSKCKDMTVKYDSRLEERKSVVVEGKALSELGKFTFDGEFLINGE CPYFTPDGGETLOCVWRIGHTPSFFLCOLILEADQUGGPSGGS PSNCLISTSLAEIFPLKKNINSSKNINSGSTFGLAASVLVVSKGAY MRSLFTYFTLDKKSLFALSRSELMSVFTFTTOMSHJFINNEGE CPYFTPDGGETLOCVWRIGHTPSFFLCOLITIERADGVLLAVIN TEHHARITVANLCTKSVSYTKYPKACLGGTTFTTOGMALSER REVKPTVQCTCHONDHINGLTENSLIGHTSSSFLINGTHALAER REVKPTVGCTCHONDHINGLTENSLIGHTSSSFLINGTHALAER REVKPTVGCTCHONDHINGLTENSLIGHTSSSFLINGTHALAER REVKPTVGCTCHONDHINGLTENSLIGHTSSSFLINGTHALAER REVKPTVGCTCHONDHINGLTENSLIGHTSSSFLINGTHALAER REVKRINGTSSFLINGTHANDHAAVANDTOKKCHGOGGGGGGGGG STORGENTALTTRICTURGSBLIVTMSPACKGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		1	ļ	QULLIAALGMKLGSPKSSVTIWOPLKT,FAYSOT,TST,VPPATT,FP
GLNAKQCSKMYNDCKEDLKHYKKVYSCLLTLYKAHTYKRYB VVDMCIRE ISSRGIMSEGLKYRGYSGULDWAFDRDGEKAD 15VMYZDINITGALKLYPROLPIPLITDAYPKIPESAKIMO PDEQLETIHEARLKLIPPAHECHIRYLKAHLKRYTHEKERIMNA EMIGIVEGPILMRSPELDAMAALINDIRYQRLVVELLIKOKDILF SKIRRESSRRPERPERPERPERPERPERRERREDPRTMPSEKTFKQRFFFE QXVEDVELIREOHPPKIPVIIERKYGKQKUVELLIKOKDILF (SXIRRESSRRPERPERPERPERPERPERPERPERPERPERPERPERPE			ĺ	NEQIPKYEKIHNFKVHTFRGPHWCEYCANFMWGLTAOGVKCADC
OVDMCHRIESRGIANSEGLYRVGGFSDLIEDVMANPDEDEKALD ISVNNYEDINITIGALKYFRDLIPJINDPRFTESKIMD PDEDLETHHSALKLIPPAHCETLRYLMAHLKRUTHEKENIMNA SAIRRESSRPREEDFGFSPERERREEDFTMPSEKTFKORFFFE OKSTUTION OKTOBER OKTOBER OKTOBER OKTOBER	1			GLNVHKQCSKMVPNDCKPDLKHVKKVVSCDI.TTI.VKahrtyppm
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BLALLIPOUTDISCOFFKYULIRVHSAPRSGAPAARSKRIVRGYK WARYHADIYDKYSOMDKOGCECLGGGRISHOSODKKHVYG YSMAYGAQHAISTEKIKAKYPDYEUTWANDGY ERAGSPEFERALERCAPORSQAPRWDEMACRESFOGSGGRAY LFINSVVNVGCGPAEERVLLTGLHAVADIYCERCKTTLGWKYCHA FESSGKYKEGKYIIELAHMIKONGWD PAVGGORGAGPPIRGGSGNARA FALTVVRHGETRFNKEKIIQGQ GVDEPLSBTGFKQAAAAGIFLNNVKFTHAFSSDLMRTKQTWHGI LERSKFCKDMTVKYDSRLERKYGVVEKGALSELRAMAKARREE CPVYPTPPGGTELDQVMRKGIDFFEFLCQLILKEADQKEGFSQGS PSNCLETSLAEIFPLGKUNISSKVNSDSGIFGLAASULIVSHGAY MRSLFDYFLTDLKCSLPATLSRSBLMSVTPNTGMSLPIINFEG REVKPTVQCICMNLQDHLNGLTENSLGINLPSKSNHFEPLKGVP LALFTSLLC AVVRAGGSRGFSGAGWRPQAAAMNFSEVFKLSSLLCKFSPDGK YLASCVQYRLVVADVNTLQILQLYTCLDOIHIEWSADSLFILC AMKKRGLVQVWSLEDDEWHKCHDEGSAGLVASKWSPDGRHILMT TEPHLRITWSLCTRSVSYIKYPKACLQGITFTRDGRYMALAER RDCKDVVSIFVCSDWQLLERHPDTDTQDLTSLBWAPNGCVLAVWB SYDGKVRILNHYTWMITEFGEPAAINDPKIVVYKRAEKSPQLG GCKSPPPPRAGGELPSSESKISTSVPVLGTLKEVTDRAMP KIGIGMLAPSPDSYFLATRNDNIPNAWWWDIQKLRLFFAVLEGL SPVRAPCWDPQOPRLAICTGGSRIYJWSPGGWSVQVPGGGFA VLSLCWHLSGDSMALLSKDHFCLFFLEVWTACRQGGGH SPEEDERRNLCLIAYPLKGDHGIVDIVDNSGCPFKSLLRWTTNK KHHVLETEKTPRUWYGCHKREKKIKLEEFFEMIKKSEVLYYY TVEKKGNISSQLKHYNPWSMKCHQQQLGRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLKWGTRQHDDASSEKAMDGTRKQQGSTG ANIGGVCHHVLEXUQGVKGGGLGGAGSPSEK GAHPSAARPLAAPTPAAPACRSSPSCAGAYAYKPIGASSUDVRM LDFAHTTCRLYGGDTVVHGQQDAGYIFGLGSLDIVTEISESGG GAHPSAARPLAAPTPAAPACRSSPSCAGAYAYKPIGASSUDVRM LDFAHTTCRLYGGDTVVHGQOAGYIFGLGSLIDIVTEISESGG GAHPSAARPLAAPTPAAPACRSSPSPCAGASFSFCKAARSPSG AARAAAAAAASSSASGGRRGGRGGRGGGGGGGKS SSSSSASAAAAAAASSSASGGRRGGRAGGRGGGGGGGKS SSSSSASAAAAAAAASSSASGGRRGGRAGGRGGGGGGGKS SSSSSASAAAAAAAASSSASGGRRGGRGGRGGGGGGGKS SSSSSASAAAAAAAASSSASGGRRGGRGGRGGGGGGGKS GCCHHVHLEEVQCPRKNOTERGOGGGGGGGKS GCCHHVHLEEVQCPRKNOTERG	1 3373]	191	GAGPWEAFPDGIGRRSRRARLPQYKRPPGRVGGGDSGRRNMAVA
6379 35 378 BRAGSPESSAALRRCAPQRSQAFRWPDEAACRRSFQGSGRAY LFNSVVNVQGSPAERVLITGLHAVADTVCENCKTTLGWKYEHA FESSQKYKEGKYI IELAHMIKONGWD 6380 1414 462 PAVGGGRAGPPIGRGSGNAARFALTVVEHGETRFNKEKIIQGQ GVDEPLSETGFKQAAAAGI FLNVKYTHAFSSDLMRTKOTMIGI LERSKFCKDMTVKYDSRLÆRRKYGVVEGKALSELRAMAKAAREE CPVFTPPGGSTLDQVKMRGIDFFEFICQLIKKEADGKEGFSQGS PSNCLETSLAEI FPLGKNISSKWASDGI PGLASVLVVSHGAY MRSJFDYFJTDLKCSLDATLSRSELMSVTFNTGMSLFI INFEEG REVKPTVQCICMNLQDHANGLTENSLGINJESKSNHFEPLKGVF LALFTSLLC AMVKRGLVQVWSLEQDEWHCKIDEGSAGLVASCKSPPDGK YLASCVQYRLVVADVANTLQILQTYCLDQIQHI ENSADSLFILC AMXKRGLVQVWSLEQDEWHCKIDEGSAGLVASCKSPPDGKI LT TEPHLRITVMSLCTKSVSYIKYPKACLQGTTFTTDGRYMALARR RDCKDVVSIFVCSDMQLLRHFTDOLTGIEMPNGCVLAVWD TCLEYKILLYSLDGRLLSTYSAYEWSIGIKSVAWSPSSQFLAVG SYDGKVRILNHTWKNITEFGHPAAINDPKIVVYKEAEKSPQLG LGCLSFPPPRAGAGPLPSSESKYIASVPVSLGTILKVTUTRANP KIGIGMLAFSPDSYFLATRMNNIPNAWWWDIQKLRLFAVLSQL LGCLSFPPPRAGAGPLPSSESKYIASVPVSLGTLKVTUTRANP KIGIGMLAFSPDSYFLATRMNNIPNAWWODIQKLRLFAVLSQL SPVRAFQMDPQQPRIALGTGGGSTLYMSPAGCSSQVDVGEGPA VLSLCHHLSGDSMALLSKOHFCLCFLETERVVCTACRQLGGHT TVEKKGNISSQLKHYNPWMKCHGODLOSEFKSKLKEMTNK KHHVLETEKTFKDWVRQRKEEKMKSKKLEEFEFWIKKSBVLLYY TVEKKGNISSQLKHYNPWMKCHGODLOSEFKSKLKLEWTYNK KHHVLETEKTFKDWVRQRKEEKMKSKKLEEFEFWIKKSBVLLYY TVEKKGNISSQLKHYNPWMCHREEKMSKIKLEEFEFWIKKSBVLLYY TVEKKGNISSQLKHYNPWMCHREENKSSKLEEFEFWIKKSBVLLYY TVEKKGNISSQLKHYNPWMCHREENKSSKLEEFEFWIKKSBVLLY GKRPEVVLDSNAEDLEDLSESSADESAGAYAVKPIGASSVOVRM IDFAHTTCRLYGGDTVVHEGQDAGYIFGLQSLDIVTBESEGG KERPEVVLDSNAEDLEDLSESSADESAGAYAVKPIGASSVOVRM IDFAHTTCRLYGGDTVVHEGQDAGYIFGLQSLDIVTBESEGG GAHPSAARPLAAPTPAAPACRSSPSGGAPASFSGRAPSEKGANPSGGADVAK ARAAAAPAAPASRSAKGRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSSPSGGABASFSEKGANPSGGADVAK PPPAPQQPPPPPAPHPQQHPQOMQAHGKGGHRGGGGGGGKS SSSSSASAAAAAAASSSASGSRRLGRALDFLFTVIAUAAAAFS GGCCHHVHLEEVQQVRSHONGSRCGHGASGSGGKGG	İ			DLALIPDVDIDSDGVFKYVLIRVHSAPRSGAPAAESKETVDGVV
6389 378 BRAKGSAGHAISTEKKAKYDDUSVTANDGY BRAKGSPSSERALERCAPGRSQAPRWPDRAACRESPGGSGRAY LFNSVVNVGCGPAEERVILITGIHAVADIYCENCKTTIGWKYEHA FESSQKYKEGKYIIELAHMIKDNGWD PAVGGGRÄGGPTURGSGENMAFFALTVVRHGETEFNKEKIIQG GVDEPLSETGFKQAAAAGIFLNNVCHTHAFSSDLMRTKQTWHGI LERSKFCKDMTVKVDSILIRERKYGVVBGKALSELRAMAKAARER CPVPTPPDGGTLDQVKMRGIDFFEPLQLILKRADGKGGPSQGS PSNCLETSLAEIFPLGKNHSSKVNSDSGIPGLAASVLVVSHGAY MRSIFDYFLTDLKCSLPATLSRESLMSVTINTGMSFFI INFEEG REVKPTVQCICMNLQDHINGLTENSLGINLPSKSNHFEPLKGVP LALFTSILC 6381 1668 218 AVVRAGSRGFSGAGWRPRQAAAMNFSEVFKLSSLLCKFSPDGK YLASCVQYRLVVZDVXTLQLLQLTTCLDQIQHIEWSADSLFILC AMYKRGLVQVWSLEQDEWHCLGGGSAGLVASCWSPDGRHILMT TEPHLRITVWSLCTKSYSYIKYPKACLQGTTFTRDGRYMALAER RDCKDYWSISVCSDWQLLARFDTDTDQLTGIBWAPNGCVLAVWD SYDGKVILHVTWRWHITEFGHPAAINDRIVVYKAERSPQLG GGLSFPPPRAGGPLPSSESKYEIASVPSLQTLKPVTDRAAP KIGIGMLAFSPDSYFLATRNDNIFNAVWWDIQKLRLPAVLEOL SPVRAFOMDPQOPRIALICTGSELYLWSPAGCMSVQVPGBGDFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRLGGTT TVEKKSNISGLKHYNPWSMKCHQOOLQRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLKMGTRGYDDDGCEPKSKLLRWTTNK KHHVLETEKTPKDWVQCHREKERMSHKLEESFEELKKSEVLLYY TVEKKSNISGLKHYNPWSMKCHQOOLQRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLKMGTRGYDGDGEPKSKLLRWTTNK KHRVLETEKTPKDWVQCHKERKGESKFFSSSLLVIYDG KRPBVVLDSDABELLBLSESSADESAGAYNYKPIGAGSVUVM IDFAHTTCRLYGEDTVVHEQQDAGYIFGLQSLIDIVTEISEESG B AVIGVRVCGMQVYQAGSGQLHMNNYHGKKLSVQOFKEALFQFF HNGRYLRELLGPVLKKLTELKAVLERGESYRFYSSSLLVIYDG KRPBVVLDSDABELDELDESSADESAGAYNYKPIGAGSVOVM IDFAHTTCRLYGEDTVVHEQQDAGYIFGLQSLIDIVTEISEESG B GAHPSAARPLAAPTPAAPACRSSPSCGAASSPSCKGHGAASPSEK GAHPSAARPLAAPTPAAPACRSSPSGCAGAASFPSGAADDVAKK PPPAPQQPPPPFAPHPQOHPQOHPQNGAHGKGGHGGGGGGG SSSSSSASAAAAAAAAAASSSSGSGRELGGALGOLOVOKKSLO	1	j		WAEYHADIYDKVSGDMOKOGCDCECLGGGRISHOSODKKTHIVG
6380 1414 462 FRANKERGAPORSQAPEWDRAACRESFOGSGRAY LIFNSVAVNGGAPAERVLITGHAWADIYCENCKTTIGWKYEHA FESSOKYKEGKYIIELAHMIKDMGWD 6380 1414 462 FAVQGGRGAPPTURGSGNMARFALTVURGETRENKIKIOG GVDEPLESTGFKQAAAGITINNVKPTHAFSSDLMRTKOTMGU LERSKECKDMTVKXDSKLRERKYGVVBGKALSELRAMAKAAREE CPVPTPPDGGETLDQVKMRGIDPFEPLCQLILKEADDKEOFSOGS PSNCLETSLAEIFPLGNNKRGIDFFEPLCQLILKEADDKEOFSOGS PSNCLETSLAEIFPLGNNKRGIDFFEPLCQUHRGYBERNFEPLKGVD LALFTSLIC AVVRAGGSRGFSGAGWRFRQAAAMNFSEVFKLSSLLCKFSPPDGK VLASCVQYRUVVADUNTLQILQTYTCLDQIQHIEWSADSLFILC AMKKRGLVQVWSLEQPBWHCKIDEGSGAGVASCWSPDGRHILNT TEPHLRITVWSLCTKSVSYIKYPKACLQGITFTRDGRYMALAER RDCKDYVSIFVCSDWQLLHHFDTDTDQLGIEWAMPNGCVLAWDD TCLBYKILLYSLOGRLLSTYSAYEWSLGIKSVAWSFSOFLAVG SYDGKVRILMYVWMNITEFGHPAAINDRIVYYKEAERSPOLG LGCLSFPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDRANP KIGIGMLAFSPDSYFLATRNDNIPNAVWWDIQKLRLFAVLSOL SPVRAFQWDPQOPRLAICTGGSRLYLWSPAGCMSVQVPGGEGFA VLSLCWHLSGDSMALLSKOHFCLCFLETEAVVGTACROLGGHT TVEKKGNISQLKHYNPMSMKCHQOQLORMKENAKHRQYKFIL LENLTSRYEVPCVLDLKMGTRGHGDDASEKAANQIRKCQOSTS AVIGVRVCCMQVVQAGSGQLMFWNKYHGRKLSVQOFKEALFOFF HNGRYLRRELLGFVLKKITELKAVLERGESTRFYSSSLVYIYDG KERPEVVLDSDAEDLEDLSESSADESAGAYAYKFIGASSVDVMM LDFAHTTCRLYGEDTVVHEQQDAGYIFGLQSLIDIVTEISEESG 6383 3159 1061 SPAPGRFSPHGSQPAARAAAAPAPSAKQRGSKGGHAASPSEK GAHPSAARPLAAPTPAAPACRS PSGCAGAASFFGRAAPSEK GAHPSAARPLAAPTPAAPACRS PSGCAGAASFFGRAAPSLASQP AARAAAAAAAAAASSSASCSRELGGALGOLOGKOKKAKK SSSSSASAAAAAAAAASASSASCSRELGGALGOLOKROKVGLOA	6379	35		ISMAYGPAQHAISTEKIKAKYPDYEVTWANDGV
6380 1414 462 FESSQKYKEGKYITELAMIKDNOWD PAVGGORGAGPPIRGSGNMARFALTVVRHGETRFNKEKIJOGO GVDEPLEBTGFKQAAAAGITLMNVKPHIAFSSDLMRTKOTMHGI LERSKFCKDMTVKYDSILRERKYGVVBCKALSELRAMAKAAREE CPVPTPPPGGETLOQVKMEGIDPFEPLCQLILKEADQKEQPSQGS PSNCLETSLAEIFPLGKNHSSKVNSDSGIBGLAASVLVVSHGAY MRSLFDYFLTDLKCSLPATLSRESLMSVTRNTGMSFJFINFEE REVKPTYQCICMNLQDHLNGLTENSLGLNLPSKSNHFEPLKGVP LALFTSLLC 6381 1668 218 AVVRAGGSRGFSGAGWRFRQAAAMNFSEVFKLSSLLCKPSPDGK YLASCVQYRLVVZDVNTLQILQLYTCLDQIQHIEWSADSLFILG AMYKRGLVQWWSLEQPBWHCDBGSAGLVASCWSPDGRHILNT TEPHLRITVWSLCTKSVSYIKYPKACLQGITFTRDGRYMALAER RDCKDVVSIFVCSDWQLLRHFDTDTDQLTGIEWAPMGCVLAVWD TCLEYKILLYSLDGRLISTYSAVEWSLGIKSVAWSPSSQFLAVG SYDGKVRILNHVTWKMITEFGHPAAINDPKIVVYKEAEKSPQLG LGCLSFPPPPRAGAGPLPSSESKYEIASVVSLQTLKPVTDRAMP KIGIGMLAFSPDSYFLATRNDIFNAVWWDIQKLRLFFAVLSQL SPVRAPQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA VLSLCWHLSGDBMALLSKOHFCLCFLETEAVVGTACRQLGGHT TUKHVLETEKTPKDWVQHKKEEKMKSHKLEEEFEBLKKSEVLYY TVEKKSNISSQLKYNPWSMKCHQOOLQMKEENAKHRNQYKFIL LENLTSRYEVPCVLDLKMSTRQHGDDASEEKAANQIRKCQQSTS AVIGVRCCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKSALFQFF HKGRYLRRELLGPVLKKTELGVLLERQESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSESADESAGAYAYKEIGASSVDVRM IDFAHTTCRLYGEDTVVHEQQDAGYIFGLQSLIDIVTEISEESG B 6383 3159 1061 SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSSPSEGGAPASFFGRAAPSEKA PPPAPQQPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGGKS SSSSSASAAAAAAAAAASSSSSCSRLLGRAMFSGGADDVAKK PPPAPQQPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGGKS SSSSSASAAAAAAAAASSSSSCSRLLGRAMFSGGALDVAKK PPPAPQQPPPPAPHPQQHPQOHPQNQAHGKGGHRGGGGGGGKS SSSSSASAAAAAAAAAASASSSSCSRLLGRAMFSGGALDVAKK PPPAPQQPPPPPAPHPQQHPQOHPQNQAHGKGGHRGGGGGGGKS SSSSSASAAAAAAAAASASSSSSCSRELGGALNFFYGLALVAAAAFS] 33	378	BRAGSPSPSRAALRRCAPQRSQAPRWPDRAACRRSFQGSOGRAY
6380 1414 462 PAVQGQGAGAPTIGRSGMMARPALTUVRHGETRFNKEKIIQQ GVDEPLSETGFKQAAAAGIFLNNVFTHAFSDLMRTKQTMHGI LERSKFCKDMTVKYDSRLRERKYGVVEGKALSELRAMAKAAREE CPUTTPPGGETLDQVKMRGIDFFEFLCQLILKEADQKEQFSQGS PSNCLETELAEIFPLGKNHSSKVNSDSGIPGLAASVLVVSHGAY MRSLFDYFLTDLKCSLPATLSRSELMSVTFNTGMSLFIINFEG REVKPTVQCICMNLQDHLMGLTENSLGINLPSKSNHFEPLKGVP LAAFTSLLC AVVRAGGSGFSGAGWRPRQAAMMFSEVFKLSSLLCKFSPDGK YLASCVQYRLVVRDVNTLQILQLVTCLDQIGHIEMSADSLFILC AMYKRGLVQWSLEQPEMHCKIDEGSAGLVASCWSPDGRHILNT TEPHLRITUWSLCYKSVSYIKYPKACLQGITFTRGRYMALAER RDCKDYVSIFVCSDWQLLRHFDTDTQDLTGIEMAPNGCVLAVWD TCLBYKILLYSLDGRLLBSTYSAFWSLGIKSVAWSPSSQFLAVG SYDGKVRILNHVTWMITTEFGHPAAINDPKIVVYKEAEKSPQLG LGGLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKPUTDRAND KIGIGMLAFSPDSYFLATMONIPNAVWWDIQKLRLFAVLEQL SPVRAFQWDPQQPRLAICTGGSRLYLWSPASCMSVQVPGEGGFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEFFEWLKKSEVLYY TVEKKGNISSQLKAYFPWSMKCHQQQLQRMKENAKHNQYKFIIL LENLTSRYEVPCVLDLKMGFRQHDDASSEKRANQIKRCQGSTS AVIGVVCCMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF HKGRYLRRELLGPVLKKLTELKAVLERGESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEBLESSADESAGAVAYKPIGASSPUVM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG B 6383 3159 1061 SPAPGRPSPHGSQPAARAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSSPSCGAPASFEKAGADSSAGAAPSEK AARAAAPAMPSAKQGSKGGHGAASPSEKGHGAASPSEK GAHPSAARPLAAPTPAAPACRSSPSCGAPASFEKGADDVAKK PPPAPQQPPPPPAPPQQPPPQQHPQQHPQQHPQQAHKGKGGHKGGGGGGGGKS SSSSSASAAAAAAASSSASCSRRLGRAANFFILALVAAAAFS GWCVHHVLEEVQVVRSLOADFSRORBELGGGLGGVSNOVVSLOA		i		LINSVVNVGCGPAEERVLLTGLHAVADIYCENCKTTI.CWKVPUA
FAVUGURGAGDIFALTVURIGETERFENERITIOGO GVUEPILSETGFRQAAAGIFILNUNETHAFSDLMRTKQTMIGI LERSKFCKDMTVKYDSRLRERKYGVVEGKALSELRRMAKAAREE PSNCLETILABIFPIGKNISSKVNSDSGIPGLAASVLVVSHGAY MRSIFDYFLTDLKCSLPATLSRSELMSVTFNTGMSLPIINFEBG REVKPTVQCICHVLQHHUNGLTENSIGINLPSKSNHFEPLKGVP LALFTSLLC 6381 1668 218 AVVRAGGSRGFSGAWRFRQAAAMFSEVFKLSSLLCKFSPDGK YLASCVQYRLVVRVDTVTLQILQLTTCLDQIGHIENSADSLFILC AMMYKGLVQVSLSQPENHCKIDEGSAGLVASCWSPDGHHILNT TEPHLRITVWSLCTKSVSYIKYPRACLQGITFTRDGRYMALAER RDCKDYVSIFVCSDWQLLRHFDTDTQDLTGIEWAPNGCVLAVWD TCLBYKILLYSLGGRLBSTYSAXEWSLGIKSVAWSPSSQFLAVG SYDGKVRILMHVTWKMITEFGHPAAINDPKIVVYKEAEKSPQLG GGCSFPPPREAGAGPLPSSKYEIASVUSLQTLKEPVIDRANP KIGIGMLAFSPDSYFLATRNDNIPNAVWNDIQKIRLFAVLEQL SPVRAFQWDPQOPRLAICTGGSRIYLMSPAGCMSVQVPGEGBFA VLSLCWHLSGDSMALLSKUHFCLCFLETEAVVGTACRQLGGHT TVEKKGNISSGUSKHYNFWSKHCHQOLQRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGVVCGMQVYQGAGSQLMFNNKYNGRKLSVQGFKEALFQFF HNGRYLRRELLGFVLKKUTFLKAVLBRGESFFFYSSLLVIYDG KERPBEVVLDSDAEDLEDLSESADESAGAYAYKPIGASSUVVRM IDFAHTTCRLYGEDTVVHRGQDAGYIFGLQSLDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSPSDGAPASFGGAASPSEKG AARAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSPSDGAPASFGGAADSPSEKG AARAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSSPGGAPASFGGADDVAKK PPPAPQQPPPPPAPQQPPPQQPPQQPQQPQNQAHGKGGHRGGGGGGGKS SSSSSAAAAAAAAASSASCSRICGRALNFIFYLALVAAAAFS GWCVHHVLEEVQQVRKSHODFSRORBELGGGLGGVSVOVANGSLOR	6380	1414	·· · · · · · · · · · · · · · · · · · ·	FESSQKYKEGKYIIELAHMIKDNGWD
GVDEPLSETGFKQAAAAGIFLINVKFTHAFSSDLMRTKQTMHGI LERSKFCKDMTVKVDSRIRERKYGVVEGKALSELRAMAKAAREE CPVFTPPGGETLDQVKMRGIDFFFLCQLILKEADQKEGFSQGS PSNCLETSLAEIFPLGKNHSSKVWSDGSIFGLAASVLVVSHGAY MRSIFDYSITDLKCSIPATISRSELMSVTPNTGMSLFIINFEGG REVKPTVQCICMNLQDHLMGLTENSLGLMLPSKSNHFFBPLKGVP LALFTSLLC AVVRAGGSRGFSGAGWRPRQAAAMNFSEVFKLSSLLCKFSPDGK YLASCVQYRLVVRDVNTLQILQLYTCLDQIQHIEWSADSLFILC AMYKRGLVQVWSLEQPEWHCKIDEGSAGLVASCMSPDGRHILNT TEPHLRITVWSLCTRSVSYIKYPKACLQGITFTRDGRYMALAER RDCKDYVSIFVCSDWQLLRHFDIDTODLTGIEWAPNGCVLAWWD TCLEYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSOFLAVG SYDGKVRILNNTVMWINTTEFGHBAAINDPKIVVYKEAEKSPQLG LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTIKEVTDRANP KIGIGMLAFSPDSYFLATRINDNIPNAVWWDIQKIRLFAVLEQL SPVRAFGWDPQOPRIALGGSRLYLWSPAGCMSVQVPGEGDFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT TVEKKGNISSQLKHYNPWSMKCHQQQLGMKKENAKHRNQVKFIL LENLTSRYSEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCCGNQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF HNGRYLRRELLGFVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDABDLEDLSESSADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEQQDAGYIFGLQSLIDIVTEISEESG B 6383 3159 1061 SPAPGRPSPHGSQPAARAAAAPAMPSAKQRSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACKSPSPGCAPASFFGRAPRSLASQP AARAAAAPAMPSAKQRSKGGHGAASPSEKGAHPSGGADDVAKK PPPAPQQPPPPPAPHQQHPQQHPQNQAHGKGGRRGGGGGGKS SSSSASAAAAAAAAAASSSASCSRLGRALNFLFYILALVAAAAFS GWCVHVLEEVQQVRRSHODFSRORELGGGLGGUGKVS		1474	462	PAVQGQRGAGPPTGRGSGNMARFALTVVRHGETRFNKEKIIQGO
LERSKFCKOMTVKYDSRLERRKYGVVEGKALSELRAMARAAREE CPVFTPPGGETLDQVMRGIDPFFPLCQLILKEADQKEQFSQGS PSNCLETSLAEIFPLGKNHSSKVNSDSGIFGLAASVLVVSHGAY MRSIFDYFLITDLKCSLPATLSREELMSVTFNTGMSLFIINFEEG REVKPTVQCICNNLQDHLNGLTENSLGINLPSKSNHFBPLKGVP LALFTSLLC AVVRAQGSRGFSGAGWRPRQAAAMNFSEVFKLSSLLCKFSPDGK YLASCVQYRLVVRDVNTLQILQLYTCLDQIQHIEWSADSLFILC AMYKRGLVQVWSLEQPEWHCKIDEGSAGLVASCWSPDGRHILNT TEPHLRITUWSLCTKSVSIKYPKACLQGITFTRDGRYMALAER RDCKDYVSIFVCSDWGLLEHFDIDTODLTGIEWAPNGCVLAVWD TCLBYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG SYDGKVRILNNTVNKMITEFGHPAAINDPRIVVYKEAEKSPQLG LGCLSFPPPRRAGAGPLPSSESKYEIASVPVSLQTIKEPVDRANP KIGIGMLAFSPDSYFLATRINDNIPNAVWVWDIQKLRLFAVLEQL SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCNSQVPGEGDFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT KHYLETEKTPKDWVRQHRKEEKMSHKLEEFEWLKKSBVLLYY TVEKKGNISSGLKHINPNSMKCHQQLQRMKEMAKHNQYKFIL LENLTSRYEUPCVULDLKWGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMKMENAKHNQVKFIL LENLTSRYEUPCVULDLKWGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMKECAKHNQVKFIL LENLTSRYEUPCVULDLKWGTRQHGDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMKECAKHNQVKFIL LENLTSRYEUPCVULDLKWGTRQHGDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMKECAKHNQVKFIL LENLTSRYEUPCVULDLKWGTRQHGDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMKECAKHNQVKFIL LENLTSRYEUPCVULDLKWGTRQHGDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMKECAKHNQVKFIL LENLTSRYEUPCVULDLKWGTRQHGDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMKECAKHNQVKFIL SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSSPGGGAPASFPGRAPRSLASQP AARAAAAPAMPSAKQRGGKGGAASPSEKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSSPGGGAPASFPGRAPRSLASQP AARAAAAPAMPSAKQRGGGAGAASPSEKGGHGAASPSEKGGHGGGGGGGKS SSSSASAAAAAAAAASSSASCSRAGRALNFLFYILALVAAAARS GWCVHVLUEEVQQVRRSHODFSROFELEGGGLGGGGGGKS GSSSSASAAAAAAAAASSSASCSRAGRALNFLFYILALVAAAARS	1 1	1	1	GVDEPLSETGFKQAAAAGIFLNNVKFTHAFSSDIMPTKOTMUCT
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SEQ	Predicted	Predicted end	Amino acid segment contains
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
-	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	-	\=possible nucleotide insertion)
			LKDLSDGIHVVKDARERDFTSLENTVEERLTELTKSINDNIAIF
			TEVQKRSQKEINDMKAKVASLEESEGNKQDLKALKEAVKEIQTS
J	}]	AKSREWDMEALRSTLQTMESDIYTEVRELVSLKQBQQAFKEAAD
4	į		TERLALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGP
			KEDGGFRHSEAFEALQQKSQGLDSRLQHVEDGVLSMQVASARQT
1		i	ESLESLLSKSQEHEQRLAALQGRLEGLGSSEADQDGLASTVRSL
-			GETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLLSQDQA
1			QAARLPPQDFLDRLSSLDNLKASVSQVEADLKMLRTAVDSLVAY
	1		SVKIETNENNLESAKGLLDDLRNDLDRLFVKVEKIHEKV
6384	738	1904	IWEVPVCLTHLLHLQQANQPLPPPSSSINEEDADEANRAIGEKR
			AAPDSGKKPKTPKTKQQKDPNEPQKPVSAYALFFRDTQAAIKGQ
	1		NPNATFGEVSQIVASMWDSLGEEQKQVYKRKTEAAKKEYLKALA
1	1		AYRASLVSKAAAESAEAQTIRSVQQTLASTNLTSSLLLNTPLSQ
1	1		HGTVSASPQTLQQSLPRSIAPKPLTMRLPMNQIVTSVTIAANMP
			SNIGAPLISSMGTTMVGSAPSTQVSPSVQTQQHQMQLQQQQQQ
•			GGGWGGWGGGCHGWHGGIGGGWGGGHEGHHWGGHLGGGGGG
ł			LQQQINQQQLQQRLQLQQLQHMQHQSQPSPRQHSPVASQI
			TSPIPAIGSPOPASOOHOSQIQSQTQTQVLSQVSIF
6385	2	1584	PRVRAADVAAGAQAVVSAGMAKSNGENGPRAPAAGESLSGTRES
1			LAQGPDAATTDELSSLGSDSEANGFAERRIDKFGFIVGSQGAEG
}			ALEEVPLEVLRQRESKWLDMLNNWDKWMAKKHKKIRLRCQKGIP
1			PSLRGRAWQYLSGGKVKLQQNPGKFDELDMSPGDPKWLDVTERD
1			LHRQFPFHEMFVSRGGHGOODLFRVLKAYTLYRPERGYCOAGAD
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			FSLLQKVSPVAHKHLSRQKIDPLLYMTEWFMCAFSRTLPWSSVI.
1 1			RVWDMFFCEGVKIIFRVGLVLLKHALGSPEKVKACOGOVETIER
			LRSLSPKIMQEAFLVQEVVELFVTEROIEREHLIOLRRWOETRG
	j		ELQCRSPPRLHGAKAILDAEPGPRPALOPSPSTRIPTDAPLEGS
	·		KAKPKPPKQAQKEQRKQMKGRGOLEKPPAPNOAMVVAAAGDACD
6386			PQHVPPKDSAPKDSAPQDLAPQVSAHHRSOESLTSOESEDTYI.
1 0000 1	819	195	TVCGSFYLGIMQRASRLKRELHMLATEPPPGITCWQDKDQMDDL
}	1		RAQILGGANTPYEKGVFKLEVIIPERYPFEPPQIRFLTPIYHPN
1			IDSAGRICLDVLKLPPKGAWRPSLNIATVLTSIQLLMSEPNPDD
1 1	1		PLMADISSEFKYNKPAFLKNARQWTEKHARQKQKADEEEMLDNL
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1			REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS
6388			STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
	*	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR
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1	1	!	NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK
1]	REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS
6389	1074	407	STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
	20,2	497	AEPGDRMAGHRLVLVLGDLHIPHRCNSLPAKFKKLLVPGKIQHI
-		ļ	LCTGNLCTKESYDYLKTLAGDVHIVRGDFDENLNYPEQKVVTVG
1		i	QFKIGLIHGHQVIPWGDMASLALLQRQFDVDILISGHTHKFEAF
			EHENKFYINPGSATGAYNALETNIIPSFVLMDIQASTVVTYVYO
6390	158		LIGDDVKVERIEYKKP
	730	535	GEERKEGRAPGKAFAPERNPAKMEKEETTRELLLPNWQGSGSHG
			LTIAQRDDGVFVQEVTQNSPAARTGVVKEGDQIVGATIYFDNLQ
6391	5386		SGEVTQLLNTMGHHTVGLKLHRKGDRFFPSLGQTWDP
0331	2386	2897	VRWNSKTECYLSIQTQENFPANLNELVNCIVISSLVTTQRKLKA
1		l l	MSLLGSRNQLARAVLNPNPMDFCTKDLLTTTSERIIAYLRDFNE
			DOKKAIETAYAMVKHSPSVAKICLIHGPPGTGKSKTIVGLLYRL

	· · · · · · · · · · · · · · · · · · ·		
SEQ	Predicted	Predicted end	Amino
ID	beginning	nucleotide	
NO:	nucleotide		
110.		location	TO TO THE PROPERTY OF THE PROP
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	Deleucine Memortionie, Kelysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- 1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of		S=Serine, T=Threonine, V-Valina
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine y=Inknorm # 5
1		sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
- 1			LTPNOPYCHEDENON
l l	1	1	LTENQRKGHSDENSNAKIKQNRVLVCAPSNAAVDELMKKIILEF
1	1	1	A THE COLON OF THE PROPERTY OF
i	1	1	I MANGUESHVQAMHKRKEFLDYOLDELSDODALCDCCDBTODOD
		i	DENISKVSKERQELASKIKEVQGRPQKTQSIIILESHIICCTLS
Į.	i	1	TSGGLLIESAFDCOCGUDECGUTTETTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
j			TSGGLLLESAFRGQGGVPFSCVIVDEAGQSCEIETLTPLIHRCN
1		ł	KLILVGDPKQLPPTVISMKAQBYGYDQSMMARFCRLLEENVEHN
İ		j.	MICRUPILICATIVO YRMHPDICLEPSNOVONDNI PONTROMPRIN TO A
ŀ	ľ	ł	1 SSUMPT QPILVEDVGDGSERRDNDSVTNDORTET TOTAL TOTAL
	1		KRKDVSFRNIGIITHYKAQKTMIQKDLDKEFDRKGPAEVDTVDA
1		i	FOGROKDCVIVICUE PROTOGO TO
i	1		FQGRQKDCVIVTCVRANSIQGSIGFLASLQRLNVTITRAKYSLF
1	1		TEGRETAL TERENORMNOLIODAOKRGATTVTCDVNVDVDVTDDVTTCT
1	1	ł	DAPVIORSLITHPPTTAPEGSRPOGGI.DCCVI.DCCDAVMGTTA
1			I INTESUSKETTETVTSKDPERPPVHDOLODDDI I VDMOTOVICE
l.			IFLWDPQPSSPQHPGATPPTGEPGFPVVHQDLSHVQQPAAVVAA
ł	1 1	ľ	LSSHKPDVPCPDDA COTT CHECKTPV VHQDLSHVQQPAAVVAA
L	. [LSSHKPPVRGEPPAASPEASTCQSKCDDPEEELCHRREARAFSE
6392	972	186	GEQEKCGSETHHTRRNSRWDKRTLEQEDSSSKKRKLL
[]	186	GRTGVDLASSMAHRLOIRLITUDVKDTLLDLDUDICERVACOVE
[1		ARGUEVEPSALEUGFROAYRAOSHSEDNYGI.guct genouwer por
ł	1 1		VLQTFHLAGVQDAQAVAPIAEQLYKDFSHPCTWQVLDGAEDTLR
1	i i		ECRTRGLRLAVISNFDRRLEGILGGLGLREHFDFVLTSEAAGWP
1	1		VPDDPIEGEAL DIAGRAGE ILGGLGLREHFDFVLTSEAAGWP
1	i		KPDPRIFQEALRLAHMEPVVAAHVGDNYLCDYQGPRAVGMHSFL
6393	2017	720	VVGPQALDPVVRDSVPKEHILPSLAHLI,PAI,DCI,PCCTDCI
1	1	730	TGGSKMAAVATCGSVAASTGSAVATASKSNUTSSAGROOD
i	1 1		NDSGPRDVSIAGTRPSVRNGOLLVSTGI.DAI.DOLICGGI ALIGNE
1	;		LLIEEDKYNIYSPLLFKYFLAEGIVNGHTLLVASAKEDPANILQ
	i I		ELPAPLLDDKCKKEFDEDVYNHKTPESNIKMKIAWRYQLLPKME
1			TCDVCCCDECTURE
1	ł i		IGPVSSSRFGHYYDASKRMPQELIEASNWHGFFLPEKISSTLKV
1	l l		EFCSDIPGITALDOFIONITYERGEDGGNDOVVODATE TOTAL
İ	!		DOS FUNGUUL CCAENGGNSHST, TKPT, VIT, DGT, T, DTCT, C3, G7 - TT.
j	i i		
	1 1	i	IHIRQIPRLNNLICDESDVKDLAFKLKRKLFTIERLHLPPDLSD
L			TVSRSSKMDLAESAKRLGPGCGMMAGGKKHLDF
6394	1418	511	GAAAGGEGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
	1		GAAAGGEGARRPAAMATVMAATAAERAVLEEEFRWLLHDEVHA
1	,		VLKQLQDILKEASLRFTLPGSGTEGPAKQENFILGSCGTDQVKG
1 :	ł J	1	VOI LOGUALSQADVNLKMPRNNOI.I.UFAFDFDVOWVI OOZODA
į l	1	1	MAYSQALIDLISKDOSYOFKTGAEVI, KI, MDAVMI OT MDA DAVE - 1
1		i	TEAT DI DESTAASGLIERMEAPALPSDIJIANNEVINI NEEL OF THESE
i i		i	LHALQPNSTKNFRPAGGAVLHSPGAMFEWGSQRLEVSHVHKVEC
<u> </u>	<u></u>	ļ	VIPWLNDALVYFTVSLQLCQQLKDKISVFSSYWSYRPF
6395	13	658	PECEDENTY CONTROL OF THE PECEDENCY CONTROL OF
]	1	- 1	PSGRPTRPLCCAARRGAARHGGSVSGWPAGRTPTETSNPGSSVM
j i	ı		ESVITEDVAVEFIQEWALLDSARRSI.CKVPMr.DOCPER a cnome
1	j	•	FUNESUVSULGORARDRATEDITT.DATINATION TO THE TOTAL TOTAL
	į.	1	DLLEEASSRDMQMGPGLFLRMQLVPSIEERETPLTREDRPALQE
		1	PPWSLGCTGLKAAMQIQRVVIPVPTLGHRNPWVARDSGE
6396	1	1221	ANTI-SCREENCOVOR
	1	1	ANILSSPSKRGQKGTLIGYSPEGTPLYNFMGDAFQHSSQSIPRF
	ĺ	1	TRESURGI DEESDSROIFYFLCLNLLFTFVELFVCVLTNICLCLT
	1	1.	SUGFHMLFDCSALVMGLFAALMSRWKATRIFSVGVGDIETICCE
j	l l		INGLFLIVIAFFVFMESVARLIDPPELDTHMLTPVSVGGLIVNL
ļ	ľ	1	IGICAFSHAHSHAHGASQGSCHSSDHSHSHHMHGHSDHGHGHSH
}		1.	GSAGGGMNANMEGUELUTT ARTT GG
1	ļ	1.	GSAGGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFIAD
ĺ	ĺ	1 4	FUCSUFIALLIFLSVVPLIKDACOVILIRI, PPEVEKET, UTATER]
j		1.	QALEGEISYRDPHFWRHSASIVAGTIHIOVTSDVI.FORTWOOM
}	ı	1:	IGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES
		1	MKYCKDGTYIM
6397	391	122	PAGGVGREEATDADADMTERWANDS
			BAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK
			CLIAAQTGTRWNKIVLKKWYTIFKDHVSLGDYEIHDGMNLELYY

SEQ	Predicted	[D - 32 - 1	
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide location	Marianine, Cacysteine, Dalanastic hara -
	location		Gracianic Acid, Fephenylalanina G.Gl.
	corresponding	corresponding to first	n=H1SC1Gine, I=Isoleucine K-Tyeino
1	to first	amino acid	L=beucine, M=Methionine N=Asparagina
ı	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ļ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
-	sequence	sequence	Codon, /=possible nucleotide deletion
—			\=possible nucleotide insertion)
6398	353	1306	Q
		1306	HKQMGPLINRCKKILLPTTVPPATMRIWLLGGLLPFLLLLSGLQ
1			RPIEGSEVAIKIDFDFAPGSFDDOYOGCSKOVMPKLTOCDVPTK
- [1	1	DIEAQKNYFRMWQKAHLAWLNQGKVLPQNMTTTHAVAILFYTLN
i	1	l	SNVHSDFTRAMASVARTPQQYERSFHFKYLHYYLTSAIQLLRKD
- 1			SIMENGTLCYEVHYRTKDVHFNAYTGATIRFGQFLSTSLLKEEA
1	1	:	QEFGNQTLFTIFTCLGAPVQYFSLKKEVLIPPYELFKVINMSYH
i			PRGDWLQLRSTGNLSTYNCQLLKASSKKCIPDPIAIASLSPLTS VIIFSKSRV
6399	75	1245	
1		1213	PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKRGVAVSGPTK
	1		RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQKKMAECEAEN
İ	1 1		EDLLKKLELYKEACEGQHKLECDLQQREEELAELQKALSDMQVC
			LFQEREHVLRLYSENDRLRIRELEDKKKIQNLLALVGTDAGEVT
	1 1		YFCKEPPHKVTILQKTIQAVGECEQSESSAFKADPKISKRRPSR
Į	1 1		ERKESSEHYQRDIQTLILQVEALQAQLGEQTKLSREQIEGLIED RRIHLEEIQVQHQRNQNKIKELTKNLHHTQELLYESTKDFLQLR
			SENQNKEKSWMLEKDNLMSKIKQYRVQCKKKEDKIGKVLPVMHE
			SHHAQSEYIKVMSLCRNEVVYFSGRVEGIPKNLQFVM
6400	2520	1053	KTMKCDEVVYEVQSAILRHNCGYAMKTGKFFHNLMERKDPETWL
l	1		DNISVTFLSLTDLQKNETLDIILISLSGAVQLRHLSNNLETLLKR
	1		DFLKLLPLELSFYLLKWLDPQTLLTCCLVSKQWNKVISACTEVW
	1		QTACKNLGWQIDDSVQDALHWKKVYLKAILRMKQLEDHEAFETS
	1 1		SLIGHSARVYALYYKDGLLCTGSDDLSAKLWDVSTGQCVYGIQT
ı			HTCAAVKFDEQKLVTGSFDNTVACWEWSSGAPTOUFDGUTGAVE
	1		SVDYNDELDILVSGSADFTVKVWALSAGTCINTITCUTPUTTURE
İ			VLQKCKVKSLLHSPGDYILLSADKYEIKIWDIGDEINGKOIVUU
			SVSEDRSICLOPRLHFDGKYIVCSSALGLVOWDERSUNTI BILLY
	1		TPEIANLALLGFGDIFALLFDNRYLYIMDI.PTRGI.TCPMDI.DEV
1 1	1		RKSKRGSSFLAGEASWLNGLDGHNDTGLVFATSMPDHSTHLVLW
6401	109		KENG
	209	766	PGAAWSRPDLRGCCTGPQPALRMLVLPSPCPQPLAFSSVETMEG
1 1			PPRKICKSPEPGPSSSIGSPOASSPPRPNHVI.I.TDTOGUDVTHII
1			VDEESQREPGASGAPGOKKCYSCPVCSRVFEVMCVLOBUGTBUG
			EVEPPECDICGKAFKRASHLARHHSIHLAGGGPPHGCDLCDDDD
6402	1196	270	RDAGELAQHSRVHSGERPFOCPHCPRRFMEONTLOKUTPWVUP
-		279	TTSQCGGIRQSSAIPVASMEFAAICLRNALLLIPEECODEVORN
	l		GAKNSNQLGGNTESSESSETCSSKSHDGDKPTDADDGCDLDKOR
] [LENLKCS I LACSAYVALALGONT MAI NHADKI TOODKI GOOT WE
1 1			LGHLYAAEALISLDRISDAITHLNPENVTDVSLGISSNEQDQGS
	1	į	DKGENEAMESSGKRAPQCYPSSVNSARTVMLFNLGSAYCLRSEY
L /	í	1	DKARKCLHQAASMIHPKEVPPEAILLAVYLELQNGNTQLALQII
6403	2	1690	KRNQLLPAVKTHSEVRKKPVFQPVHPIQPIQMPAFTTVQRK
			RGIHTSVLQGNLQNQMYSHNVVIMNLNNLNLTQVQQRNLITNLQ RSVDDTSQAIQRIKNDFQNLQQVFLQAKKDTDWLKEKVQSLQTL
1			AANNSALAKAMADTI EDMASOV NO BERGOVENIO EL TELEVICIONE DE LA RANNSALAKAMADTI EDMASOV NO BERGOVENIO EL TELEVICIONE DE LA RANNSALAKAMADTI EL MANGOVENIO EL TELEVICIONE DE LA RANNSALAKAMADTI EL MANGOVENIO EL TELEVICIONE DE LA RANNSALAKAMADTI EL MANGOVENIO EL TELEVICIONE DE LA RANNSALAKAMADTI EL MANGOVENIO EL TELEVICIO EL TELEVICIONE DE LA RANNSALAKAMADTI EL MANGOVENIO EL TELEVICIO EL T
		ĺ	AANNSALAKANNDTLEDMNSQLNSFTGQMENITTISQANEQNLK DLQDLHKDAENRTAIKFNQLEERFQLFETDIVNIISNISYTAHH
		1	LRTLTSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLR
1			MQQDLMRSRLDTEVANLSVIMEEMKLVDSKHGQLIKNFTILQGP
- 1			PGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGPAGERGPIG
j.	1		PAGPPGERGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGPP
ļ	ĺ	ł.	GKEGLPGPQGPPGFQGLQGTVGEPGVPGPPGLPGLPGVPGMPGP
f	j	1	KGPPGPPGPSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYY
ł	1	1.	FSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH
J		1	WIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC
5404		14	AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAI.
6404	1012	222	AAALAMAAPAPGLISVFSSSQELGAALAQLVAQRAACCLAGARA
			ANADALIZATION

SEQ	Predicted	Predicted end	Amino
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Deucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			RFALGLSGGSLVSMLARELPAAVAPAGPASLARWTLGFCDERLV
1			PFDHAESTYGLYRTHLLSRLPIPESQVITINPELPVEEAAEDYA
1			KKLRQAFQGDSIPVFDLLILGVGPDGHTCSLFPDHPLLQEREKI
	1		VAPISDSPKPPPQRVTLTLPVLNAARTVIFVATGEGKAAVLKRI
		<u></u>	LEDQEENPLPAALVQPHTGKLCNFLDRAARIJTVPPEKHSPI.
6405	1	1456	AALPRPTPRAPLGREGTGSDSEMAASMFYGRI.VAVATI.DNHDDD
1			TAQRAAAQVLGSSGLFNNHGLOVOOOOORNI,SI,HEVMSMETT,OF
			AGVSVPKGYVAKSPDEAYAIAKKLGSKDVVIKAOVLAGGDGKGT
ł			FESGLKGGVKIVFSPEEAKAVSSOMIGKKLFTKOTGEKGPTCMO
			VLVCERKYPRREYYFAITMERSFOGPVLIGSSHGGVNTEDVAAR
ļ			TPEAIIKEPIDIEEGIKKEOALOLAOKMGFPDNIVESAAFMMVV
			LISTELKIDATMIEINPMVEDSDGAVLCMDAKINFDSNSAVPOV
	ļ i		KIFDLQDWTQEDERDKDAAKANLNYIGLDGNTGCLANGAGLAMA
i			TMDIIKLHGGTPANFLDVGGGATVHOVTEAFKI,ITSDKKVI.A TI
1			VNIFGGIMRCDVIAQGIVMAVKDLEIKIPVVVRI.OGTPVDDAVA
	[LIADSGLKILACDDLDEAARMVVKLSEIVTLAKOAHVDVKFOLD
6406	1036	167	1 ↓
	1050	10/	HPRQMRGEDTPEAPPYSSGRYDSIKTEVSGCPEDLTVGRAPTAD
			DDDDDHDDHEDNDKMNDSEGMDPERLKAFNMFVRLFVDENLDRM
			VPISKQPKEKIQAIIESCSRQFPEFQERARKRIRTYLKSCRRMK
			KNGMEMTRPTPPHLTSAMAENILAAACESETRKAAKRMRLEIYO
] [SSQDEPIALDKQHSRDSAAITHSTYSLPASSYSQDPVYANGGLN
1 1			YSYRGYGALSSNLOPPASLQTGNHSNGESGEARALASRPAPSWV CRAALGSGMGRGKQRPVMERGCLTA
6407	492	150	VGLCLAVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGV
i i			SWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNAC
			VLTISPVQPEDDADYYCSVGYGFSP
6408	1458	903	RGCITSSQAWRLFGGVTRGFNMRIEKCYFCSGPIYPGHGMMFVR
}			NDCKVFRFCKSKCHKNFKKKRNPRKVRWTKAFRKAAGKELTVDN
			SFEFEKRRNEPIKYQRELWNKTIDAMKRVEBIKQKRQAKFIMNR
			LKKNKELQKVQDIKEVKQNIHLIRAPLAGKGKQLEEKMVQQLQE
7100			DVDMEDAP
6409	150	446	NTALANLLRCFTCDRLCGGCTAPAPPAHQGIVLQPVMPSCDPGP
		:	GPACLPTKTFRSYLPRCHRTYSCVHCRAHLAKHDELISKSFOGS
6410			HGRAYLFNSV
9410	85	607	RGGTAGCVACLGCWGQSSSPKAAFPAGSACLPADSCPCLLFQAC
I	1		AISGLENCITIHPLNIAAGVWMIMNAFILLLCEAPECCOFTERA
1	1		NTVAEKVDRLRSWQKAVFYCGMAVVPIVISITI.TTI.I.CNATABA
6411	302		TGVLYGLSALGKKGDAISYARIOOOROOADEEKIAETI.EGRI.
A-11	202	772	RLSIMASSLNEDPEGSRITYVKGDLFACPKTDSLAHCISEDCEM
		ļ	GAGIAVLFKKKFGGVQELLNOOKKSGEVAVLKRDGRYTYVIITE
			KRASHKPTYENLQKSLEAMKSHCLKNGVTDLSMPRTGCGLDPLO
6412	61	1700	WENVSAMIEEVFEATDIKITVYTL
2	61	1709	RPVTSFSPLPGSCGGRLGTRTMLGRSLREVSAALKQGQITPTEL
i			CQKCLSLIKKTKFLNAYITVSEEVALKOAEESEKRYKNGOSLOD
J	1		LDGIPIAVKDNFSTSGIETTCASNMLKGYIPPYNATVVOKLLDO
[ł	ł	GALLMGKTNLDEFAMGSGSTDGVFGPVKNPWSYSKOYREKRKON
ĺ	!		PHSENEDSDWLITGGSSGGSAAAVSAFTCYAALGSDTGGSTPND
- 1		•	AAHCGLVGFKPSYGLVSRHGLIPLVNSMDVPGILTRCVDDAATU
[Ī	LGALAGPDPRDSTTVHEPINKPFMLPSLADVSKLCIGIPKEVLV
1	}		PELSSEVQSLWSKAADLFESEGAKVIEVSLPHTSYSIVCYHVLC
	}		TSEVASNMARFDGLQYGHRCDIDVSTEAMYAATRREGFNDVVRG
		ļ	RILSGNFFLLKENYENYFVKAQKVRRLIANDFVNAFNSGVDVLL
1		j	TPTTLSEAVPYLEFIKEDNRTRSAQDDIFTQAVNMAGLPAVSIP
			VALSNOGLPIGLOFIGRAFCDQOLLTVAKWFEKQVQFPVIQLQE
			LMDDCSAVLENEKLASVSLKQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	_	\=possible nucleotide insertion)
6413	2	885	HEPRCAGMAASLWMGDLEPYMDENFISRAFATMGETVMSVKIIR
			NRLTGIPAGYCFVEFADLATAEKCLHKINGKPLPGATPAKRFKL
Į.	ı	1	NYATYGKQPDNSPEYSLFVGDLTPDVDDGMLYEFFVKVYPSCRG
1			GKVVLDQTGVSKGYGFVKFTDELEQKRALTECQGAVGLGSKPVR
1	J	ĺ	LSVAIPKASRVKPVEYSQMYSYSYNQYYQQYQNYYAQWGYDQNT
1			GSYSYSYPQYGYTQSTMQTYEEVGDDALEDPMPQLDVTEANKEF
	<u></u>		MEQSEELYDALMDCHWQPLDTVSSEIPAMM
6414	1	538	RGGRAALLPWRRFPCCRPRPQPARPSSRATPGPRSPGMATSIGV
]			SFSVGDGVPEAEKNAGEPENTYILRPVFQQRFRPSVVKDCIHAV
	İ		LKEELANAEYSPEEMPQLTKHLSENIKDKLKEMGFDRYKMVVQV
1			VIGEORGEGVFMASRCFWDADTDNYTHDVFMNDSLFCVVAAFGC
			FYY
6415	2	1168	FVRQWQSSHRRACGLGCEARAGGGEEPRGRASSVAGWVGAFRAP
1]		FIEAAVAGLGAGSGKRRRGWKMPVHSRGDKKETNHHDEMEVDYA
1			ENEGSSSEDEDTESSSVSEDGDSSEMDDEDCERRRMECLDEMSN
i			LEKQFTDLKDQLYKERLSQVDAKLQEVIAGKAPEYLEPLATLOE
1			NMQIRTKVAGIYRELCLESVKNKYECEIOASROHCRSEKIJIVD
i			TVQSELEEKIRRLEEDRHSIDITSELWNDELOSRKKRKDPFWPD
1			KKKPGVVSGPYIVYMLQDLDILEDWTTIRKAMATLGPHRVKTRP
1			PVKLEKHLHSARSEEGRLYYDGEWYIRGOTICIDKKDECPTSAV
6416	410		ITTINHDEVWFKRPDGSKSKLYISQLQKGKYSIKHS
0410	410	1519	EIAPADLEIPACAPVLLSRATSSTMSVTGGKMAPSLTQEILSHL
i i			GLASKTAAWGTLGTLRTFLNFSVDKDAQRLLRAITGQGVDRSAI
1 1			VDVLTNRSREQRQLISRNFQERTQQDLMKSLQAALSGNLERIVM
1 1	!		ALLQPTAQFDAQELRTALKASDSAVDVAIEILATRTPPQLQECL
	Ì	}	AVYKHNFQVEAVDGITSETSGILQDLLLALAKGGRDSYSGIIDY
1 1		Ì	NLAEQDVQALQRAEGPSREETWVPVFTQRNPEHLIRVFDQYQRS
1 1			TGQELEEAVQNRFHGDAQVALLGLASVIKNTPLYFADKLHQALQ
1	i		ETEPNYQVLIRILISRCETDLLSIRAEFRKKFGKSLYSSLQDAV KGDCQSALLALCRAEDM
6417	1	845	RGESRVLWSELEGEAGGAGGWASSLNARMDNRFATAFVIACVLS
]			LISTIYMAASIGTDFWYEYRSPVQENSSDLNKSIWDEFISDEAD
1 1		Ĭ	EKTYNDALFRYNGTVGLWRRCITIPKNMHWYSPPERTESFDVVT
]]	1		KCVSFTLTEQFMEKFVDPGNHNSGIDLLRTYLWRCQFLLPFVSL
1 1		}	GLMCFGALIGLCACICRSLYPTIATGILHLLAGLCTLGSVSCYV
1 1		1	AGIELLHQKLELPDNVSGEFGWSFCLACVSAPLQFMASALFIWA
		į.	AHTNRKEYTLMKAYRVA
6418	2	662	TRTRPRRPPGLGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH
			TPAPPPPPPCGGIACHGEPAKFYGYDNLOROPIFTTOOFAELVO
ļ i			YFDCKSSSGNIGEDPDHLNQSSSPSQMFPWMRPQAAPGRRRGRQ
	i	Į.	TYSRFQTLELEKEFLFNPYLTRKRRIEVSHALALTEROVKIWFO
			NRRMKWKKENNKDKFPVSRQEVKDGETKKEAOELEEDRAEGITN
6419	1	973	PGRPRVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIFP
!!	•	1	MARSISTSGPLDKEDTGRQKLISTGSLPATLOGATDSLGLEWHI.
1	i	1	PSPDPVTVPYLSPLVVWKELESLLENEGDHAITVADFVDHHDIV
[FWNLVWYFRRLDLPSNLPGLILSSBHCNKYSKIPRHCMSEDSKY
	. [J	VLIQMLWDNMKLHQDPGQPLYILWNAHTOKYPMVHLLOKSDNSF
	{		NQELLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRORSLYRET
1		1	LFLSLVALGRENIDIDAFDKEYKMAYDRLTPSQVKSTHNCDRPP
6420	300	i	STGVMECRKTFGEPYL
0320	207	1187	RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN
	ł	1.	YLLWVFTPLILLILPYFTIFLLYLTIIFLHIYKRKNVLKEAYSH
		1 1	NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPEDGPALIIFYH
		1 (GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC
1	1	. [4	ALHGPREKCVEILRSGHLLAISPGGVREALISDETYNIVWGHRR
LL			GFAQVAIDAKVPIIPMFTQNIREGFRSLGGTRLFRWLYEKFRYP

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide		**- PAGMAMANC, C=CVSCEINE, D=AgnayFig Nata =
1.77	location	location	TOTAL CHILD ACIO, PEPRANO 19 19 19 0 0 0 0 1 1 1 1
- 1	1	corresponding	n=nistidine, l=Isoleucine V-Lucino
- 1	corresponding	to first	L=Leucine, M=Methionine N_Agramain-
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W-Truntonhan V W-valine,
i	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	Doquence	Codon, /=possible nucleofide deletion
		 	\=possible nucleotide insertion\
ı		ì	FAPMYGGFPVKLRTYLGDPIPYDPOITAEELAEKTKNAVOALID
6421			MORIPGNIMSALLERFH
0421	1844	362	WALSLRRQPERMSNKLLSPHPHSVVLRSEFKMASSPAVLRASRL
İ	ŀ	ĺ	YOWSLKSSAOFLGSDOLDOVCOLTDVDARWASSPAVLRASRL
1			YQWSLKSSAQFLGSPQLRQVGQIIRVPARMAATLILEPAGRCCW
ı]		DEPVRIAVRGLAPEQPVTLRASLRDEKGALFQAHARYRADTLGE
1	1		LDLERAPALGGSFAGLEPMGLLWALEPEKPLVRLVKRDVRTPLA
ł	1		VELEVEDGHDPDPGRLLCOTRHERYFI, PPGVDPEDVDVGDUDGm
1			DEDPERGREPGIVDMFGTGGGLLEVRASIJAGVGRAIMAT AVD
1	1		NYEDLPKTMETLHLEYFEEAMNYLLSHPEVKGPGVGLLGISKGG
ı)		ELCLSMASFLKGITAAVVINGSVANVGGTLRYKGETLPPVGVNR
]		NRIKUTKDEVADTUDUI NODI TERROS VANVGGTLRIKGETLPPVGVNR
1	1		NRIKUTKDGYADIVDVLNSPLEGPDQKSFIPVERAESTFLFLVG
	· i		QDDHNWKSEFYANEACKRLQAHGRRKPQIICYPETGHYIEPPYF
	1		PLCRASLHALVGSPIIWGGEPRAHAMAOVDAWKOLOTERUKULO
6422	+		GREGIIPSKV
0722	181	2133	EGENLSWFQEFWGDIAKEFYWKTPCPGPFLRYNFDVTKGKIFIE
1	j		WMKGATTNICYNVLDRNVHEKKLGDKVAFYWEGNEPGETTQITY
	1 1		HOLLVOVCOFSWII PROCTURODDIN TORRESPECTOTTY
ľ	1 1		HQLLVQVCQFSNVLRKQGIHKGDRVAIYMPMIPELVVAMLACAR
i	1		IGALHSIVFAGFSSESLCERILDSSCSLLITTDAFYRGEKLVNL
	1		KELADEALQKCQEKGFPVRCCIVVKHLGRAELGMGDSTSQSPPI
i	i i		AKSCPDVQ1SWNQGIDLWWHELMOFAGDRCFDFWCDARDDY BILL
	f i		113GSIGKPKGVVHTVGGYMLYVATTFKVVPDFHARDVPWCTAD
ļ	1.		IGWITGHSYVTYGPLANGATSVLFEGIPTYPDVNRLWSIVDKYK
ŀ	ľ		VTKFYTAPTAIRLLMKFGDEPVTKHSRASLQVLGTVGEPINPEA
			WLWYHRVYGAODCDTYDTEWOTTETTCCTT
1	1 1		WLWYHRVVGAQRCPIVDTFWQTETGGHMLTPLPGATPMKPGSAT
1	i 1		FPFFGVAPAILNESGEELEGEAEGYLVFKQPWPGIMRTVYGNHE
	1		RFETTYFKKPPGYYVTGDGCQRDQDGYYWITGRIDDMLNVSGHL
			LOIAEVESALVEHEAVAEAAVVGHPHPVKGECLVCEVEL COCKE
1	1 1		FSPKLIEELKKQIREKIGPIATPDYTONADGI, DYTDGGYTMDDY.
6423			DRAIAQNDHDLGDMSTVADPSVISHLPSHRCITTO
0423	614	1237	ANLKEIPRDLPPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLS
1 1		Į.	KNGIEFIDEHAFKGVAETLQTLDLSDNRIQSVHKNAFNNLKARA
1 1	1		RIAMNEHUCOCOTI COLLI BOLL COLLIS DINRI OSVHKNAFNNLKARA
1			RIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRP
1 1		i	FLNAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQN
6424	ı		VEDARRHLE ILKSLPSROKKADEPDDISTIA/
	- 1	1188	KKVSWPVAAMVHCSCVLFRKYGNFIDKLRLFTRGGSGGMGYPRL
l 1	1	1	GGEGGREGDVWVVAHNRMTLKOLKDRVDRVDEVACUGANGVTGA
1 1	i	į	DAGSAGROWEI PVPVGISVTDENGKTIGELNKENDDIT TA OCCU
ľ	i	ļ	GGKLLTNFLPLKGQKRIIHLDLKLIADVGLVGFPNAGKSSLLSC
1 1	ł .	ì	VSHAKPAIADYAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH
1		1	MNKGMGHKRI KUTEDMROLE STEED SOFKQISVADLPGLIEGAH
	-		MNKGMGHKFLKHIERTRQLLFVVDISGFQLSSHTQYRTAFETII
			LLTKELELYKEELQTKPALLAVNKMDLPDAQDKFHELMSQLQNP
1	1		AUFUHUFERNMI PERTVEFOHTTPTSAVTCEGTERI VACTORGE
6425			DECANCENDALHKKOLLNLWISDTMSSTEPPSKHAUTTSVMDTT
0123	1850	1144	LAMEGGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWGFLLTG
	1	j	LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR
[l l	[CRRGSLUDIGGEDGETUIAAAWGCEFFVPAIMKQLENVVKMLR
	ĺ		CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA
	j	1.	WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE
1		1.	RELEDDARVIACRFPFPHWTPDHVTGEGIDTVWAYDASTPDCDF
6426	30		ARPCISMHFQLPIQA
0140	30	565	SRGAAVGGMSVAGGEIRGDTGGEDTAADGDESESDEDTLEDIDE
	1	1 1	LHAEFAAERDWEQFHQPRNLLLALVGEVGELAELFQWKTDGEPG
1		};	POGMSDEEDAT OFFI COM THE STATE OF THE PROPERTY
1	ſ	1.	PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI
l	i] -	WRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT
6427	145		sr ,
	113	959	ASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK
			VIREYVRWMYWIVFALFMAAEIVTDIFISWFPFYYEIKMAFVL
			TOTELIBLANAFVL

D Deginning nucleotide location corresponding to first mino acid maino acid maino acid maino acid maino acid maino acid sequence mino acid seq	SEO	Predicted	Predicted end	1 Amino and 1
No: nuclectide location corresponding to first amino acid residue of amino acid residue of amino acid sequence	ID			Amino acid segment containing signal peptide
corresponding to first amino acid amino acid as an acid conting to first amino acid amino acid as amino acid as amino acid sequence acid sequence acid seque	NO:			Glutamic Acid E-Phonelal
to first amino acid residue of smino acid sequence Peroline, Q-Golutamine, R-Arginine, sequence Sequence				H-Wistiding T-Iselandanine, G=Glycine,
to first amino acid residue of sequence sequence sequence sequence sequence sequence sequence sequence sequenc	- {	corresponding		LeLeucine M-Mathionine, K-Lysine,
residue of amino acid sequence				P=Proline O-Glutamine D number
amino acid sequence s	į.	amino acid		Seserine Temponine, KeArginine,
sequence Sequence Sequence Codon, /-possible nuclectide insertion		residue of	1	W=Truntonhan V=Truncia
V=possible nuclectide insertion		amino acid		Codon /-nossible muslestia di di di di
### ### ### ### ### ### ### ### ### ##	1	sequence		\=nossible nucleotide detetion,
LSFGRRGINTARSAWOARTKSGALAGRIKRSTSMQDIRSTSIDE PARAYNPILYLEDQUSHRPPIGYRAGGLOSPITEBECKSITEA VPRAPARPREKPILYLEGOGSHERPIGYRAGGLOSPITEBECKSITEA VPRAPARPREKPILTSGGLRVURKEPPVREGTSRSLKVRTRKXT VPRAPAR 6428 1982 444 SGSGGKMEDIGHYDIGTSKLLDWINDRERESLKKGGLIVLTRE EKINAALODLOSSYSTHYPHCLRILDLIKGTEAST KNIFGRYSSORMKOMEILALSGSYTHYPHCLRILDLIKGTEAST KNIFGRYSSORMKOMEILALSKONTYLVELSLLVINNVNYLI PSILKVOLAKCOLOGOSYSTKEBECQAGAARMRQGEHCKOYGOTI TGENNRGELLALVKOLPSGYSTKEBECQAGAARMRQGHCEATOVQASVOP VCESPTEQVILDMLRVQKGRONSTVISHRTGTEBSVHCKGYGTI TGENNRGELLALVKOLPSGYGLABEAGGIGEATOVQASVOP VCESPTEQVILDBLEBLEILFAGARVELSEEADAGIDMGIFFESISS KOPGGDEIDMGDRAVALQITVLBAGTQAPEGVARGDALTILLEY TETRIQPIDELMELBIITAGARAVELSEEADALSVSGYGLAPALL QGGYTKERWYMWSVLEDLIGKLISLOLGHIFMILASPRYVDRVT TETRIQPIDELMELBIITAGARAVELSEEADALSPKULDLILKK TRELQKLIBADISKRYSGRPVAINMTGL GESSKTAMARGGLLARVELWYKQQGALEQALBPKULDLILKK TRELQKLIBADISKRYSGRPVAINMTGL BYSSKTAMARGGLLANVKORGALBARALSPKSTRYVDRVT VVKSVTDKDAGDYLCVARNKVGDDVVLKVDVWRASHATSHKSE HOKKYFKGGOLLVOPHSPEISSNELDGGSINSSMGSDDS GGRTKRYVVENNGTLYRNEVGRBEGDYTCFABNOVKDEDMRYN VAVVTAPATIRNKCLLAVOVPKSDLEVTVHOKGGLDIFNSAMGSDDS GGRTKRYVVENNGTLYRNEVGRBEGDYTCFABNOVKDEDMRYN VAVVTAPATIRNKCLAVOVPKSDLEVTVHOKGGLDIFNSAMGSDDS GRRTVRHVNOPPKINGPNPITTVYELGRGGDIFNSAMGSDDS GRRTVRHVNOPPKINGPNPITTVYELGRGGDIFNSAMGSDS DEKTVHHVNOPPKINGPNPITTVYELGRGGDIFNSAMGSTRN VAVVIPABATIRNKCLAVORTSTRUKTLANGSGENKLIDCKABG PITRULMAPPSGVULDAPYCONTTVLORMGERIFNSAMGYINN USINGSTLKLDCTPPQAAQGRFSWTLINKVOLKPARROYHNIL LDNGTLTVREASYPDAGGSSSPLAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG			 	WILEDVINGACITYER FRANCE CONTROL CONTRO
### PARAYIDELYLED/USHRRPP1GYRGGLQDSDTEDEGUSTTER ### VPRAPARPREKPLIRSQLRUVRKRPDVREGTSRILKVRTRKKT ### VPRAPARPREKPLIRSQLRUVRKRPDVREGTSRILKVRTRKKT ### VPRAPARPREKPLIRSQLRUVRKRPDVREGTSRILKVRTRKKT ### SGSGKMEDMIGHTP1DTSKLLDMILVDRERGSLKWGGLULTTR ### SGSGKMEDMIGHTP1DTSKLLDMILVDRERGSLKWGGLULTTR ### SGSGKMEDMIGHTP1DTSKLLDMILVDRERGSLKWGGLULTTR ### SCHANGLOLD/STRIKEBELOLLSGSYTHYPHCLRILDLIKGTEAST ### KNIFGRYSSGMEDMIGHT ILLYEKDNTYILUTLISLUVRIVNYBIL ### PERVAEDALDWIGDFOVERVSEGTDSGISABAAGIDWIJONGSVUG ### VCUSSTER/UN-DELMELISTLAGRAVELSGERDVLJSVSSGFOLAPALI GOGTTERKYVMTWSVLEDLIGKKIJSLOLD/BEDARAGDALTILLEY ### TETRNQFIDELMELISTLAGRAVELSGERD/ULSVSSGFOLAPALITLEY ### TETRNQFIDELMELISTLAGRAVELSGERD/ULSVSSGFOLAPALITLEY ### TETRNQFIDELMELISTLAGRAVELSGERD/ULSVSSGFOLAPALITLES ### TETRNQFIDELMELISTLAGRAVELSGERD/ULSVSSGFOLAPALITLES ### TETLOKLIBADISKRYSGRAVULIGKKIJSLOLD/HTLASPRYVDRVT ### BELQKILKOSGLLALKKLMVVKQGEALEEQAALEPKDLILLEK ### TETLOKLIBADISKRYSGRAVULIGKKIJSLOLD/HTLASPSTYUDRVT ### BELGKLIBADISKRYSGRAVULIGKKIJSLOLD/WIGHENEKSIN ### VAWYTAPALTRIKTCLAVQVPYGDVVTVACEAKGEPMEKVTIMLS ### VAWYTAPALTRIKTCLAVQVPYGDVVTVACEAKGEPMEKVTIMLS ### PERVINARPPEGVULPAPYYGNRITTHGRGSILLICKAEG ### GORTKYVVILYPROGTATIVACEAKGEPMEKVTIMLS ### PERVINARNAGEGRALLIVOLTVLLEMMERP JEHDPISEKITAMAGH ### TISLINGSAAGTSTTSLWVLIPNGTDLQSGGOLQRPYKHARGMLIH ### BEGLSSVDAGAYRCVARNAGETRILTVAGGSSKLILDCKAEG ### TISLINGSAAGTSTTSLLWVLIPNGTDLQSGGOLQRPYKHARGMLIH ### TISLINGSAAGTSTTSLLWVLIPNGTDLQSGGOLQRPYKHARGMLIH ### TISLINGSAAGTSTTSLLWVLIPNGTDLQSGGOLQRPYKHARGMITH ### TISLINGSAAGTSTTSLLWVLIPNGTDLQSGGOLQRPYKHARGMITH ### TISLINGSAAGTSTTSLLWVLIPNGTDLQSGGOLQRPYKHARGMITH ### TISLINGSAAGTSTTSLLWVLIPNGTDLQSGGOLQRPYKHARGMITH ### TISLINGSAAGTSTTSLLWVLIPNGTDLGTCKTSTLLVTAPPR ### TISLINGSAAGTSTTSLLWVLIPNGTDTLQSGGOLQRPYTHAGGGOLGAAGEPUT ### TISLINGSAAGTSTTSLLWVLIPNGTDTLQSGGOLGAAGEPUT ### TISLINGSAAGTSTTSLLWVLIPNGTDTLGTTSLLGKRSSVLIPNGTTSLLEKKNIPNGTAAGTSTSLLEKKNIPNGTAAGTSTSLLEKKNIPNGTAAGTSLLEKKNIPNGTAAGTSLAGAAGTSCHLEKKNIPNGTAAGTSLAGAAGTSCHLEKKNIPNGTAAGTSLAGAAGTSCHLEKKN				LSEGREGINIAGENICALTICOGAL DOLL DOLL DOLL DOLL DOLL DOLL DOLL DO
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PSIKKQIAKCQLOCOBYSRREESCQAGABEREOFYSISCKQYGI TGENVARGELLALVKULPSQLAE IZAAQOSIGEATDVQASVOF VCESPPEQULPMLEFUQKRONSTVYENRTGTB PSVVERPHLEEL PEQVAZEDATINGEDFOVEAVSEGTDSGISAEAAGIDMGIFFESDS KDEGGDGIDWGDDAVALQITVLEAGTQAFEVAKEPGTBAILLERY TETRROFIDBLMELEIFLAQRAVELSEEADULSVSQFQLAPATL QGGTKRWYTMVSVLEDLIGKLISJOLOHLPMILASPRYDRWY BEHQQKLKOSQLIALKKELMVQKQQEALEEQAALEPKLDILLEK TRELQKLKOSQLIALKKELMVQKQQEALEEQAALEPKLDILLEK TRELQKLIFADISKRYSGRPVLMATTSL 6429 3413 3442 BPSSMTAAPROPLAAMPLERAAVGEDDRRALSPDERTKVFANGTL WINKSYTEDGLKVDCVARTKVEDWYUKVDVVMKPAKIEHKEE NDHKVFYSGDLKVDCVATGLPNPEISWSLPDGSLVNSFRQSDDS GGRTKRYVVFNNTTLIFREVGKREEGDYTCFAENOVGKDEMRVR VKVVTADATIRNKTCLAVQVFYEGDVVTVACEAKGEMPKYTMLS PINKVIPTSGSKYQIYQDGTLLIOKAQRSDSGNYTCLVENNSAGE DRKTVWHINVNQPPKINGNPNPITVVREIAAGGSRKLIDCKAGE IPTRVLMAPPEGVVLDAPYYGNRTTVHGNSIDIISSLRKSDSV QLVCMARNEGEBALIVOLTVLERBANGSKILIDCKAGE IPTRVLMAPPEGVVLDAPYYGNRTTVHGNSIDIISSLRKSDSV QLVCMARNEGGALIVOLTVLERBANGSKILIDCKAGE IPTRVLMAPPEGVVLDAPYYGNRTTHYBROSLDIISSLRKSDSV QLVCMARNEGGALIVOLTVLERBANGSKILICKAGE IPTRVLMAPPEGVVLDAPYYGNRTHVHGNSIDIISSLRKSDSV QLVCMARNEGGALIVOLTVLERBANGVRINL VSIINGETLKLPCTPGAQQGFSWTLPNMCHLEEGPCTLGRWSL LDNGTLTVREASYFDRGTYVCMMETETGESVTSIPVIVIAYPPR ITSSPTVTYTREGRITVKINCMAGIFKADITTHELPDKSHLKAG VOARLYGNRRLHEQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYHIVF ITSPTVTYTREGRITVKINCMAGIFKADITTHELPDKSHLKAG VOARLYGNRRLHEQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYHIVF TY				KNIFGPYGGODMYDWOGITALWSWATHOLRILDLLKGTEAST
TERNYRGELLALVKDLPSQLAFIGARAQQSIGEAIDVYQASVGP VCESPTEQVLMILTSPVQKRGNTSVERMTCTEPS VYREPHLEEL PEQVAEDAIDWGDFGVEAVSEGTDSGISAEAAGIDWGIFPESDS KDRGGGGIDWGDDAVALQITVLEAGTQAFEVARGPDAITLEY TETRNQPLDELMELEIFLAQRAVELSEEADVLSVSGCLAPAIL QGGTKERWYTWSVLEDLIGKLTSLOLGHLMTLASSRYVDRVT EFLQKLKGSGLLALKKELMVQKDEALEGAALEGYALEGYGCLAPAIL QGGTKERWYTWSVLEDLIGKLTSLOLGHLMTLASSRYVDRVT EFLQKLKGSGLLALKKELMVQKDEALEGAALEGYALEGYGCLAPAILLEY TRELQKLIEADISKRYSGRPVALMGTSL BESSTTAARFOFLAAAVGEDDRRALSFDERIKVFANGTL VKSVTDKDAGDVLCVARNKVGDDVVVLKVDVVMKPAKIEHKEE NDHKVFYKGGLKVDCVATCHPNPEISWSLEPDGSLVNSFMQSDDS GGRTKRVVVENNTLLYNEVGMREEGDVTGAEROVGKDEMRWR VKVVTAPATIRNTCLAVQVPYGDVVTVACEAKGEPMFKVTMLS PINKVIPTSSEKVGIVQDGTLLIGAGSSRKLIDCKAEG DRKTVWHIHVNQPPKINGHPNPITTVREIAGGSRKLIDCKAEG DRKTVWHHVNQPPKINGHPNPITTVREIAGGSRKLIDCKAEG DRKTVWHHVNQPPKINGHPNPITTVREIAGGSRKLIDCKAEG DRKTVWHHVNQPPKINGHPNPITTVREIAGGSRKLIDCKAEG DRKTVWHHVNQPPKINGHPNPITTVREIAGGSRKLIDCKAEG DRKTVWHHVNQPPKINGHPNPITTVREIAGGSRKLIDCKAEG DRKTVWHHVNQPPKINGHPNPITTVREIAGGSRKLIDCKAEG DRKTVWHFFTSSEKVGIVADAYVGARSDSGMYTCHANGAGS DRKTVWHFTSSEKVGIVADAYVGARSDSGMYTCHANGAGS DRKTVWHTVNQFPKINGHPNPITTVREIAGGSRKLIDCKAEG DRKTVWHFTSSEKVGIVADAYVGARSDSGMYCHVANGAGSBCGOLQRFYHKADGMLH ISGLSSVDAGAYRCVARNAGGTERUVSUKGERDSGNTLIVKAEG DRKTVWHFTYNQFPFTVARPORGTVCRMFKIEGYBVTSIPVIVIAYPPR ITSENTCAARAGAGTPTGSLVWLONGTSDGSVTKTAMAGH TISLNCSAAGTFTPSLVWARNAGGTFTSVAVGGSTKTSLKAGK VAXLKACHARLPFTTPGAATTVANGAGSTKCAAKAILGSDSKT TYHVF 6430 1946 602 RTRVSTGLRFHLWSEAVGASSTRGDTGIFGSGGGGGGGGGG AMLEAMABESPSBPPPTLKPETGPPEKRTSTERLQAPDSATLLEMW LKDSLFPLDGFKVARSSKRBAADAGFTGPGFGGRKRSRIKKSK KRIKKKAEGRELPPFGPQAPPFGFGAPPSDTDSEEGEBEEREEMEN TVVGGEAPPVULPTPPEAPRPPATUTPEGGRKRSRIKKSK KRIKKARAGRGRLPPFGPQAPPFGPQAPPDFDGAPBDESKEVGSTE TSQGGLASSECGHWRMDEITMFETGGGRKRGAYAGKMEATTAGVGR MECSLCGTWHLSCAKKKTNVPDFFYCQKCKELRPEARGG GPPKSGEP MTMCSLCGTWHLSCAKKKKTNVPDFFYCQKCKELRPEARGG GPPKSGEP WHSCSCP IESVILANLAPRKPDWDLKRGDVAKKLEKLKKRTQRAIAELIRER LKGGEDSLASAVDAATEQKTQROVERVKGGLEAAVPEV IESVILANLARSKTGRKLKALREKTGRKKLENLTKGRAIAELIRER LKGGEDSLASAVDAATEQKTQDSLTKULLUTLIDIDSKGR FFSCKLISKGAKSCFCLISLYMPW				RATTORISSORMADWOETTALYEKDNTYLVELSSLLVRNVNYET
VCSSTEGVLPMLKFVGKROSTVVENRIGTEBSVVERPHLEEL PROVAEDALDINGSDEVARNSEGTGSARAAGIDMGIFPESDS KDRGGGGIDMODDAVALGITVLEAGTQAPEGVARGPDALTLLEY TETRNOPILDELMELEIFLAQRAVELSERADUSVSGPGLAPAIL QGQTKERKWYMVSVLEDLIGKLISJOLGHLPMILASPRYVDRAVI EFLQQKLKGSGLLAALKKELMVQKQGEALEPKIDLLIEK TRELQKLKGSGLLAALKKELMVQKQGEALEPKIDLLIEK TRELQKLKGSGLLAALKKELMVQKQGAALEPKIDLLIEK TRELQKLIFADISKRYSGRPVILMGTSL 6429 3413 3442 BESSMTAARROPLAAMPLEAAVGEDDRRALSFDSRIKVFANGTL UVKSVTDKDAGDYLCVARNKVGDDYVLKVVLVVWKFAKIHKEE NDHKVFYGGLLKVDCVATGLNPDEISWSLPDGSLVWFANGTL UVKSVTDKDAGDYLCVARNKVGDDYVTVACHAGFAKIHKEE NDHKVFYGGLKVDCVATGLNPDEISWSLPDGSLVWSFMGSDB GGRTKRYVVENNGTLLFNSUGKREEGDYTCFAENOVGKDEMRVR VKVVTAPATIRNKICLAVQVPYGDVTVACHAGRSDEIMFKTMLS PINKVIPTSSEKYGIVQDGTLLIOKAGRSDSGNYTCLVRNSAGE DRKTVWHINVNOPPKINGRNPDITVELPAGRGSRKLILOCKAEG IPTPRVLWAPPEGVVLPAPYYGNRITVHGMSSLDIRSLKXSDSV QLVCMARNEGERALLVOLTVLEPMERY IPHDISSKITAMAGH TISLNCSAAGTPTPSLVWVLPNGTDLOGSQOLOGFYKAGDGMLH ISGLSSVDAGAYRCVARNAAGHTGRLVSLKVGLKPBANKQYINL VGINNGSTLKLPCTPPGAQQGFSTLIPMOHLEGPQTLGRVSL LDNGTLTVREASVPDRGTYVCRMETEGSPSVTSIPVIVIAYPPR ITSEPTFVTYTRRGHTVKLNCMANGIFKADITHELPDKSHLKAG VQARLVARNRLEHGGSLTIGHATORDAGFYKCMAKNILGSDSKT TYHVF ITSEPTFVTYTRRGHTVKLNCMANGIFKADITHELPDKSHLKAG VQARLVARNRLEHGGSLTIGHATORDAGFYKCMAKNILGSDSKT TYHVF GTFVKKAKSSKRAAQAGPTOPGPFBSTFSRIQAPDSATLLEKM KLKOSLSPDLLGFKVASSLSSPTSLTHTSRPPAALTPVLGSCGLE HPPKKKORNNKLIGGGAAGMFUGPBFSTFSRIQAPDSATLLEKM KLKOSLSPDLLGFKVASSLSSPTSLTHTSRPPAALTPVLGSCGLE HPPKKKORNNKLIGGGAAGMFUGPBFTFFTGVAPCSSVLA KRKLKKAERGDRLPPPGPQAPPSDTDSEBEBEEEEEBREMM TVVGGEAPVPULPTFPEAPRPATUTHEGVPPADESSKEVASTE TSQGGASSSGEGMRVMDEDIMMESPRTFTGLAPDSATLLEKM KRKLKKNEWNENDEIMMESDDBMDLITCYCKKPPAGR MIECSLCGTWHLSCAKIKKTNVPDFFYCQKCKELRPEARLG GPPKSGEP 6431 3 605 WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEBALRREBRLKALRRKTGRKDKEGGEBKTFHLREEEEBGEKH RELIKRNYPBEDELKKRRVPQAKPEKVKGGLEARAFEBF IEBVLAMILAPRKPDWDLKKBUVAKKLEKLKKRTQRATAELIRER LKGGEBSLAASVDAATCKKTORD LKGGESCLASSVDAMSCLIKKHTVATKDOEMO GGLGTMGSRIKQNPETTFEVYVEVAPPRTGGTLSDPEVQRGFFE DYSDGEVLQTILTKFCFFFYVOSLTVAUMFVLLMILLDLDYTKKOGEMO	1	,		TGPN/PGELLALUKUL DOOLADIAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
PEÇVAEDAIDWGDFGVEAVSEGTDSGISAEAAGIDWGI FPESDS KDEGGGIJWGDDAVALQITVURGOPAGHGVARGDAICHLISF TETRNOFIDELMELEI FLAQRAVELSEEADVLSVSQFQLAFAIL QCGYTEKWYTMYSVLEDLIGKLTSLOLGHLFMILASSRYVDRVT EFLQKLKGSQLLALKKELMVQKQEALEGAALEGPAALEFYLDLLEK TRELQKLIEADISKRYSGRFVAILMGTSI. 6429 3413 3442 EFSSKTAARRGPLAAHBILEAVGLEDDRRALSFDSRIKVFANGTL VVKSYTDKDAGDVLCVARKVGDDVVLKUDVWKRAKIEHKEE NDHKVYFGGLKVDCVAATGLPNET SIGNLPDGSLVNSFMQSDDS GGRTKYVVFNNGTLYFNEVGMREEGDYTGFAENOVGKDEMRVR VKVYTAPATIRNKICLAVQVFYGDVVLKVDVWKRAKIEHKEE DRKTVWHINVQPPKINGRPNPITTVREIAAGGSRKLIDCKAEG DRKTVWHINVQPPKINGRPNPITTVREIAAGGSRKLIDCKAEG DRKTVWHINVQPPKINGRPNPITTVREIAAGGSRKLIDCKAEG DRKTVWHINVQPPKINGRPNPITTVREIAAGGSRKLIDCKAEG DRKTVWHINVQPPKINGRPNPITTVREIAAGGSRKLIDCKAEG DRKTVWHINVQPPKINGRPNPITTVREIASGSRKLIDCKAEG DRKTVWHINVQPPKINGRPNPITTVREIAGGSRKLIDCKAEG DRKTVWHINVQPPKINGRPNPITTVREIBAGGSRKLIDCKAEG DRKTVWHINVQPPKINGRPNPITTVREIBAGGSRKLIDCKAEG DRKTVWHINVQPPKINGRPNPITTVREIBAGGSRKLIDCKAEG DRKTVWHINVQPPKINGRPNPITTVREIBAGGSRKLIDCKAEG DRKTVWHIPTSGEBOULDAYVGNGSDBJGCHQFFYHRADGHL TISLNCSAAGTPPPGLVWUPNGTDLUGSGDLGRFYHRADGHL TISLNCSAAGTPPFUVWUPNGTDLUGSGDLGRFYHRADGHL TISLNCSAAGTPPFUVWUPNGTDLUGSGDLGRFYHRADGHL TISLNCSAAGTPFDFUVWUPNGTDGSBYNTGHNGWHILGSDSKT TYLHVF 6430 1946 602 RTRVSTGLRTTLLWSEAVGASSTRGDTGIFGSGGGAGAGGGGG AMLEAMAEPSPBDPPPTLXPETQPPERKRTIEDFNKFCSFVLA YAGYIPPSKESDWPASGSSSPLRGSSADSOMDSAPSDLRTI QTFVKKAKSSKRRAAQAGPTQDPPERGDGSKRSRIKKSK KLKLKKASKGRLPPPGGPQAPPSDTDSEEGEBEEBEREMA TVVGGEAPPVUPTPPEAPRPALITVPUPLSQGDLS HPPRKKDRKNRKLGPGAGAGRGVGURRPRFFTGGGSKRSRIKKSK KRLKKAERGRLPPPGGPQAPPSDDDSSEEBEEBEEBEREM TVVGGEAPPVUPTPPEAPRPDATTVHEGUPPADGESKEVGSTE TSQGGDASSSEGEMRVMDEDIMESGDSWMDLITCYCKKPPAGR PMIECSLCGTWHLSCAKIKKTNVPDFFYQKKERLREEEEBEREM TVGGGASSGEGEMRVMDEDIMESGDSWMDLITCYCKKPPAGR PMIECSLCGTWHLSCAKIKKTNVPDFFYQKKERLREEEBEREME RELERANTERIKALREKTGRKDKEGEBKHTHLREEEBERGEKH RELERANTYPBEDELKKREVQAKKLEKLKKRTQRAIAELIRER LEGGBSJASAVDAATEOKTODSD 6431 3 605 WWSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEPALARKERLKALREKTGRKDKEUGKKHVKAGARAPEPY IEEVDLANLARRKPDDWDLKROPAVERKVKGOLBARAPEPY IEEVDLANLARRKPDD	1	l		VCECPEROUI DMI DELOVEDANOMINICATION DELOVEDANOMINIC
KORGOBGIUMGDDAVALQITVLEAGTQAPEVARGEDALTLLEY TETRNOFLDEBLESIFLAGAVELSEADAULSVSOFOLAPAIL GCGCYKEKAVTWYSVLEDLIGKLTSLQLQHLFMILASPRYUDRVT EFLQKLKGSQLLAKKELMVQKQGALEEQAALEFKLDLLLEK TRELQKLEADISKRYSGRPVINMGTEL 6429 3413 3442 EPSSWTAAPRGPLAAHPLEAAVQEDDRRALSFDSRIKVFANGTL VVKSVTDRDAGDYLCVARNKYDDVVJKKVDVMKPAKLEHKEE NDHKVFYGGDLKVDCVARGLPNPEISWSLPDGSLVNSFMQSDDS GGRTKRYVVFNNGTLYPNEVGMEEGDYTCFAENOVGKDEMRVR VKVVTAPATIRNKTCLAVQVFYOVTVACEAKGEMPKVTULS PINKVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLVENSAGE DRKTYWHINNOPPKKINGNPHTTVREIAAGSGRKLIDCKAEG IPTPRVLMAPPEGVVLDAPYYGNRITVHGNGSLDIRSLKKSDSV QLVCMARNEGGEARLIVQLTVLEPMER, FIFHDPISEKITAMAGH ISGLSSVDAGAYRCVARNAAGHTERLVSKKVGLKPEANKQYHNL ISGLSSVDAGAYRCVARNAAGHTERLVSKKVGLKPEANKQYHNL ISGSSVDAGAYRCVARNAAGHTERLVSKKVGLKPEANKQYHNL ISGSSVDAGAYRCVARNAAGHTERLVSKKVGLKPEANKQYHNL ITSEPTPVIYTRPGNTVKLNCMAMGIRGFOXGGRVSKTLAKAG VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMARNILGSDSK LDNGTLTVTRRASVPDRGTTYCRMETSYGPSVTSIPVIVIAYPPR ITSEPTPVIYTRPGNTVKLNCMAMGIRGFOXGAGGGGG AMLEAMAEPSPEDPPPTLKPETQPPEKRRTIEDFNKFCSFVLA YAGYIPPSKEESDWPASGSSSPLRGBSAADSGGNDSAPSDLRTI QTFVKKAKSSKRRAAQAGFTQGPPRSTTSILQAPDSATLLEKK KLKDSLFDLLGFKVASPLSPTSITHTSRPPAALTPVPLSQGDLS HPPRKKNRKNKLGGGAGAGFGGFPRSTTSILQAPDSATLLEKK KLKDSLFDLLGFKVASPLSPTSITHTSRPPAALTPVPLSQGDLS HPPRKKNRKNKLGGGAGAGFWRPPPTDTAHPEGGEKSRIKKSK KRILKKAERGDRLPPDGPDQAPPSDTDSEEEEEEEEEEMA TVVGGBAPVPVLPTPPBARPPATVHPEGGEKSGSVGSTT TSGDGDASSEGGMRWMDEDIWURSGDDSNDLITCYCRKPPAGR PMIECSLCOTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRG GPPKSGEP WIECSLCOTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRG EEEALRRUKGRRLKAARREKTGRKDKEDGEPKWHLHREEEEEGEHK RELRLKNYVPEEDDLKKRRVQARVAVEEKVKSOLBAARPEV IEEVDLANLAPRKPDWDLKRDVAKKLELKKRTGRAIAELIRER LKGGEDSLASAUDAATEGKTCDSD GGGGTKKGNPFTFEVVVEVAYPRTGGTLSDEVÇGRPFE DYSDGEVLQTLTKFCFFFYVDSLTVSQVGONFTFULTDIDSKQR FGFCKLSSGAKSCFCLISLYLDWTKKLDEDTKKROENO	1			PEOVAEDA TOWODEGUEANGEGEROS COLOR DE CO
TETRROFIDELMELSITIAORAVELSEERDVLSVSOFLAPAIL QGGYERKWATWSVLEDLIGKUTSLOLOHLFMILASPRYDRUT EFLQOKLKOSQLLALKKELMVOKQQEALEEQAALEPKLDLLLEK TKELQOKLKOSQLLALKKELMVOKQQEALEEQAALEPKLDLLLEK TKELQOKLKOSQLLALKKELMVOKQQEALEEQAALEPKLDLLLEK TKELQOKLKOSQLLALKKELMVOKQQEALEEQAALEPKLDLLLEK TKELQOKLKOSQLLALKKELMVOKQQEALEEQAALEPKLDLLLEK TKELQOKLKOSQLLALKKELMVOKQQEALEEQAALEPKLDLLLEK TKELQOKLKOSQLLALKKELMVOKQQEALEEQAALEPKLDLLLEK UVKSVTDKDAGDYLCVARNKVGDDYVVLKVDVVMKPAKTEHKEE NDHKVYKGDLKVDCVATGHDYVACEAKGEBMPKVTHLIS GGRTKRYVVFNNGTLYPNEVGMREEGDYTCFAENOVGKDEMRVR VKVVTAPATIRNKTCLAVQVYYGDVVTVACEAKGEBMPKVTHLIS PTNKVIPTSSKSKYQIYQDGTLLOKAQRSDSGNYTCLVENSAGE DEKTYWHINNOPPKINGNNPTTTVRETAAGGSRKLIDCKAEG DEKTYWHINNOPPKINGNNPTTTVRETAAGGSRKLIDCKAEG DEKTYWHINNOPPKINGNNPTTTVRETAAGGSRKLIDCKAEG TYSLMCSAAGTPTPSLVWLPNGTDLIGSQQLQFFYHKADGMLH 1SGLSSVDAGARVCVARNAAGHTERLVSLKVCHAEPBAKQYHINL VSIINGETLKLPCTPPGAGGGRSWTLPNGMELEGPQTLGRVSL LDNGTLTVREASVPDRGTTVCRMETSYGGSVTSIPVIVAYPPR TISLNCSAAGTPTPSLVWLPNGTDLIGSGQTQGGGGGGG AMLEANAEPSPEDPPTTLKPETQPSKKRRTIEDFNKRCSFVLA VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYLHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGGGAGPGGGGG AMLEANAEPSPEDPPTLKPETQPPSKRRTIEDFNKRCSFVLA KLKOSLPPLUEDFNAGSSSPLRGSSAADSDCMDSAPSDLRTI QTFVKKAKSSKRRAAQAGPTQPPPRSTFSRLQAPDSATLLEKM KLKOSLPPLUEDFNAGSSSPLRGBSAADSDCMDSAPSDLRTI QTFVKKAKSSKRRAAQAGPTQPPPPSTPSALTTVPLSQCDLS HPPRKKDRNKKLGPGAGAGGVLRFRPPTPSDCEKKERIKSS KRKLKKAERGDRLPPPGPPQAPPSTDSEEEEEEEEERERMA TVVGGAPVPVLUTTPPEARPPADDSESKEVGSTE TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKFFAGR MILECSLCTWHILSCAKIKKTNVPDFFYCQKCKELKPEARRIG GPPKSGPP MILECSLCTWHILSCAKIKKTNVPDFFYCQKCKELKPEARRIG GPRKSGPP IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRATAELIRER RELRERNVPPEBEDLKKRRVQAKPVAVEEKVKRQLEAARPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTCRATAELIRER LKQGEDSLASAUDAATECKTCOG				KDPGGDGTDWGDDAVALOTTULEAGTON BROWN BROWN
GQQTKKMYTMYSVLEDLIGKLITSLQLGILFMILASPRYDRAVDEPELGOKLKOSQLIALKKELWOKQGAALEPKLDLIEK TKELOKLISAGILALKKELWOKQGAALEPKLDLIEK TKELOKLISAGILALKKELWOKQGAALEPKLDALLEK TKELOKLISAGILAKKELWOKQGAALEPKLDALLEK TKELOKLISAGISKRYSGRPVNIMGTSL EPSSWTAAPROPLAAHPLEAAVOEDDVVLKDVVMKPAKIEHKEE NDHKVYFGGDLKVDCVATSLPHPEISWSLPDGSLINSFMOSDDS GGRTKRYVVFNNGTLYFHEVREEGDVTCAFAENOVGKDEMRVR VKVVTAPATIRNKTCLAVQVPYGDVTVACEAKGEPMRKVTWLS PTNKVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLVRNSAGE DRKTVWIHVNVQPPKINGNPRPITTVREIAAGGSRKLIDCKAEG IPTPRVLNAFPEGVVLPAPYYGNRITVHGNGSLDIRSLRKSDSV QLVCMARNEGEGRALIVOLLPEMEKIPHPIPISEKITAMAGH TISLNCSAAGTPTPSLVWVLPNGTDLQSGQQLQRFYHKADGMLH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGIKPEANKQYHNL VSIINGETLKLEPCTPGAGGGRFSWTLDNGMLESGPQTLGRVSL LDNGTLTVREASVPDRGTYVCRMETEYGPSVTSIPVIVIAYPPR ITSSPTPVIYTYPENTVKLMAMGIPKADTTWELPDKSHLKAG VQARLYGNRFLHPQGSLTIQHATQRDAGFKKCMAKNILGSDSKT TYIHVF TYHVF TYHVF G430 6430 1946 602 RTRYSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG AMLEAMAEPSPEDPPPTLKPETQPPEKRRRTIEDFNKFCSFVLA VAGYIPPSKESSWPASGSSSPLRGESAADSDGWDSAPSDLRTI TYHVF QTPVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGPKVASFLSFTSILTHTSRPPAALTPVLSGGDLS HPPRKKDRKNRKLGPGGAGGVLRRPPPTPGGGEKRSTIKKSK KRILKKARGGRLPPPGGPPARPPATVHPEGGEKRSTIKKSK KRILKKARGGRLPPPGGPQAPPSDTDSEEEBEEBEEBEEBEEBEE HPRKKDRKNRKLGPGGAGGURRPPPTGGGEKRSTIKKSK KRILKKARGGRLPPPGGPPARPPATVHPEGGPKRSTIKKSK KRILKKARGGRLPPPGGPPARPPATVHPEGGPKRSTIKKSK KRILKKARGGRLPPPGGPPARPPATVHPEGGPKRSTIKKSK KRILKKARGGRLPPPGGPPARPPATVHPEGGPKRSTIKKSK KRILKKARGGRLPPPGGPCARSTIKKSK KRILKKRYUPEDEDLIKGRYPQAKPVAVEKWKOLLEAARPBFV IESUDLANLAPRKPDMDLKRDVAKKLEKKRTORAIAELIRER RELRLRNYVPEDEDLIKGRYPQAKPVAVEKWKOLLEAARPBFV IESUDLANLAPRKPDMDLKRDVAKKLEKKRTORAIAELIRER LKGGDSLASAVDAATEGKTOLDED 6432 56 1692 GGLGTMGSRIKNPETTFEVYVEVAYPRTGGTLSDPEVORGFPE DYSDGEVLOTLTKFCFFFYVDSLITVSQVQGNFTFULIDLDSKGR FGFCRLSSGARSACGCTLISJVEFVEVYKLIILLADDTTKROENO	1			TETRNOPLDELMELETELACDAMES CONTROL CONTROL
6429 3413 3442 EPSEWTAPRGPLANDISHKYSGRPVNIMGTSL EPSSWTAPRGPLANDLEARAVQEDDRRALSFDSRIKVFANGTL VVKNVTDKDAGDYLLCVARNKVGDDYVVLKUDVMKPAKTEHKEE NDHKVFYGGDLKVDCVARTLENDETISMSLPDGSLINSFMOSDDS GGRTKRYVVFNNGTLIYFNEVGMREEGDYTCFAENOVGKDEMRVR VKVVTAPATIRKTCLAVQVPYGDVTVACEAKGEPMFKVTUKG PTNKVIPTSSEKYGIYQDGTLLIQKAQRSDSGNYTCLVRNSAGE DRKTVWIHNVQPFKINGNPRITTVERIAAGGSRKLIDCKAEG DRKTWHIHNVQPFKINGNPRITTVERIAAGGSRKLIDCKAEG DRKTWHIHNVQPFKINGNPRITTVERIAAGGSRKLIDCKAEG DRKTWHIHNVQPFKINGNPRITTVERIAAGGSRKLIDCKAEG DRKTWHIHNVQPFKINGNPRITTVERIAAGGSRKLIDCKAEG DRKTWHIHNVQPFKINGNPRITTVERIAAGGSRKLIDCKAEG DRKTWHIHNVQPFKINGNPRITTVERIAAGGSRKLIDCKAEG DRKTWHIHNVQPFKINGNPRITTVERIAAGGSRKLIDCKAEG DRKTWHIHNVQPFKINGNPRITTVERIAAGGSRKLIDCKAEG DRKTWHIHNVQPFKINGNPRITTVERIAAGGSRKLIDCKAEG DRKTWHIHNVQPFKINGNPRITTVERIAAGGSRKLIDCKAEG DRKTWHIHNVQPFKINGNPRITTVERIAAGGSRKLIDCKAEG DRKTWHIHNVQPFKINGNPRITTVERIAAGGSRKLICKAED VAGALYGRAFLHPGGSUTIQHATQRDGSQQLQFFYHAADGMLISGUSVDAGAPSTUWLLPGGQQQRFSWTLDRGHLISGUSTIAAGG TISLMCSAAGTPFPGGGGGRFSWTLDWGLERGPTVINAPPR ITSEPTPVIYTRPGNTVKLNCMAMGIFKADITWELPPKSHLKAG VQARLYGRRFLHPGGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYHUF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRDTGIPGSGGGAGPGGGGG AMLEAMAEPSPEDPPTILWPETQPSGERGAAPGGGGGGGGGGGGGGGAPGGGGGGGGGGGGGGGG	1		1	OGOTKEKMYTMYSVI.EDI.TCKT.TSI.O. OUT TOUT A GOVERNMENT
TRELOKLIBADISKRYSGRPVAILMTSL SEPSWTAAPGEPLAAMPLEAAVQEDDRRALSFDSRIKVFANGTL VVKSVTDKDAGDYLCVARNKVGDDYVVLKVDVMKPAKLEHKEE NDHKVFYGGLLKVDCVATGLPNPEISWSLPDGSLVNSFMQSDDS GGRTKRYVVFNNGTLYFNEVREEGDYTCFAENOVGKDEMRVR VKVVTAPATIRNKTCLAVQVPYGDVTVACEAKGEPMPKVTWLS PTNKVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLVRNSAGE DRKTWNIHVNVQPPKINGNPPHITTVREIAAGGSRKLIDCKAEG IFTPRVLNAFPEGVVLPAPYYGNRITVHGMGSLDIRSLRKSDSV QLVCMARNEGGEARLIVQLTVLEPMEKPIFIDPISEKTTAMAGH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL VSIINGETLKUDCTPPGAGGGFSWTLDNGHLEGPQTLGRVSL LDNGTLTVREASVPDRGTYVCRMETEYGPSVTSIPVIVIAYPPR ITSSPTFVIYTRPGNTVKLNCMAMGIPKDJUTKELPDKSHLKAG VQARLYGNRFHHPQGSLTIQHATORDAGFYKCMAKNILGSDSKT TYIHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGE AMLEAMAEPSPEDPPPTIKPETQPPEKRRRTIEDFNKFCSFVLA YAGYIPPSKESDWPASGSSPLRGESAADSDGWDSAPSDLRTI QTPVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGPKVASSLSFTSITHTSRPPAALTPVPLSGGDLS HPPRKKORKNRKLGPGAGAGFGULRRPRPTPGGGEKRSRIKKSK KRLKLKAERGGRLPPDGPDQAPPSDTDSEEEEEEEEEEEEEEEE TSQDGDASSSEGEMRVWDEDIMVESGDBMDLTCYGRKPFAGR PHIECSLCGFWHILSCAKIKKTNVPDFFCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WWNSSYNLPAYAFYLFCEACAMQDGRKGGAYAGKMEATTAGVGR EEEALRRNYVPEDEDLKKRRVFQAKPVAVEEKVKEGLEAAKPERV IEEVDLAANLAPRRDDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGGESLASAVDAATEGKTGDD 6432 56 1692 GGGTMSSIKNOPETTFEVYVEVAYPRTGGTLSDPEVQRGFFE DYSDGEVLGTLTKFCFFFYVDSLTVSQVGGNFTFFLITDDLSKGR				REPOOKINGSOFFFFEEFFEEFFEEFFEEFFEEFFEEFFEEFFE
### 1945 ### 3442 ### BEPSWTAAPRGPLAHPLEAAVGEDDRRALGFDSRIKVFANGTL VVKSVTDKDAGDYLCVARNKVGDDYVVLKUDVNKPANTEHKEE NDHKVFYGGDLKVDCVATGLPNPEISWSLPPGSLVNSFNGSDDS GGRTKRYVVFNNGTLYFNEVGMREEGDYTCFAENOVGKDEMRVR VKVVTAPATIRKTCLAVQVPYGDVVTVACEAKGEPMFKVTWLS PTNKVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLVRNSAGE DRKTVWHHVNVQPPKINGPRPITTVREIAAGGSRKLIDCKAEG IPTPRVLWAPPEGVULPAPYYGRNITVHGNSLDIRSLKXSDSV QLVCMARNEGGEARLIVQLTVLEFMEKPIFHDFISEKITAMAGH ISGLSSVDAGAYRCVARNAGHPERLVVLKVGLKPEANKQYHNL VSIINGETLKLPCTPPGAGQGRFSWTLPNGMHLEGPCTLGRVSL LDNGTLTVREASVFDRGTTVCRWETEYGPSVTSIPVIVIAYPPR ITSSETPVIYTTRPGATVKLNCMAMG;PKADITMELPHKSHLKAG VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYHUF ### 1946 ### 602 ### RTRVSTGLRTTLLWSEAVGASSTRGDTG PGSGEGGAGPGGGG AMLEAMAPPSPDDPPTTLKPETQPPEKRRTIEDFNKFCSFVLA YAGVIPPSKEBSDWPASGSSSPLAGSAADSDCWDSAPSDLRTI QTFVKKAKSSKRRAAQAGFTQFBPRSTFSRLQAPPDSATLLEKM KLKDSLFDLDGFKVASPLSFTSLLTHTSRPPAALTPVPLSGGDLS HPPRKKDRINKLGFGAGAGGVGVLRRPRPTPGGDGERSRIKKSK KRKLKKAERGDRLPPGFDQAPPSDTDSEEBEBEBEEBERBMA KRKLKKAERGDRLPPGFDQAPPSDTDSEEBEBEBEBEBERMA TVVGGBAVPVUPTPPEAARPPATVHPEGVPPADSESKEVGSTE PMIECSLCGTWHIHSCAKIKKTNVPDFFYCQKCKELRPEARRIG GPPKSGEP ### 15 605 ### 1692 ##				TKELOKI JEADI SKRYSGPDINI MOTTEL
WKSYTKKNÄGDYLCVARNKYGDTYVLKVDVVMKPAKIEHKEE NDHKVFYGGDLKVDCVARGLPNPEISMSLPDGSLVNSFMQSDDS GGRTKRYVVFNNGTLYFNEVGMEEGDYTCFAEROVGKDEMEVR VKVVTAPATIRKKTCLAVQVYYGDVTVACEAKGEPMEKTWILS PINKVIPTSEKYGIVJDGTLLIOKAGRSDSGNYTCLVRNSAGE DRKTWHIHVNVQPPKINGNPNPITTVREIAAGGSRKLIDCKAEG DRKTWHHVNVQPPKINGNPNPITTVREIAAGGSRKLIDCKAEG LIPTPRVLWAFPBGVVLDAPYYGNRITVHGNGSLDIRSLRKSDSV QLVCMARNEGGEARLIVOTLSPMEKEP JFHDPISEKITAMAGH TISLNCSAAGTFTPSLVWVLPNGTDLQSGQQLQRFYHKADGMLH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL VSIINGETLKLDCTPFGAGQGRFSWTLPNGMHLEGPGTLGRVSL LDNGTLTVREASVFDRGTVVCRMETEFYGPSVTSIPVIVIAYPPR ITSSPTPVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG VQARLYGRRFLHWSEAVGASSTRGDTGIPGSGGGAGFGGGE AMLEAMAEPSPEDPPTLKPETQPFEKRRTIEDFHKFCSFVLA YAGYIPPSKESDWPASGSSSPLRGBAADSDUMDSAPSDLRTI QTFVKKAKSSKRRAAQAGFTQFGPPRSTFSRLQAPDSATLLEM KLKDSLFDLDGPKVASPLSPTSLITHTSRPFAALTPVPLSQGDLS HPPKKNRKNRKLGPGACAGWGVLRPRPTFGGGEKRSRIKKSK KRKLKKAERGDRLPPFGDAPPSDTDSSEEBEEEEEBBEMA TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADESKEVGSTE TSQDGDASSEGGMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWIHLSCAKIKKTURPDFFYCQKCKELRPEARRIG GPPKSGEP MIECSLCGTWIHLSCAKIKKTURPDFFYCQKCKELRPEARRIG GPPKSGEP MWSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLEEEEBEGEKH RELRLRNYVPEDEDLKKRRVPQAKPAVEEKVKEQLEAAKPBFV LEEVDLANLAPRKFDWDLKRRDVAKKLEKLKKRTQRAIAELIRER LKGGEDSLASAVDAATEGVTCDSD 6432 56 1692 GGLGTMSSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRGFFE DYSDGEVLGTLTKFCFFFYYDSLTVSQVGQNFTFVILTDIDSKOR FGFCRLSSGAKSCFCLLSVLJWFFEVFYLLNILADAYTKROBNO	6429	3413	3442	EPSSWTAAPRGPLAAHPLEAAVOEDDPPALSEDGDIVVEAWORE
NDHKVFYGGLKVDCVATGLPNPEISWSLPDGSLVNSFMQSDDS GGRTKRYVVPNNGTLYPNEVGMREEGDYTCFAENOVGKDEMRVR VKVVTAPATIRNKTCLAVQVPYGDVVTVACEARGEPMFKYTWLS PTNKVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLJVRNSAGE DRKTVHIHVNVQPPKIMOPMPITTVREIAAGGSRKLIDCKAEG DRKTWHIHVNVQPPKIMOPMPITTVREIAAGGSRKLIDCKAEG DRKTWHIHVNVQPPKIMOPMPITTVREIAAGGSRKLIDCKAEG DRKTWHIHVNVQPPKIMOPMPHITVHONGSLDIRSLRKSDSV QLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGH TISLNCSAAGTPTPSLWVLDNTDLQSGQQLQRFYHKADGMLH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL VSIINGETIKLPCTPPGAGQGRFSWTLPNGMKLEGPOTLGRVSL LDNGTLIVREASVYDRGTVCKMETEYGPSVTSIPVIVIAYPPR ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG VQARLYGRRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYHHVF TYHHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG AMLEAMAPPSPEDPPPTLKPETDPPEKRRTIEDPMKFCSFVLA YAGYIPPSKESDWPASGSSSPLRGBSAADSDGWDSAPSDLRTI QTFVKKAKSSKRAAQAGFTQPGPPRSTFSKLQAPDSATLLEKM KLKOSLFDLDGFKVASPLSFTSIHTSRPPAALTPVPLSGGDLS HPPRKKDRKIRKLGPGAGAFGVLRRPRPTPGDGEKKRSRIKKSK KRLKKAERGDRLPPPGPPQAPPSDTDSEEEBEBEEEBEBMA TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADBESKEVGSTE TSQDGDASSSEGEMRVMDDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWHHISCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP MMSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR EEEPALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEEGEKH RELRRHYVPREDEDLKKRRVPQAKPVAKKLEKLKRTQRAIAELIRER ELEVDLANLAPRKPDWDLKKRVPQAKPVAKKLEKLREEEEGEKH RELRRHYVPREDEDLKKRRVPQAKPVAKKLEKLRETGRAIAELIRER LKGQEDSLASAVDAATECKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRGFFE DYSDQEVLQTILTKFCFPFYVUSLITVSQVGGNFTFVLIDJDSKQR FGFCRLSSGAKSCFCILSYLDWFEVYFKLINILADYTKRORNO				VVKSVTDKDAGDYLCVARNKVGDDVVVI KVDVVMKDAVTBUVBB
GGRTKRYVVPNOGTLYPNEVGMREEGDYTCFAENQVGKDEMRVR VXVVTAPATIRNKTCLAVQVPYGDVTVVACEAKGEPMFKVTWLG PTNKVIPTSSEXYQIYQGTTLLIQKAQRSDSGNYTCLJVRNSAGE DRKTVWIHUNVQPKINGNPMPITTVREIAAGGSRKLIDCKAEG IPTPRVLWAPPEGVVLPAPYYGNRITVHGNGSLDIRSIRKDDSV QLVCMARNBGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGH TISLMCSAAGTPTPSLWWLPNGTDLQSGQQLQRFYHKADGMLH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL VSIINGETLKLPCTPPGAGQGGFSWTLPNGMLEGPQTLGRVSL LDNGTLTVREASVFDRGTYVCRMETEYGPSVTSIPVIVIAYPPR ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYIHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG AMLEAMAPPSPBDPPPTLKPETQPPEKRRRTIEDFNKFCSFVLA YAGYIPPSKEESDWPASGSSSPLRGESAADSDWDSAPSDLRTI QTFVKKAKSSKRRAAQAGFTOPGPPRSTFSRLQAPDSATLLEKM KLKOSLFDLDGPKVASPLSPTSLTHTSRPPAALTPVPLSGGDLS HPPRKKDRKNKKLGPGAGAGFGVLRRPRPTPGGGEKRSRIKKSK KRKLKKAERGDRLPPPGPDQAPPSDTDSEEEBEEBEEBEEBEE HPPRKKDRKNKKLGPGAGAGFGVLRRPRPTPGGGEKRSRIKKSK KRKLKKAERGDRLPPPGPPDQAPPSDTDSEEEBEEBEEBEEBEE TSQDGDASSSGGEMEWDDDIMVESGDDSWDLITCYCRKPPAGR PMIBCSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP MIBCSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP MWNSSYNLPAVAPYLPCEACAMQGGRKGGAYAGKMEATTAGVGR LEEEALRRYVPEDBDLKKRRVPQAKFVAVEEKVKSQLEAAKPEPV LEEGALRRYVPEDBDLKKRRVPQAKFVAVEEKVKSQLEAAKPEPV LEEGALRRYVPEDBDLKKRRVPQAKFVAKLEKKKRTQRAIAELIRER LKGQEDSLASAVDAATECKTCDSD 6432 56 1692 GGLGTMGSRIKONPETTFEVYVEVAYPRTGGTLSDPEVQRGFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGGNFTFVLIDDISKQR FGFCRLSSGAKSCFCILSYLDWFEVFYKLINILADPTTKROBNO	1			NDHKVFYGGDLKVDCVATGLPNPEISWSLPDGSLVNSEMOGDDS
VKVVTAPATIRKTCLAVQVPYGDVUTACEARGEPMEKVTWLS PINKV1PTSSEKYQ1YQGTLLIQKAQRSDSGNYTCLVRNSAGE DRKTVWIHVNVQPFKINGNPNPITTVREIAAGSSRKLIDCKAEG IPTPRVLWAPPEGVVLPAPYYGRRITVHENGSLDIRSLRKSDSV QLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGH TISLNCSAAGTPPTSLVWVLPNGTDLQSGQQLQRFYHKADGMLH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL VSIINGETLKLPCTPPPGAGQRFSWTLPNGMELEGPQTLGRVSL LDNGTLTVREASVPDRGTYVCRMETEYGPSVTSIPVIVLAYPPR ITSEPTPVTYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYHHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG AMLEAMAEPSPBDPPPTLKPETQPPEKRRTIEDFNKFCSFVLA YAGYIPPSKEESDWPASGSSSPLRGBSAADSGDMSAPSDLRTI QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGFKVASFLSFTSLTHTSRPPAALTPVPLSQGDLS HPPRKKDRKNRKLGFGAGAGGGVLRPPPTGGEKRSRIKKSK KRKLKKAERGDRLPPPGPPQAPPSDTDSEEEBEEEBEEMA TVVGGEAPVPVLTPPEARPPATTVHPEGVPPADSESKEVGSTE TSQDEGDASSEGEMRVMDEDIMVESGDDSWDLITCYCRKPPAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WWMSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRYVPREDEDLKKRRVPQAKPVAVBEKVKEQLBAAKPEPV IEEVOLANLAPRKPDWDLKRDVAKKLEKLKKRTQRATAELIRER RELRRRYVPBEDEDLKKRRVPQAKPVAVBEKVKEQLBAAKPEPV IEEVOLANLAPRKPDWDLKRDVAKKLEKLKKRTQRATAELIRER LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGLGTMSSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRGFFE DYSDGEVLQTLTKFCFFFYVUEVAYPRTGGTLSDDEVQRQFFFE DYSDGEVLQTLTKFCFFFFYXLEUNILADVTYKROENO				GGRTKRYVVFNNGTLYFNEVGMREEGDYTCFAENOVCKDEMBUR
PINKVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLJVRNSAGE DRKTVNIHVNVQPPKINGNPNPITTVREIAAGGSRKLIDCKAGE IPTPRVLWAPPEGVUPAPYYGRITUHGNGSLDIRSLRKSDSV QLUCMARNEGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGH TISLNCSAAGTPTPSLVWUPPRGTDLQSGQQLQRFYHKADGMLH ISGLSSVDAGAYRCVARMAAGHTERLVSLKVGLKPEANKQYHNL VSIINGETLKLPCTPPGAGQGRFSWTLPNGMELEGPQTLGRVSL LDNGTLTVREASVPDRGTTVCRMETEYGPSVTSIPVIVIAYPPR ITSFPTPVTYTRPTAVTKLNCMAMGIPKADITWELPDKSHLKAG VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYHHV 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG AMLEAMAEFSPEDPPPTLKPETQPFPKKRRTIEDFNKFCSFVLA YAGYIPPSKESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI QTFVKKAKSKRAAQAGPTPOPPPRSTFSRLQAPDSATLLEKM KLKDSLFPLLDGFKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS HPPRKKDRKNRKLGPGAGAGFGVLRRPRPTFGDGEKRSRIKKSK KRKLKKAERGDRLPPDGPQAPPSDTDSEEEEEEEEEEEEMEMA TVVGGGAPPVPULTPPBAPPPPATVHPEGVPPADSESKEVGSTE TSQDGDASSSEGEMRWMDEDIMVESGDDSWDLTTCYCKKPFAGR PMIECSLCGTWHLLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WWMSSYNLPAYAPYLFCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKYPEDEDLKKRRVQAKFVAVEEKVKEQLBAAKPEPV LEEVDLANLAPKKEDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRGFFE DYSDGEVLQTLTKFCFFFYVVEVAYPRTGGTLSDPEVQRGFFE DYSDGEVLQTLTKFCFFFFYVSLETVSQUQNFTFVLIDIDSKGR				VKVVTAPATIRNKTCLAVOVPYGDVVTVACEAKGEDMDKVTWLC
DRKTVNIHVNVQPPKINGPNPITTYREIAAGGSRKLIDCKAEG IPTPRVLMAPPEGVVLDAPYYGNRITVHGNGSLDIRSLRKSDSV QLVCMARNEGEARLIVQLTVLEPMEKPI FHDPISEKITMAGH TISLNCSAAGTPTPSLVWVLPNGTDLQSGQQLQRFYHKADGMLH ISGLSSVDAGAYRCVARNAAGHTERLUSLKVGLKPEANKQYHNL VSIINGETLKLDCTPPGAGQGRFSWTLPNGMŁLEGPQTLGRVSL LDNGTLTVREASVFDRGTVVCRMETEYGESVTSIPVIVIAYPPR ITSEPTPVIVTRPGMTVKLNCMAMGIPKADITWELPDKSHLKAG VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYIHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAPGGGEG AMLEAMAEPSPEDPPPTLKPETQPPEKRRRTIEDFNKFCSFVLA YAGYIPPSKEESDWPASGSSSPLRGESAADSDCWDSAPSDLRTI QTFVKKAKSSKRRAAQAGFTQPGPPRSTTSRLQAPDSATLLEKM KLKOSLFDLDGPKVASPLSPTSITHTSRPPAALTPVPLSQGDLS HPPRKKDRKNRKLGPGAGAGFGVLRRPPTFGGGEKRSRIKKSK KRKLKKAERGDRLPPPGPPQAPPSDTDSEEEBEEEEBEBMA TVVGGEAPVPVLPTPPEARPPDATVHPEGVPPADSESKEVGSTE TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPPAGR PMIECSLCGTWHLLSCAKIKKTNVPDFFYCQKCKELKPEARRLG GPPKSGEP 6431 3 605 WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR EEEEALRRKGRLKALREKTGRKDKEDGEPKTKHLREEEEEGBKH RELLRLRNYVPEDEDLKKRVPQAKKPVAVEEKVKGQLEAAREEPV LEEEDLANLAPRKRPWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDEVQROFFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVQQNFTFVLTDLIDSKQR FFFCRLSSGAKSCFCLLSYLDWFEVFYKLINILADYTTKRGENO	1			PTNKVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLVPNSAGE
OLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGH TISLINCSAAGTPTPSLVWUPNGTDLQSGQQLQRPYKADGMLH ISGLSSVDAGGYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL VSIINGETLKLPCTPFGAGQGFFSWTLPNGMELEGPQTUGRVSL LDNGTTVRZASVPDRGTYVCRMETEYGPSVTSIPVIVIAYPPR ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITMELPDKSHLKAG VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYIHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGFGGGEG AMLEAMAEPSPEDPPPTLKPETQPPEKRRTIEDFNKFCSFVLA YAGYIPPSKEESDWPASGSSSPLRGESSADSDGWDSAFSDLRTI QTFVKKAKSSKRRAAQAGFTQPGPRSTFFSLQAPDSATLLEKM KLKDSLFDLDGPKVASPLSPTSITHTSRPPAALTPVPLSQGDLS HPPRKKDRXNRKLGPGAGAGFGVLRRPRPTPGGGEKRSRIKKSK KRKLKKAERGDRLPPPGPPQAPPSDTDSEEBEBEBEBEBEBMA TVVGGEAPVPVLIPTPBEAPRPPATVHPEGVPPADSESKVGSTE TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEBEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEBGEKH RELLRRNYVPEDEDLKKRRVQAKPVAVEEKVKGQLEAARPBPV LEEWDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDEVQROFFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVQQNFTFVLTDLIDSKQR FGFCRLSSGAKSCFCLLSYLDWFEVFYKLINILADYPTTKRGENO	1			DRKTVWIHVNVQPPKINGNPNPITTVREIAAGGSRKLIDCKAEG
QLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGH TISLNCSAAGTPTPSLVWVLPNGTDLQSGQQLQRFYHKADGMLH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL VSIINGETLKLPCTPPGAGQGRFSWTLPNGMHLEGPQTLGRVSL LDNGTLIVREASVFDRGTYVCRMETEYGPSVTSIPVIVIAYPPR ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYIHVF 6430 1946 602 RTRVSTRILWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG AMLEAMAEPSPEDPPPTLKPETQPPEKRRRTIEDFINKFCSFVLA VAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGPKVASPLSFTSLTHTSRPPAALTPVPLSQGDLS HPPRKKDRKNRKLGPGAGAGFGVLRRPRPTPGDGEKRSRIKKSK KRKLKKAERGDRLPPPGPPQAPPSDTDSEEEBEEBEEBMA TVVGGEAPVPVLPTPPEAPRPDATVHPEGVPPADSESKEVGSTE TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPPAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDREDGEPKTKHLREEEEEGEKH RELRLNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV LEEVDLANLAPRRPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRGPPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FFFCRLSSGAKSCFCILSYLPWFEVFYKLINILADYTTKROENO	1 1			IPTPRVLWAFPEGVVLPAPYYGNRITVHGNGSLDIRSLRKSDSU
TISLNCSAAGTPTPSLVWULPNGTDLQSGQQLQRFYHKADGMLH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNI VSIINGETLKLPCTPPGAGQGRFSWTLPNGWHLEGPQTLGRVSL LDNGTLTVREASVFDRGTYVCRMETEYGPSVTSIPVTVIAYPPR ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG VQARLVGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYIHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG AMLEANAEPSPEDPPPTLKPETQPFEKRRTIEDFNKFCSFVLA YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS HPPRKKDRKNRKLGPGAAGAGVGURRPRPTPGDGEKRSRIKKSK KRKLKKAERGRLPPPGPPQAPPSDTDSEEEEEEEEEEEEMA TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE TSQDGDASSEGGEMRWDEDINVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WWNSSYNLPAYAPYLFCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEEGEKH RELRRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGLGTMGSRIKQNEETTFEVYVEVAYPRTGGTLSDPEVQRGFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLINILADYTTKROENO		1		QLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGH
ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL VSIINGETLKLPCTPPGAGQGFFSWTLPNGMHLEGPQTLGRVSIL LDNGTTJVREASVFDRGTTVVCRMETEYGPSVTSIPVIVIAYPPR ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELDKSHLKAG VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYIHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG AMLEAMAEPSPEDPPPTLKPETQPPEKRRRTIEDFNKFCSFVLA YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM KLKDSLFPLDGPKVASPLSPTSLTHTSRPPPAALTPVPLSQGDLS HPPRKKDRKNRKLGPGAGAGFGVLRRPRPTPGDGEKRSRIKKSK KRKLKKAERGDRLPPPGPPQAPPSDTDSEEEEEEEEEEEEEEMA TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WWMSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALRKTRKKDEDGEPKTKHLREEEEEGEKH RELRRLNYVPBCBEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER EKGGEDSLASAVDAATEQKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVQQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLINILADYTTRROENO				TISLNCSAAGTPTPSLVWVLPNGTDLOSGOOLORFYHKADGMLH
VSIINGETLKLPCTPPGAGQGRFSWTLPNGMHLEGPQTLGRVSL LDNGTLTVREASVFDRGTYVCRMETEYGPSVTSIPVIVIAYPPR ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG VQARLYGNRFLHFQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYIHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG AMLEAMAEPSPEDPPPTLKPETQPPEKRRRTIEDFNKFCSFVLA YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI QTFVKKAKSSKRRAAQAGFTQPGPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS HPPRKKDRKNRKLGPGAGAGFGVLRRPRPTPGDGEKRSRIKKSK KRKLKKAERGDRLPPPGDPDAPPSDTDSEEEEEEEEEEBEMA TVVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKSRLKALREKTGRKDKEDGEPKTKHLREEEEGEKH RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLINILADYTTKROENO	1	1		ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKOYHNI.
LDNGTLTVREASVFDRGTYVCRMETEYGPSVTSIPVIVIAYPPR ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG VQARLYGRRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYIHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAFFGGGEG AMLEAMAEPSPBDPPPTLKPETQPPEKRRRTIEDFNKFCSFVLA YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI QTFVKKAKSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGPKVASPLSFTSLTHTSRPPAALTPVPLSQGDLS HPPRKKDRKNRKLGFGAGAGFGVLRRPRPTPGDGEKRSRIKKSK KRKLKKAERGDRLPPGPPQAPPSDTDSEEEBEEEEEBEEMAA TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRYKPFBEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRATAELIRER LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGLGTMGSRIKONPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLINILADYTTKROENO				VSIINGETLKLPCTPPGAGQGRFSWTLPNGMHLEGPOTLGRVSI.
ITSEPTFVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYIHVF RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG AMLEAMAEPSPEDPPPTLKPETQPPEKRRRTIEDFNKFCSFVLA YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALITVPLSQGDLS HPPRKKDRKNRKLGFGAGAGFGVLRPRPTPGDGEKRSRIKKSK KRLKKAERGDRLPPPGPPQAPPSDTDSEEEBEEEEEEBEBMA TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE TSQDGDASSSEGBMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEEGEKH RELRLRNYVPEDEDLKKRRVFQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLAASAVDAATEQKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILAPYTTKROENO	1	J		LDNGTLTVREASVFDRGTYVCRMETEYGPSVTSIPVIVIAYPPR
VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYIHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG AMLEAMAEPSPEDPPPTLKPETQPPEKRRTIEDFNKFCSFVLA YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS HPPRKKDRKNRKLGPGAGAGFGVLRPRPTPTGDGEKRSRIKKSK KRKLKKAERGDRLPPPGPQAPPSDTDSEEEBEBEEEEBEMA TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEBGEKH RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDGSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLINILADYTTKROENO	1 1	ĺ		ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG
6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG AMLEAMAEPSPEDPPPTLKPETQPPEKRRTIEDFNKFCSFVLA YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM KLKDSLFPLLDGPKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS HPPRKKDRKNRKLGPGAGAGFGVLRPPRTPTGDGEKRSRIKKSK KRKLKKAERGDRLPPPGPPQAPPSDTDSEEEBEEBEEBEMAA TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEBGEKH RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFVVVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLINILADYTTKROENO	}	i		VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT
ARKYSIGHKYLLMSEAVGASSTRGDTGIPGSGEGGAGPGGGEG AMLEAMAEPSPEDPPPTLKPETQPPEKRRTIEDFNKFCSFVLA YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS HPPRKKDRKNKLGPGAGAGFGVLRPPRTPTGDGEKRSRIKKSK KRKLKKAERGDRLPPPGPPQAPPSDTDSEEEEBEEEBEEMEMA TVVGGBAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEBEGKH RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEOKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFFYYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLINILADYTTKROENO	6430	1075		TYIHVF
AMLEAMAEPSPEDPPTLKPETQPPEKRRRTIEDFNKFCSFVLA YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS HPPRKKDRKNRKLGPGAGAGFGVLRRPRPTFGDGEKRSRIKKSK KRKLKKAERGDRLPPPGPPQAPPSDTDSEEEEEEEEEEEEEMA TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWHILSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEEGEKH RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLINILADYTTKROENO	0430	1746	602	RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG
YAGYIPPSKEESDWPASGSSSPLRGBSAADSDGWDSAPSDLRTI QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGPKVASPLSPTSITTTSRPPAALTPVPLSQGDLS HPPRKKDRKNRKLGPGAGAGFGVLRRPRPTFGDGEKRSRIKKSK KRKLKKAERGDRLPPPGPPQAPPSDTDSEEEBEEEEEEBEMA TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWHLLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WWWSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEEGEKH RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLINILADYTTKROENO]			AMLEAMAEPSPEDPPPTLKPETQPPEKRRRTIEDFNKFCSFVIA
GTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALITPVPLSQGDLS HPPRKKDRKNRKLGPGAGAGPGVLRPRPTPGDGEKRSIKKSK KRKLKKAERGDRLPPPGPQAPPSDTDSEEEBEEEEEBEBMA TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEBGEKH RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLINILAPYTTKROENO	į į	1	ľ	YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI
KLKDSLFPLLDGPKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS HPPRKKDRKNRKLGPGAGAGFGVLRRPRPTTGDGEKRSRIKKSK KRKLKKAERGDRLPPPGPPQAPPSDTDSEEEBEEEEEEBEMA TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEBGEKH RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLINILAPYTTKROENO				QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLOAPDSATLLEKM
KRKKKKAERGDRLPPPGPPQAPPSDTDSEEEBEBEEEEBEEMA TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEEGEKH RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASADAATEQKTCDSD GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLINILAPYTTKROENO	ļ i			KLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS
TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE TSQDGDASSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWHILSCAKIKKTNVPDFFYCQKCKELRFEARRLG GPPKSGEP 6431 3 605 WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEEGEKH RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLINILADYTTKROENO	j l		1	HPPKKKURKNRKLGPGAGAGFGVLRRPRPTPGDGEKRSRIKKSK
TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRFEARRLG GPPKSGEP 6431 3 605 WWMSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEEGEKH RELRLRNYVPEDEDLKKRRVFQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLINILADYTTKROENO] [1	1	AKALAKAERGURLPPPGPPQAPPSDTDSEEEEEEEEEEEMA
PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEEGEKH RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLINILADYTTKROENO] [1	ŀ	TOODGDAGGEOUNDERSTEERS
GPPKSGEP GPPKSGEP WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEBGEKH RELRLRNYVPEDBEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKROENO]		ļ	DMIRCOL GGENTUL CONTROL OF THE CONTR
6431 3 605 WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEEGEKH RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASADAATEQKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKROENO]	1	İ	CREWSCHE CONTROL OF T
6432 56 1692 GGLGTMGSRIKQNATTEVLYCVEVEVEVEVEVEVEVEVEVEVEVEVEVEVEVEVEVEVE	6431	3	60E	
RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKROENO		-	T .	HINDS INDPAYAPY DECEACAMODER KGGAYAGKMEATTAGVGR
1EEVOLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDATEQKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKROENO				DELEGERALKALKELKALKEKTGRKDKEDGEPKTKHLREEEEEGEKH
6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKROENO		}		VETICITY IN A DEMODRANT AND THE CONTROL OF THE CONT
GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKROENO			1	LEGOEDEL AGNIDA AMBOLIMONAKKLEKLKKRTQRAIAELIRER
DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKROENO	6432	56	1692	CCI COMCCOT PONT DOMESTIC CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF T
FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKROENO		-	1037	DVCDOPH ON THE TRANSPORT OF THE TRANSPOR
FGFCKLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENQ	1		1	DISDUE VLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR
	ſ		i .	rereads GAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENQ
WWELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN	ł			WNELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN
LTEYFVAVDVNNMLHLYASMLYERRILIICSKLSTLTACIHGSA		İ	1	LIEYFVAVDVNNMLHLYASMLYERRILIICSKLSTLTACIHGSA
AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGIHLSLMEKVRN	ŀ	ŀ	1:	AMLY PMYWQHVYIPVLPPHLLDYCCAPMPYLIGIHLSLMEKVRN
MALDDVVILNVDTNTLETPFDDLQSLPNDVISSLKNRLKKVSTT			<u></u>	MALDDVVILLNVDTNTLETPFDDLQSLPNDVISSLKNRLKKVSTT

SEQ	Predicted	Predicted end	Amino noid commit
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=HlStldine, I=Isoleucine, Kalvaine
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine
}	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
i	residue of	residue of	S=Serine, T=Threonine, V=Valine.
İ	amino acid	amino acid sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
1			TGDGVARAFLKAQAAFFGSYRNALKIEPEEPITFCEEAFVSHYR SGAMRQFLQNATQLQLFKQFIDGRLDLLNSGEGFSDVFEEEINM
Ī			GBYAGSDKLYHQWLSTVRKGSGAILNTVKTKANPAMKTVYKFDI
			AENGCAPTPEEQLPKTAPSPLVEAKDPKLREDRRPITVHFGQVR
			PPRPHVVKRPKSNIAVEGRRTSVPSPEQNTIATPATLHILQKSI
6433			THFAAKFPTRGWTSSSH
6433	1524	484	APVTKRKEVFAKDSKGSALDAGRDPKRPALPETLCESGWASNTA
1			PTTPPQPGWCLCGKDFKSSCOTPGREKERRI, ATMUGGCG PI MI I
ľ	}		LPLLLLVATTGPVGALTDEEKRLMVELHNLYRAOVSDTASDMI
ł			HMRWDEELAAFAKAYAROCVWGHNKERGRRGENLEATTDECMDU
	1		PLAMEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCG
			SHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP
1	}		SGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMG
6434	40	2002	AEGPDKPSVVSGLNSGPGHVWGPLLGLLLLPPLVLAGIF MPQLNFGMADPTQMGGLSMLLLAGEHALGTPEVFSGTCRPDVSE
ļ			SPELRQKSPLFOFAEISSSTSHSDASTKQCQTSALFQFAEISSN
1			TSQLGGAEPVKRCGKSALFQLAEMCLASEGMKMEESKLIKAKES
ľ			DGGRIKELEKGKEEKEIKMEKTDETRLQKEAEFEKSAKENLRDS
			KELRNFEALQIDDIMAIKMEDPKEIRKEELEEDHKCGHEDDEGV
			SASSKIIISDVPSRKDHMCHPHGIMIIEDPAAT,NKPEKT,KKKKK
			KSKMDRHGNDKSTPKKTCKKROSSESDIESVIVTIFAVAKCDMC
	1		IEKLGDTPRKKVRTSSSGKGSILDAKPPKKVKSPEKKMSKEKS
	1	!	SDTTKESRPPDFISISASKNISGETPEGIKAEPLTPMEDALPPS
.			LSGQAKPEDSDCHRKIETCGSRKSERSCKGALYKTLVSEGMLTS
1			LRANVDRGKRSSGKGNSSDHEGCWNBESWTFSQSGTSGSKKFKK
			TKPKEDCLLGSAKLDEEFEKKFNSLPQYSPVTFDRKCVPVPRKK KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT
[MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ
			DIQRAGYHHEEVLWMTNLMNNCGGVYLKOLRHTAMTNA
6435	2227	657	ALQRDAAAAYAHPEYEERFLOEETVSOOTNSTELLOTPDLALDE
			VVKSQRPLQRQVHLRGRPASOPTVIRGITYVKAKUSEEENDIEE
- 1			QQDEFFSGDNGVDLLIEDOLLRHNGLMTSVTPRDAATDOGUGTA
ı			VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLOTTQUEDD
	!	}	PTRESVLOPSPOVPATTVAHTATQQPAAPAPPAVSPREALMRAM
- 1		1	HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY
1			GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR
[AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA
}		i	VDBNGLWLIYPALDDEGFSOBVIVLSKLNAADI.STOKETTWDTG
1			LRRNFYGNCFVICGVLYAVDSYNORNANISVAFDTHTNTOTUDD
6436	1295		LLFENEYFYTTQIDYNPKDRLLYAWDNGHOVTYHVIFAY
3230	1495	341	GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGTLEHCVM
- 1	ľ		YPIDCVKTRMOSLOPDPAARVRNVI.EAT.WDTTPTEGTWDDWG.
ł	1	i	NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC
	[VATLUMDAAMNPAEVVKORMOMYNSPYHRVTDCVRAVWONEGAG
		1	AFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVL
1		ļ	SGACAGAVAAAATTPLDVCKTLLNTQESIALNSHITGHITGMAS AFRIVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLIT
			KRQEEWRAGK
6437	1828		PPAPAPPASPARHVTRTARGHLEGGSRAPPLLQAVFLQIKNMVK
1		4 :	LIHTLADHGDDVNCCAFSFSLLATCSLDKTIRLYSLRDFTELPH
- 1	1	[]	SPLKFHTYAVHCCCFSPSGHILASCSTDGTTVLWNTENGQMLAV
-	i) [MEQPSGSPVRVCQFSPDSTCLASGAADGTVVLWNAOSYKLYRCC
1	1	[5	SVKDGSLAACAFSPNGSFFVTGSSCGDLTVWDDKMRCLHSEKAH
į		j I	DLGITCCDFSSQPVSDGEQGLOFFRLASCGODCOVKIWIVSFTH
			ILGFELKYKSTLSGHCAPVLACAFSHDGQMLVSGSVDKSVIVYD

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
İ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-st
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
1			TNTENILHTLTOHTRYVTTCAFAPNTIJJATGSMDKTIMIMOED
			DETLCQARSTEHOLKOFTEDWSEEDVSTWI.CAODI.KDI.VGT.PVM
			NNIDGKELLNLTKESLADDLKIESLGLRSKVLRKTERLDTKVVC
İ			LSSGIPDEFICPITRELMKDPVIASDGYSYEKEAMENWDPAKRN
6438	109	901	RTSPP
1	100	301	EVQILRAKMFQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNV
j	1		NPALPLSPTGLAGSLTNALSNGLLSGGLLGILENLPLLDILKPG
ł		ĺ	GGTSGGLLGGLGKVTSVIPGLNNIIDIKVTDPQLLELGLVQSP
			DGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRD
			KQERIHLVLGDCTHSPGSLQISLLDGLGPLPIQGLLDSLTGILN
6439	23	412	KVLPELVQGNVCPLVNEVLRGLDITLVHDIVNMLIHGLQFVIKV SIQTASAITTEMASQSQGIQQLLQAEKRAAEKVADARKKARRL
			KQAKEEAQMEVEQYRREREHEFQSKQQAAMGSQGNLSAEVEQAT
			RRQVQGMQSSQQRNRERVLAQLLGMVCDVRPQVHPNYRISA
6440	3	517	RARWINSDMGDLPGLVRLSIALRIQPNDGPVFYKVDGQRFGQNRT
		•	1 KLLTGSSYKVEVKIKPSTLOVENISIGGVIAPI, ELKEKPROGR
ļ	i i		RVVYTGTYDTEGVTPTKSGEROPIOITMPFTDIGTPETUMOUVE
6441	234		INTHKRDHCQWGSPFSVIEYECKPNETRSIMWUNKESET.
0441	234	1373	KSGGLRRRQRPGRSAAVGEEELPPGMEKFKAAMLLGSVGDALGV
1			RNVCKENSTVGMKIQEELORSGGLDHLVLSPGEWDVSDNTIMHI
1			ATAKALTIDYWCLDDLYREMVRCYVEIVEKLPERPDDATIEGG
			AULKPNNYLLAWHTPFNEKGSGFGAATKAMCIGLRYWKDRDI.rm
			LIEVSVECGRMTHNHPTGFLGSLCTALFVSFAAQGKPLVQWGRD
i l	1		MLRAVPLAEEYCRKTIRHTAEYQEHWFYFEAKWQFYLEERKISK
			DSENKAIFPDNYDAEEREKTYRKWSSEGRGGRRGHDAPMIAYDA LLAAGNSWTELCHRAMFHGGESAATGTIAGCLFGLLYGLDLYPK
			GLYQDLEDKEKLEDLGAALYRLSTEEK
6442	34	796	AEDPAGGLAGODTMFARGLKRKCVGHEEDVEGALAGLKTVSSYS
			LORQSLLDMSLVKLQLCHMLVEPNLCRSVLIANTVRQIQEEMTQ
]			DGTWRTVAPQAAERAPLDRLVSTEILCRAAWGOEGAHDAGGIGD
1 [f		GHTQGPVSDLCPVTSAQAPRHLOSSAWEMDGDDENDGGEUVELD
1 1			QIFETLETKNPSCMEELFSDVDSPYYDLDTVI,TGMMGGAPDGDG
6443	2		EGLEGLAPATPGPSSSCKSDLGELDHVVEILVET
""	2	555	MASPAASSVRPPRPKKEPOTLVIPKNAAEEOKLKLERLMKNPDK
1	İ		AVPIPERMSEWAPRPPPEFVRDVMGSSAGAGSGEFHVVPULDDD [
1 1	1		EYQRQDYMDAMAEKQKLDAEFQKRLEKNKIAAEEQTAKRRKKRQ
!!!	į		KLKEKKLLAKKMKLEOKKOEGPGOPKEOGSSSSAFASGTEEREE VPSFTMGR
6444	390	899	
] [1		GSTPRGKMRAPIPEPKPGDLIEIFRPFYRHWAIYVGDGYVVHLA
	ļ.	ĺ	PPSEVAGAGAASVMSALTDKAIVKKELLYDVAGSDKYQVNNKHD DKYSPLPCSKIIQRAEELVGQEVLYKLTSENCEHFVNELRYGVA
		ł	RSDQVRDVIIAASVAGMGLAAMSLIGVMFSRNKRQKQ
6445	2	753	AGAAGAAGAARSPRPQAHTKGVRGLPSRRRSPDCGRMELAAGSF
			SEEQFWEACAELQQPALAGADWQLLVETSGISIYRLLDKKTGLY
	1	ſ	EYKVEGVLEDCSPTLLADIYMDSDYRKOWDOVVKELVEGEGMOR
ľ		•	TVVYWEVKYPFPMSNRDYVYLRORRDLDMEGRKTHVTLAPGTCM
' i	İ	1	PULGERSGVIRVKQYKQSLAIESDGKKGSKVFMYVFDNpccotb
6446			SWILLNWAAKNGVPNFLKDMARACONYLKKT
0440	1	1651	RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLDELG
			DSGDEAAWEDEDDADLPHGKOOTPCLFCNRLFTSAFFTFGUCVC
1	ļ		EHQFNIDSMVHKHGLEFYGYIKIINFIRIKNPTVEVMNSTVNDV
		Ť	PWEKEEYLKPVLEDDLLLOFDVEDLYEPVSVPFSYPNGLSENTS
		i	VVEKLIKHMEARALSAEAALARAREDLOKMKOFAODFVMHTDUDT
1	[1.	CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMI,KDKTRTEGVPD
			FIYQNPHIFKDKVVLDVGCGTGILSMFAAKAGAKKVLGVDQSEI

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	\n-nighthere C=CVsteine
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	sequence		Codon, /=possible nucleohide deletion
			\=possible nucleotide insertion)
			LYQAMDIIRLNKLEDTITLIKGKIEEVHLPVEKVDVIISEWMG
{			FLLFESMLDSVLYAKNKYLAKGGSVYPDICTISLVAVSDVNKH
1	}		DRIAFWDDVYGFKMSCMKKAVIPEAVVEVLDPKTLISEPCGIK
}	1		IDCHTTSISDLEFSSDFTLKITRTSMCTAIAGYFDIYFEKNCHN
Ĭ			RVVESTGPQSTKTHWKOTVFLLEKPPSVKAGEALKGVGETGWAN
6447	1554	1068	KDPRSLTVTLTLNNSTQTYGLQ
ļ		1000	RLGPAEWHLSGPCHATLGAANRGRALGVRAAWRGAPLCQRVMMF
	ſ		SKINLAIGIPSSKVKYSRLSSTDDGVIDLOFKYTDDVIDVVA TA
	l		HAIVLELIGAFLIIIGSLLLSGYISKGGADDAUDUT TTOTTUN
6448	74	PEA	PGF THERTAYYASKGYRGYSYDDIPDFDD
	/ -	559	GQVLSHCYHYRSSRWRRGGLSRGRGAGVMALVPYEETTEFGLQX
			FRAPLATESFANHTIOIRODWRHIGVANWWDAATM CTVI ENG
			AVELKGKSAVELGAGTGLVGIVAAI, ACDIDVEDDAMED AMI UD
6449	597		QFIVEKVHYDPEKDVHIYEAOKRNOKEDI.
	39,	1876	EYGVCENLRKLEITGVSCRDVYAKLIHRYPHTLGLWODDIGDYG
i			GLENVVVDGLFIIGWMYLPPHDPHVDDPMPFKDI.FDIUIMEDUR
i	1		ATVECMIGHKGPHHGHIOIVKKDEFSTKCNOTDHHPMSCGPARE
l	1		FRINCHESEWGRTLEDIFHEHMORLTIMKFIVTSOVDMOLTUNDE
ſ	1		1 11PPSRPDDLIKPGLFKGTYGSHGLFTVMLSFHGPPAPGTV100
- [- 1		DENIFAGQQTVEIDLRHRIOLPDIENORNENELSPILLEUPPDI
	i		RVAQUEGGHEAGEGRGROGPRESOPSPAODPAFADGUCADGUDG
	1		BUGGEFGDAVAAAEOPAOCGOGOPFVI,DVGVSSDNEDVDDDODA
Į.			CFIGIGLIAGHGFTSPERTPGVFTLEDPDPGGUMTELKGBOTT
6450	848		SKVQATERNADAPSPOAFDEMLKNIOSTTS
0130	648	269	FVPAPRTVSGKRSLPGEWEERGEGEORTGREESGNGGPAVEARD
ŀ			MKLUCGLWLWLSLLKVI.OAOTPTPI.PI.PDPMOSEOCNOFOGDUD
	1		VIGUAGNSERPEHRALLNAFTATFELSDDGPFFUNNAMTDCOUG
1	1		DIWSIVELPAAQPGQFTVDHRVWTHEOAGRPODOPAGOPLWANC
6451	232		RDAGPVHLPGQSSGPLG
1.02	232	939	HSPTPPTSPRASTMEDVKLEFPSLPQCKEDAEEWTYPMRREMQE
i	1	į.	TDPGDFLGPYSSAMKSKLPVLOKHGTTHTTCTPONTPANTETEDAY
1			FQQLFRILVLDIADNPVENIIRFFPMTKEFTDGSLOMCGVVII
	}		CHAGISKSAAFVIAYIMETFGMKYRDAFAVIOEDDECTNDNAGE
- 1	1		VHQLQEYEAIYLAKLTIOMMSPLOTERSLSINISGTTGGI VDWX
6452			PEDDI-GIMOVA.IAONG
1.55	1	652	RTRGESSNMEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQ
[1	1	DAT DAPKINSFYAFEVKDAKGRTUST.EKVKGKUST UDDITA ODGO
		. [LIDRNI DGLKELHKEFGPSHFSVI.AFPCMOFGPGFDDDGVDVD
ł		1	FARRNIGVIEPIFHKIKILGSEGEPAFRFIUDSSKEPDDWIEWE
6453	827		ILVNPEGQVVKFWRPEEPIEVIRPDIAALVROVTIKKVEDT.
1	827	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLAAALGSAGGGGG
!		,	KUKKNCKVVFSOOELRKRLTPI OVHUTOFKCTECA PEOPVOLITA
i			DPGIYKCVVCGTPLFKSETKFDSGSGWDSFUDVINGERIMDER
}	Į.	i	FSIGMERVETSCSQCGAHLGHIFDDGPRPTCKPVCTMCAAL CEM
6454			PADSSGTAEGGSGVASPAQADKAEL
0434	827	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC
		1	RDKKNCKVVFSQQELRKRLTPLQYHVTQEKGTESAFEGEYTHHK
1		1:	DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD
1	1	1.	FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSFT
		Į.	PADSSGTAEGGSGVASPAQADKAEL
6455	1042	173	RVHI ATVEACAMOAT OF BURGUES
1			RVHLATVSASAAWDALGLEVRSHMQGSTRRMGVMTDVHRRFLQL
		1:	LMTHGVLEEWDVKRLQTHCYKVHDRNATVDKLEDFINNINSVLE SLYIEIKRGVTEDDGRPIYALVNLATTSISKMATDFAENELDLF
		1 4	
. 1	1	1,	PKALELITOERGER COMMITTEE TO COMMITTE TO COMMITTEE TO COMMITTEE TO COMMITTEE TO COMMITTEE TO COMMITTE TO COMMITTEE TO COMMITTEE TO COMMITTEE TO COMMITTEE TO COMMITTE TO COMMITTEE TO COMMITTEE TO COMMITTEE TO COMMITTEE TO COMMITTE TO COMMITTEE TO COMMITTEE TO COMMITTEE TO COMMITTEE TO COMMITTE TO COMMITTE TO COMMITTE TO COMMITTE TO COMMITTE TO COMMITTE TO COMMITTE TO COMMITTE TO COMMITTE TO COMMITTE TO COMMITTE TO COMMI
		1 2	RKALELIIDSETGFASSTNILNLVDQLKGKKMRKKEAEQVLQKF VQNKWLIEKEGBFTLHGRAILEMEQYIRETYPDAVKICNICHSL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
I	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	Now members of the control of the co
]	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	sequence	sequence	Codon, /=possible nucleotide deletion,
	bequence	 	\=possible nucleotide insertion)
			LIQGQSCETCGIRMHLPCVAKYFQSNAEPRCPHCNDYWPHEIPK
6456	 		VFDPEKERESGVLKSNKKSLRSRQH
0436	2	555	RPQSRSISMWRNSLLQVSSGLRWLRVCAMVDILGERHLVTCKGA
1	1		TVEAEAALQNKVVALYFAAARCAPSRDFTPLLCDFYTALVAEAR
}			RPAPFEVVFVSADGSSQEMLDFMRELHGAWLALPFHDPYRHELR
1			KRYNVTAIPKLVIVKQNGEVITNKGRKQIRERGLACFQDWVEAA
			DIFQNFSV
6457	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
1	1	ļ	KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
1		1	IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
i	ì		IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
ł			DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
	ļ		TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
<u> </u>	1		SFLTLSSQLKPKPVGEENICLDLKS
6458	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
i			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
į			DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
l			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
ļ			SFLTLSSQLKPKPVGBENICLDLKS
6459	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
į			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
1			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
1		· ·	DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
			SFLTLSSQLKPKPVGEENICLDLKS
6460	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
1			DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
		,	TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
			SFLTLSSQLKPKPVGEENICLDLKS
6461	1653	360	LQQRTLRITAVGQTHPIAWMAWEPSLGAFYGPASFITFVNCMYF
			LSIFIQLKRHPERKYELKEPTEEQQRLAANENGEINHQDSMSLS
			LISTSALENEHTFHSQLLGASLTLLLYVALWMFGALAVSLYYPL
			DLVFSFVFGATSLSFSAFFVVHHCVNREDVRLAWIMTCCPGRSS
	ľ		YSVQVNVQPPNSNGTNGEAPKCPNSSAESSCTNKSASSFKNSSQ
	İ		GCKLTNLQAAAAQCHANSLPLNSTPQLDNSLTEHSMDNDIKMHV
I	!		APLEVQFRINVHSSRHHKNRSKGHRASRLTVLREYAYDVPTSVE
			GSVQNGLPKSRLGNNEGHSRSRRAYLAYRERQYNPPQQDSSDAC
į			
i			STLPKSSRNFEKPVSTTSKKDALRKPAVVELENQQKSYGLNLAI
6462	3	773	QNGPIKSNGQEGPLLGTDSTGNVRTGLWKHETTV
1	,	113	SEELDREKKLKEDSPRKTPNKESGVPSLPVSLTSIKEEPKEAKH
l			PDSQSMEESKLKNDDRKTPVNWKDSRGTRVAVSSPMSQHQSYIQ
[YLHAYPYPQMYDPSHPAYRAVSPVLMHSYPGAYLSPGFHYPVYG
ł	}		KMSGREETEKVNTSPSVNTKTTTESKALDLLQQHANQYRSKSPA
	ł		PVEKATAEREREAERERDRHSPFGQRHLHTHHHTHVGMGYPLIP
6463	<u>2</u>	555	GQYDPFQGLTSAALVASQQVAAQASASGMFPGQRRE
0.403	2	350	VILCILGGWIFKNADRSMEKKKGEPRTRAEARPWVDEDLKDSSD
.			LHQAEEDADEWQESEENVEHIPFSHNHYPEKEMVKRSQEFYELL
6464	12		NKRRSVRFISNEQVPMEVIDNVIRTAGL
0.304		1154	GILRQKEREERNRIHKKEILFLEHLLVVPSEMSSLSGKVQTVLG

SEQ	Predicted	Predicted end	Aming agid comment
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			LVEPSKLGRTLTHEHLAMTFDCCYCPPPPCQEAISKEPIVMKNL
1]	YWIQKNAYSHKENLQLNQETEAIKEELLYFKANGGGALVENTTT
1			GISRDTQTLKRLABETGVHIISGAGFYVDATHSSETRAMSVEQL
			TDVLMNEILHGADGTSIKCGIIGEIGCSWPLTESERKVLQATAH
			AQAQLGCPVIIHPGRSSRAPFOIIRILORAGADTSKTIMSHIDD
1			TILDKKELLEFAQLGCYLEYDLFGTELLHYOLGPDIDMPDDNKP
			IRRVRLLVEEGCEDRILVAHDIHTKTRLMKYGGHGYSHILTDVV
			PKMLLRGITENVLDKILIENPKOWLTFK
6465	126	1396	KMTVFFKTLRNHWKKTTAGLCLLTWGGHWLYGKHCDNLLRRAAC
Ĭ			QEAQVFGNQLIPPNAQVKKATVFLNPAACKGKARTI FEKNAADT
	1		LHLSGMDVTIVKTDYEGQAKKLLELMENTDVIIVAGGBGTLOEV
i]		VTGVLRRTDEATFSKIPIGFIPLGETSSLSHTLFAESGNKVOHT
[[TDATLAIVKGETVPLDVLQIKGEKEOPVFAMTGLRWGSFRDAGV
	[KVSKYWYLEPLKIKAAHFFSTLKEWPOTHOASISYTGPTERDDN
1	ļ .		EPEETPVQRPSLYRRILRRLASYWAOPODALSOEVSPEVWKDVO
1	l i		LSTIELSITTRNNQLDPTSKEDFLNICIEPDTISKGDFTTIGSP
ì			KVRNPKLHVEGTECLQASQCTLLIPEGAGGSFSIDSERYRAMDU
6466	1134	· · · · · · · · · · · · · · · · · · ·	EVKLLPRKLQFFCDPRKREQMLTSPTQ
1 0400	1134	828	VARGTELSQLEKAHPPADMGRRKSKRKPPPKKKMTGTLETQFTC
1			PFCNHEKSCDVKMDRARNTGVISCTVCLEEFOTPITYLSEPVDV
6467	301		YSDWIDACEAANQ
0107	301	2571	GELRVLALAHGELACHAVLTASLLSLRSRLMDSDMDYERPNVET
			IKCVVVGDNAVGKTRLICARACNATLTQYQLLATHVPTVWAIDQ
	Ì		YRVCQEVLERSRDVVDDVSVSLRLWDTFGDHHKDRRFAYGRSDV
1 .			VVLCFSIANPNSLHHVKTMWYPEIKHFCPRAPVILVGCQLDLRY
1			ADLEAVNRARRPLARPIKPNEILPPEKGREVAKELGIPYYETSV
			VAQFGIKDVFDNAIRAALISRRHLQFWKSHLRNVQRPLLQAPFL
			PPKPPPPIIVVPDPPSSSEECPAHLLEDPLCADVILVLQERVRI FAHKIYLSTSSSKFYDLFLMDLSEGELGGPSEPGGTHPEDHQGH
1 1	ŀ		SDQHHHHHHHHHGRDFLLRAASFDVCESVDEAGGSGPAGLRAST
1 1			SDGILRGNGTGYLPGRGRVLSSWSRAFVSIQEEMAEDPLTYKSR
			LMVVVKMDSSIQPGPFRAVLKYLYTGELDENERDLMHIAHIAEL
1			LEVFDLRMMVANILNNEAFMNQEITKAFHVRRTNRVKECLAKGT
1 1	i		FSDVTFILDDGTISAHKPLLISSCDWMAAMFGGPFVESSTREVV
]			FPYTSKSCMRAVLEYLYTGMFTSSPDLDDMKLIILANRICLPHI.
j !	-		VALTEQYTVTGLMEATQMMVDIDGDVLVFLELAOFHCAYOTADW
	ĺ		CLHHICTNYNNVCRKFPRDMKAMSPENOEYFEKHRWPDVWYLKE
1 1	1	ĺ	EDHYQRARKEREKEDYLHLKRQPKRRWLFWNSPSSPSSSAASSS
6468			SPSSSSAVV
1 0400	3	1374	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLAEPG
1 i			LGRVHHLALKDDVRHKVHLNTFGFFKDGYMVVNVSSLSLNEDED
	.		KDVTIGFSLDRTKNDGFSSYLDEDVNYCILKKOSVSVTLLTLDT
1 1			SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGOSORPNVNPASAGN
1 1		l	QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFOFFFNTS
		1	TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA
1 1		1	GEIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKIHWI.MAAI.
j l			PFTKSLSLVFHAIDYHYISSQGFPIEGWAVVYYITHLLKGALLF
1 1	1	ł	ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYITIES
]		TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD
6469			GKGKFSRAHFVLLSLL
60 50	3	1374	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLAEPG
			LGRVHHLALKDDVRHKVHLNTFGFFKDGYMVVNVSSLSLNEPED
[[1	1	KDVTIGFSLDRTKNDGFSSYLDEDVNYCILKKQSVSVTLLILDI
		1	SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSOEPNVNPASAGN
1		ŀ	QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFOFFFNIS
			TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA

SEQ Degining nucleotide location will beginning nucleotide location corresponding to first amino acid residue of amino acid sequence first amino acid sequence sequen	17:40
Cocation Corresponding	
Corresponding	E=
to first amino acid residue of amino acid sequence Poptoline, Oscilutamine, Ranginine, Poptoline, Oscilutamine, Ranginine, Sescrine, T=Threonine, V=Valine, W=TryTopine, X=Unknown, *** Codon, /=possible nucleotide deletion, \ Poptoline, Oscilutamine, Ranginine, Sescrine, T=Threonine, V=Valine, w=TryTopine, Y=TryTopine, X=Unknown, *** Codon, /=possible nucleotide insertion) Colon, /=possible nucleotide insertion, Poptoline, Oscilutamine, Ranginine, Sescrine, T=Threonine, V=Valine, w=TryTopine, Y=Tr	e,
amino acid residue of amino acid sequence securine, TarThreonine, VaValine, Securine, TarThreonine, VaValine, Mariyotophan, Yaryosine, Xaunknown, **a (Codon, /*possible nucleotide deletion, \possible nucleotide disertion) GEIPLPKLYISMAFFFISGTIMIHLKRRRNDVFKIRM) FPTKSLSUFHALDYHISSAGPIEGWAVVYYTTHLIKK ITIALIGGWAPIKHILSDKOKKIFMIVIPRRYLANNAY; TEEGTTEYGLWKDSLFIVULLCCGAILFPVWSTRHLOEK (KOKKFSRAHPVLLSIL) AAASSVSSRADAPVLAQSPASAGNGRSTFRVFGSRHFE GOLDFREGOKTOPGOLLPLPGALDYVYSTHLOEK (SKKFSRAHPVLLSIL) AAASSVSSRADAPVLAQSPASAGNGRSTFRVFGSRHFE GOLDFREGOKTOPGOLLPLPGALLAPRYLLSSAAETGRS OHPSGGCRGCTSSPSAAGRFASMAEAEDCHSDTVRF ENESPASTDLQAQLOMFRAQWMFELAGVVSSSMLENRPCG SLOKTSADTGKGCOAKEKAREFLKAVEEGOMALYSE RRAMQLVPDIEFRITYTRSPDGDGVGNSY1EDNDDDSKMA YFQQUIFGESVLKLCOPELESSOITSVFRWENT SUDLIRSLEQLSLVCRGFY1CARDPEIWLLACKKWGRSC PYYSRRMPLERPRVFFGOVISKTTYTGGGSLDGFTF VEYFRYTRIFFPDGHVMMLTTEBETGSLSSGLAGFFTR VEYFRVHREPFPGSVVFRAKTROEGSLDGFTR VEYFRVHREPFPGSVVFRAKTROEGSLDGFTR VEYFRVHREPFPGSVVFRAKTROEGSLDGFTR VEYFRVHREPFPGSVVFRAKTROEGSLDGFTR VEYFRVHREPFPGSVVFRAKTROEGSLDGFTR VEYFRVHREPFPGSVVFRAKTROEGSLDGFTR VEYFRVHREPFPGSVARAKKLRRKEQSLPREVDAGAAREVLAGAGSGGGGGRASSKSDADSGFLGGRPTSVDFALRT LLNDSATRAKGGPGCTVSRFFYDUMADNFLDRFLVGGOB QTKKKCVKRPAKHTKFSQAPAVEVAPAGATSGSLTSLETL, NILBPATRAKGGPGCTVSRFFYDUMADNFLDRFLVGGOB QTKKKCVKRPAKHTKKFKGVARALHTKFSQAPAVEVAPAGATSTFSCHCE ESIGGEGFQGSGPBAGDAEVCPPARATTSKKTGOORN VHELVGOAAREAARLHROELFPERTVUDCHHEFPARGFGAAVEVAPAGATSTFSCHCE ESIGGEGFGGGSGPBAGDAEVCPPARATTSKKTGOORN VHELVGOAAREAARLHROELFPERTVUDCHHEFPARFGF ARVDLQQIMTIIDELGKASAKAQNISAPITTSASRMQSNT LKDSSAPPAGKGA IIGFIKVGAARALHROELFPARFGF ARVDLQQIMTIIDELGKASAKAQNISAPITTSASRMQSNT LKDSSAPPAGKGA IIGFIKVGAARALHROELFPARFGF ARVDLQQIMTIIDELGKASAKAQNISAPITTSASRMQSNT LKDSSAPPAGKGA IIGFIKVGAVARPPARFSCHCE DESTREGOFTARFTAN VEYPTAAPARALPFRCHGCTANDANTKYKKVEVLERPERFORM AVDPTPAAPARKALFTARGFTCHGCTANDANTKYKKVEVLERPERFORM AVDPTPAAPARKALFTARGFTCHGCTANDANTKYKNSRAAQMYREN LCCMQVGONANATAFFRQHGCTANDANTKYNSRAAQMYREN LGCMQVGONANATAFFRQHGCTANDANTKYNSRAAQMYREN LGCMQVGONANATAFFRQHGCTANDANTKYNSRAAQMYREN LGCMQVGONANATAFFRQ	
residue of amino acid sequence Sequence	
amino acid sequence Sequence	
Sequence Codon, /=possible nucleotide deletion Codon, /=possible nucleotide insertion GEIPLPKLYISMAFFFFLSGTIWIHILRKRNNDVFKIHW PFTKSLSLVFHAIDTHYISSGFFIEGWAVVYYITHLKK ITIALIGTGWAFIKHLISKKKIFMTVIPREVLANNAY TEEGTTEYGLWKDSLPLVDLLCCGAILFPVVWSIRHLQER CKGKFSRAHPVLASLL AAASGVSSRADAPVLAQSPASAGNGRSTFRVFGSRRHPS GPLPREDGCRTPGPOLLPLEGALLRFATLLSSAAFTGRSF GPLPREDGCRTPGPOLLPLEGALLRFATLLSSAAFTGRSF GPLPREDGCRTPGPOLLPLEGALLRFATLLSSAAFTGRSF GPLPREDGCRTPGPOLLPLEGALLRFATLLSSAAFTGRSF GPLPREDGCRTPGPOLLPLEGALLRFATLSSAAFTGRSF GPLPREDGCRTPGPOLLPLEGALLRFATLSSAAFTGRSF GPLPREDGCRTPGPOLLPLEGALLRFATLSSAAFTGRSF GPLPREDGCRTPGPOLLPLEGALLRFATLSVLPMSVLMYIFR SLOKTSADTKSKOSDAKEKARRLFLAVEEDONGSYLENDDDSKM FRAMQLUPDI IFFKITYTRSPIGGCVGNSY1EDDDDSKM YFQQLIFTGESVLKLCOPELESSQIHISVLPMSVLMYIFR SULDLIRSLEGISLVCRGFVLARPEIWRLACLKVWGRSC PYTSWREMFLERPRVRFDGGVVGNSYLLKVWGRSC PYTSWREMFLERPRVRFDGGVVGNSYLLKVWGRSC PYTSWREMFLERPRVRFDGGVVGNSYLLKVWGRSC PYTSWREMFLACEPIGLEVQOPILSVLQGETSGGLLS GPRNKKRGWRRLAQEPIGLEVQOPILSVLQGETSGGLLS EKLFPVDTGSKKGGLKKKRKKGLWEKLAKQGELPREVKR LAMPSATRAKPGPQDTVERFFYDLWASDNPLDRFLVGQDE GPRNKKRGWRRLAGLERVQAPDIDVALGETSGGLLS CKKGVKRPARHTHYRSOAFWAYAPAGASNYDSFEDHO AAHEVELQRGKEAEKLERQLADATQAATQESTFQLCE ESGGGEGEGGGGGGGSKASSAAGNALATTEKKTEQORR VHRLRVQAALRAARRHGELFRLRGIKAVQVALRIAELART RQARREAEADKPRICGRKWQAPDIDVLSSELTTSLETTL NILDRFKSFGGRMMEPPFDVDALFPERAKTFKKVKVKVLVERRARE; DFYIHSSVQRHGHGRELFQYMLQKSFRYBHOLAIDRSGKILKVANSTATUSASARPAGKGALAIGFIKVGYKKLFVLDDREAINEVEPIDPYIHSSVQRHGHGRELFQYMLQKSFRYBHOLAIDRSGKILKNANSTATSSARMQSNRI LIKMSSARPAGKGALAIGFIKVGYKKLFVLDDREAINEVEPIDPYIHSSAAFPAGKGALIGFIKVGYKKLFVLDDREAINEVEPIDPYIHSSAAFPAGKGALIGFIKVGYKKLFVLDREAINEVEPIDPYIHSSAAFPAGKGALIGFIKVGYKKLFVLDREAINEVEPIDPYIHSSAAFPAGKGALIGFIKVGYKKLFVLDREAINEVEPIDPYIHSSAAFPAGKGALIGFIKVGYKKLFVLDREAINEVEPIDPYIHSSAAFPAGKGALIGFIKVGYKKLFVLDREARFSITTENSAMONNANTIKUNSRAAGHTATSKYTARAFTATTEKTATTEKTATTATTEKTENDANNANTIKVNSRAAGMYRIK AVDPTPAAPARKLPCAGGAAFFAGGGGATASTATTEKTARAFTATGKTATTEKTATTATTEKTATTATTATTATT	
GEIPDRALY ISAMPFFIGGTI HITLERKERNDVFKIHWI PFTKSLSLVFHAIDYHTISSGGFFIEGWAVYYYITHLIK LTIALIGTGWAPIKHILSDKOKKI FMIVIPERRULANVAY. TEEGTEEGUKMESLIPLUGCAILIPPVWSIRHLOER CKGKFSRAHFVLLSLL AAASGVSSRADAPVLAGSPASAGNGRESTRVPGGSRRHPS GPLPREDGCRTPGPOLLIPLEGALLRPRTLLSSAAETGRSS GPLPREDGCRTPGPOLLIPLEGALLRPRTLLSSAAETGRSS GPLSPSABTDLQAQLQMFRAGWMFELAPGVSSSALERPFC SLOKTSADTKGKOSCAKEEKARELFILKAVEERONGALYER RRAMQLVPDIEFKITYTRSPDGDGVGNSYIEDNDDDSKM YFQQQLFFGESVLKLCOPELESSGIHISVLPWEERONGALYER RRAMQLVPDIEFKITYTRSPDGDGVGNSYIEDNDDDSKM YFQQQLFFGESVLKLCOPELESSGIHISVLPWEEROPYTSWREMFLERREVRPDGVYISKTYTYRGGSGSLDGFYR VEYYRYTRFFPDGHVMMLTPTEEPOSIVPRLRTR GPRNKKGWRRLAGOPFLGEVOOFLEERTS GPRNKKGWRRLAGOPFLGEVOOFLEERTS GPRNKKGWRRLAGOPFLGEVOOFLEERTS LLMPSATRAKPGPDTVERFPDVARSDMPLDRPLVGQDE QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQ AAHEVELQROKEABKLERQLADPATSQAATQSSTFOELCE ESGGEGFGGGFGEAGDALVFTRALTTEKKTEQORR VHALRVQGAALRAARLRHOELFRLIGIKAQVALRALAELAR ROARREAEADKPRLGRUKYQAAPDIDVQLSSELTDSLTTL, NILRDFKSFGRRNMIEPRERKFKRKVKVKLVEKRAFRE LIMPSKSFRRAGGALIGFIKVGYKKLFVLDGHLRPPARRGG ARVDLQQQIMTI IDBLGKASAQANLSAPITSASRMQSNR ILKDSSARPAGKGALIGFIKVGYMLYSERSHDLATDRSOKI LIKDSSARPAGKGALIGFIKVGYKKLFVLDGREANNSVEP DFYHESVQRHGHGRELFCYMLQKEKVSPHQLAIDRPSOKI LIKDSSARPAGKGALIGFIKVGYKKLFVLDGREANNSVEP DFYHESVQRHGHGRELFCYMLQKEKVSPHQLAIDRPSOKI LIKDSSARPAGKGALIGFIKVGYKKLFVLDGREANNSVEP DFYHESVQRHGHGRELFCYMLQKERVSPHQLAIDRPSOKI LIKDSSARPAGKGALIGFIKVGYKKLFVLDGREANNSVEP AVDPTPAAPARLLPFKRAGGIKFYSSSGREPLKVAVEPDW RAPRRATPPAAPARLLPFKRAGGIKFYSSSGREPLKVAVEPDW RAPRRATPPAAPARLLPFKRAGGIKFYSSSGREPLKVAVEPDW RAPRRATPPAAPARLLPFKRAGGIKFYSSSGREPLKVAVEPDW NPSMASITYGVFLCIDCSGVURSLGVHLISFIRSTELDSNM LECMGYGGNANATAFFFGHGCTAANANTKYNSRAAQMYREK LGSAALARHGTULWIDMSSAVPNHSFEKKDSDFFTEHTOG DAFATEPSGTQQPAPSTESSGLAQPENGPNTDLLGTSPKAS KSSIIGKKKPAAAKKGLGAKGAGANXSSOFSETERDOA	top
GEIPLPKLYISMAFFFISGTIWHILLKKRRNDVFKIHW PFTKSLSUVFHAIDYHYISSQOFFIEGWAVVYYITHLKK ITIALIGTGWAFIKHIJDKDKKKIFMIVIPRVLANVAY. TEEGTTETGLWKDSLFLVDLLCCGAILFPVVWSIRHLQE GKGKPSRAHPVLISLL AAASGVSSRADAPVLAQSPASAGNGRPSTPRVPGSRRHPS GPLPREDGCRTPGPQLLPLEGALLRFTLLSSAAETGRS OHPSSGGRCRGESPSSAAGRPASMARAEDCHSDTVRF ENESPAETDLQACLOWFRAGMMFELAPGVSSSMLENRPCK SLOKTSADTKGKEQAKEEKARELFIKKVEEEONGALYER RRAMQLVPDIEFKITYTRSPLGDGVCKNSYLEDNDDDS KMA YFQQQLIFGESVIKLCOPELESSQIHISVLPMEVLMYIFR SDLDLRSLEGLSLVCRGFYLCARDPEIWHLACLKWWGRSC PYTSWREMFLERPRVRFDGGVISKTTYIRQGEQSLDGFYG SPYTSWREMFLERPRVRFDGGVISKTTYIRQGEQSLDGFYG PYTSWREMFLERPRVRFDGGVISKTTYIRQGEQSLDGFYG PYTSWREMFLAGEPIGLEVDQFLEDSVILORETS GPYTSWRSMFLAGEPIGLEVDQFLEDVLQCRETSGGLLS EKLFPUTGSKEKGLTKKRFVGKKSLLLKKPLRVDLILE VPAPKDULAHQVPNAKKLRKKGCLUKKKLLLKKPLRVDLILE VPAPKDULAHQVPNAKKLRKKGCLUKKKALLLKKPLRVDLILE VPAPKDULAHQVPNAKKLRKKGCLUKKLAKGGSLPREVRR LNPSATRAKPGFQDJTVERFFDLWBANDFLDRFLVGQDE QTKKKGVKRPARLHTKPSQAPAVEVAPAGASTVPSFEDIOL AAHEVELQRGKEAEKLERQLADPATQAATQESTFOELCE ESIGGEFPGGGEGFEAGDAEVCFTPARLATTEKKTEQORR VHRLRVQAALRAARLRHGELFRLKGIKAQVALRLAELARI RQARREAEADKFRRLGRLKYQAPDIDVGLSSELTDSLKTL NILDRFKSFGRRMMIEPPERVAFRKFKKVKVKLVEKARPE; DFYIHSSVQRHGHGRELFQYMLQKSRVEPHOLATDRFAKMSH ARUDLQQIMTIIDBLGKASAKAQNLSPISASRMQSNR ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPI DFYIHSSVQRHGHGRELFQYMLQKSRVEPHOLATDRFSOKI LIKHVNLETIVZVVNNFVIFFGFHAURTPPABLRARTHS AVDPTPAAPARKLPPKRAEGDIKPYSSCREPHPLAA PUPTPAAPARKLPPKRAEGDIKPSVSSCREPLKVAVEPD DFYIHSSVQRHGHGRELFQYMLQKSRVEPHOLATDRFSOKI LIKHVNLETIVZVVNNFVIFFGFHAURTPPABLRARTHS AVDPTPAAPARKLPPKRAEGDIKPSSCREPHPLAAPFORMACH LECMQGGNAMATAFFROGGCTANDANTKYNSRAAQMRR LECMQGGNAMATAFFROGGCTANDANTKYNSRAAQMYRK LGSAALARHGTDLWIDMNSSAVPHSEEKKDSDFFTEHTOG DAFATEPSGTQQPAPSTESSGLAQPENGPNTDLLGTSPKLS KSSIIGKKKPARAKKGLGAKAGANCSSSFSTERDOA	
PTKSISLVFHAIDYHISSOGPIEGMAVYYITHLLK ITIALIGTGWAFIKHLISKÖKKIFMIVIPRRVLANVAYI TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEI CKKFSRAHFVLLSLL AAASGVSSRADAPVLAQSPASAGNGRPSTFRVPGSRRHPS CPLPREDGCRTPGPQLLPLPGALLRFRTILSSAAETGRSF CPLPREDGCRTPGPQLLPLPGALLRFRTILSSAAETGRSF CPLPREDGCRTPGPQLLPLPGALLRFRTILSSAAETGRSF CPLPREDGCRTPGPQLLPLPGALLRFRTILSSAAETGRSF CPLPREDGCRTPGPQLLPLPGALLRFRTILSSAAETGRSF CPLPREDGCRTPGPQLLPLPGALLRFRTILSSAAETGRSF CPLPREDGCRTPGPQLLPLPGALLRFRTILSSAAETGRSF CPLPREDGCRTPGPQLLPLPGALLRFRTILSSAAETGRSF CPLPRAQMOVPDIEFKITYTRSPBOGVSSSINLENRPCK SLOKTSADTKGKOBCOKEKKARELFLKAVEEEQNGALYEA RRAMQLVPDIEFKITYTTRSPBOGVSSSINLENPTG SJLDLRSLEQLSLVCGFFYLCARDEPIMRLACLKWGRSC PYTSNEMPHERPRVRFPDGHVMMLTTPEEPQSIVPRLETR SJLDLRSLEGLSLVCGFFYLCARDEPIMRLACLKWGRSC PYTSNEMPHERPRVRFPDGHVMMLTTPEEPQSIVPRLETR CFRNKKRGWRPLACHFTYTYRPDGHVMMLTTPEEPQSIVPRLETR CPRNKKRGWRRLAGEPLGLEVDQFLEDVALGETSGGLLS CKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLRVDLILE VPAPKDVLAHQVPHAKKLRREGUEMKLAKGGELPREVRR LLMPSATRAKFGPQDTVSRFFYDLMSSINPLDRPLVGQDE QTKKKGVKPARLHTKFSQAPAVEEVAPAGASYNPSFEDHQ AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCE ESDGEGEPGGGGEGFEAGDBEVCPTPARLATTEKKTEQORR VHALRVQQAALRAARLRHGELFRLRGIKGVAARLAELAR RQARREAEBAKPRRLGRLYQAPDIDVQLSSELTDELBTIL NILRDRFKSFQRRNMIEPRERAKFKRKYKVKLVBKRAFRE: SCGSDRAQWMEFFFDVDALFPERITVLDQHLRFPARFBGF ARVDLQQQINTIIDELGKASAKAQNLSAPTASSARMOSNR LLKDSSARPAGKGALIGFIKVGYKKLFVLDDREAHNEVEPI DFYHIESVQRHGHGRELFQVMLOKERKPEHQLALDRFSQKI LKMSYNLETTVPCVNNEVIFEGFFAHCHRPPAPSILRATRH AVDPTPAPAPARKLFFRAEGDIKYSSSDREPLKVAVEPPM RAPRRATPPAPPPPRSSCHARPPPRSSCHARRTHR AVDPTPAPAPARKLFFRAEGDIKYSSSDREPLKVAVEPPM RAPRRATPPAPPPPRSSCHARPFTPRAFFTON LKCMQVGGKANATAFFRGHCTANDANTKYNSRAAQMYREK LGSAALARHGTDLWIDNMSAVPNHSPEKKOSDFFTEHTOP DAPATEPSGTQQPAPSTESSGLAQPEHGPNTOLLGTSPKAS SSSIIGKKKPAAAKKGLGAAKKSOSSSETEREDONN	MANAY
TITIALIGTGWAFIKHILSDKOKKI FMIVIPRRULANNAY: TEEGTETYCHWRDSLEJUDLCCGAILFPUVWSIRHLQEI GKGKFRAHFVLLSLL AAASGVSERADAPVLAQSPASAGNGRPSTPRVPGSRRHPE GPLPREDGGRTEOPQLLPDGALLRPRTLLSSAAETGRSE QHPSSGGRCRGTESPSSAAGRPASMAEAEEDCHSDTVRI ENESPAETDLQAQLOMFRAQWHFELAPGVSSSNLERRPCG SLOKTSADTYKGKOEQAKEKARELFIKAVEEEQNGALYEA RRAMQLVPDIEFKITYTRSPDGDGVGNSYIEDNDDDSKMA YFQQQITFQESVLKLCQPELESSQIHISVLPMEVLMYIFR SDLDLRSLEGLSLVCRGFYICARDESIMRLACLKVWGRSC PYTSWREMFLERPRVRFDGVYISKTTYIRQGEQSLDGFYR VEYYRYIRFFDGHWMMLTTEEPQSIVPRLETTR FFFDKMAAGGSVGGKRSKSDADSGFIGLEPTSVDPALR GPRNKKGWRRLAQPLGLEVDQPLEDVRLQERTSGGLIS EKLFFVDTGSKEKKSLTKKRTKVQKKSLLLKKPLRVDLILLE VPAPKDVLAHQVPNAKKLRKEGUMEKLAKQGELPREVR LLNPSATRAKPGPQDTVRRPFYDLWASDNPLDRPLVQDDE QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQ AAHEVELQRGKEABELLEGLALPFATGAATGESTFOELCE ESDGEGEPGGGEGFAGDAEVCPTPARLATTEKKTEQOKR VHELRVQOAJARAARLRHQELFRLRGIKAVQAALBAELARI RQARREABADKPRLGRIKKVQAPDIDVQLSSELTDSIRTL NILRDRFKSFQRRMMIBPRERAKFKYKVKLVBKRAFRE: ARVDLQQQIMTIIDEIGKASAKAQNLSAPITSASRMOSNRI LIKDSSARPAGKGALIGFIKVGYKKLFVLDDREAHNEVEPJ DFYTHESVGRHGIGRELFYKRJKKVKLVPLDDREAHNEVEPJ DFYTHESVGRHGIGRELFYKSSDREFFLKVAVEPPP RAPRRATPPAAPARKLPFPKRAEGDIKYSSDREFFLKVAVEPPP RAPRRATPPAHPPPRSSLCMSPERGPLRPFVD 6473 22 912 SSAVEPVWEGEKMAAEPNKTEIQTLFKRLRAVFTNKACPPC NPSWASITYGVFLCIDCSGYHRSLGHLSFIRSTELDSNIN LECKGVGGRANATAFFRGHGCTANDANTKYNSRAQMYREK LGSAALARGGTDLWIDNMSSAVPNHSPEKKDSDFFTTENDA	MAAL
TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEE GKKFSRAFVLLSLU 6470 2726 1437 AAASGVSSRADAPVLAQSPASAGNGRPSTPRVPGSRRHPS GPLPREDGCRTPGPQLLPLPGALLRPRTILISSAAETGRSE OPHSSGGRCRGGTBS PSSAAGRASMAREAEGDCHSDTVRP ENESPAETDLQAQLQMFRAGMMFELAPGVSSSNLENRPCR SLQKTSADTKGKQEQAKEEKARELFLKAVEEEQNGALYRR RRAMQLVPDIEFRITYTRSPDGDGVGNSYIEDNDDSKMA YFQQQLTFQESVLKLCQPELESSQIHISVLPMEVLMYIFR SDLDLRSLEQLSLVCRGFYICARDPEIWRLACLKVWGRSC PYTSWREMPLERPVRRPDGVYISKTTYIRQGGEQSLJGFYR VEYYRYIRFPDCHVMMLTTPEEPQSIVPRLETT 6471 1750 299 FFFDKMAAGGSGVGGKRSSKSDADSGFLGRFTSVDDPALE GPRNKKRGWRRLAQEPLGLEVDQPLEDVRLQERTSGGLLS EKLFFVDTGSKERGLTKKRTKVQKKSLLLKKPLRVDLILE VPAPKDVLAHQVPDAXKLRKKQUKSLLLKKPLRVDLILE LLNPSATRAKPGPQDTVERPFYDLWASDNPLDRPLVGGDE QTKKKGVKRPARLHTKPSQAPAGVAPAGASYNPSFEDHQ QAHEVELGQCKEAEKLERQLADPATEGAATQESTFQELCE ESDGGEGEGGGGEGEGEGGEGEAGDAEVCPTPARLATTEKKTEQGRR VHRLRVQQAALRAARLRHGLEFFLRGIKAQVARLAELARI, NILRDRFKSFQRRMMLERQLADPATEGAATQESTFQELCE ESDGGEFGQGGGPEAGDAEVCPTPARLATTEKKTEQGRR VHRLRVQQAALRAARLRHQELFFLRGIKAQVARLAELARI, NILRDRFKSFGRRNMIEPRERAKFKRKYKVKLVEKRAFRE. 6472 3 897 SCGSDRAQWAMEFPFDVDALFPERITVLDQHLRPFDARFGG ARVDLQQQIMTIDELGKASARAQNLSAPITSASRMGNRR ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPI DFYYHESVQRHGHGRELFQYMLQKERVEPHQLAIDRPSQKI LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPARSLRTHK AVDPTPAAPARKLPPKRRAEGIKKPSSSDREFLKVAVEPPR RAPRRATPPAHPPPRSLGMSPERGPLRFVD SSAVEFVWEGEKMAAEPNKTEIQTLFKRLRAVPTNKACPPC NPSWASITYGVFLCIDCSGVURSLGVHLSFIRSTELDSNNN LECRQVGGNANATAFFRGHGCTANDANTXYNSRAAQMYREK LGGSALARHGTDLWIDNMSAVPNHSPEKKNSDFFTEHTQD DAPATEPSGTQQPAPSTESSGLADPEHGPTDLLGTSPKAS KSSIIGKKRPAAKKGLGAKKGLGAKKGLGADKVSSOSFSEIERDAN	TIDE
6470 2726 1437 AAASGYSRADAPVLAGSPASAGNGRPSTPRVPGSRRHPS CPLPREDGCRTPGPQLLPLEGALLRPRTILSSAAETGRSE OHPSSGRCRGGTESPSSAAGRAMAEAEEDCHSDTVRF ENESPAETDLQAQLQMFRAQWMFELAPGVSSSNLENRPCR SLQKTSADTKGKQEQALQMFRAQWMFELAPGVSSSNLENRPCR RAMQLVPDIEFRITYTRSPDGDGVGNSYIEDNDDSKMA YFQQQLTFGESVLKLCQPELESSQIHISVLPMEVLMYIFR SDLDLRSLEQLSLVCRGFY1CARDPETWRLACLKVWGRSC PYTSWREWFLERPRVRFDGGV71SKTTYIRQGEQSLDGFYR VEYRYIFPPDGHVMMLTTPEEPQSIVPRLETR GPRINKKGWRRLAGEFIGLEVDGFLEDVRLOGERTSGGLLS EKLFFVDTGSKEKGITYKKPTKVQKKSLLLKKPLRVDLILE VPAPKDVLAHQVPNAKKLRKRGLWEKLAKQGSLPREVWR LLMPSATRAKPGPQDTVERFFYDLWASDNPLIDRFLVGQDE GYKKKGKRFARLHTKPSQAPAVEVAPAGASYNPSFEDHQ AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCE ESIGGEBGGGGBEAGDAEVCFTPARLATTEKKTEQORR RQARREAEADKPRRIGRLKYQAPDIDVQLSSELTDSLRTLI, NILKDRFKSFQRRNMIEPERRAKFKRKYKVKLVEKRAFRE: DFYHLSSQAMAMEFPPDVDALFPERTIVLQPHLEPPARRFG ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRI LLKDSARPAGKGAIIGFIKVGYMLQKERVEPHQLAIDRPSQKI LNKHYMLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATRIH AVDPTPAAPARKLPFKRAEGDIKFYSSDREFLKVAVEPPP RAPRRATPPAHPPPRSSLGNPPEGPLRFVFV RAPRRATPPAHPPPRSSLGNPPEGPLRFVFV RAPRRATPPAHPPPRSSLGNPPEGPLRFVFV RAPRRATPPAHPPPRSSLGNPPEGPLRFFVF RAPRRATPPAHPPPRSSLGNPPEGPLRFFVF RAPRRATPPAHPPPRSSLGNPPEGPLRFFVF RAPRRATPPAHPPPRSSLGNPPEGPLRFFVF RAPRRATPPAHPPPRSSLGNPPEGPLRFFVF RAPRRATPPAHPPRFSSLGNPPEGPLRFFVF RAPRRATPPAHPPRFSSLGNPPEGPLRFFVF RAPRRATPPAHPPRFSSLGNPPEGPLRFFVF RAPRRATPPAHPPRFSSLGNPPEGPLRFFVF RAPRRATPPAHPPRFSSLGNPPEGPLRFFVF RAPRRATPPAHPPRFSSLGNPPEGPLRFFVF RAPRRATPPAHPPRFSSLGNPPEGPLRFFFF RAPRRATPPAHPPRFSSLGNPPEGPLRFFF RAPRRATPPAHPPRFSSLGNPPEGPLRFFF RAPRRATPPAHPPRFSSLGNPPEGPLRFFF RAPRRATPPAHPPRFSSLGNPPEGPLRFFF RAPRRATPPAHPPRFSSLGNPPEGPLRFFF RAPRRATPPAHPPRFSSLGNPPEGPLRFFF RAPRRATPPAHPPRFSSLGNPPEGPLRFFF RAPRRATPPAHPPRFSSLGNPPEGPLRFFF RAPRRATPPAHPPHPFF RAPRRATPPAHPPHPFF RAPRRATPPHPPHPF RAPRRATPPHPPHPF RAPRRATPPHPHPPHPF RAPRRATPPHPHPPHPHF RAPRRATPPHPHPHPHF RAPRRATPPHPHPHPHF RAPRRATPRATPPHPHPHF RAPRRATPRATPPHPHPHF RAPRRATPTPHPHPHF RAPRRATPRATPPHPHPHF RAPRRATPTPHPHPHF RAPRRATPTPHPHPHF RAPRRATPRHF RAPRRATPRHF RAPRRATPRHF RAPRRATPRHF RAPRRATPRHF RAPRRATPH	CULUS
GPIPREDGCRTDGPGCLIPLPGALLRPRTILISSAAETGRSF GPIPREDGCRTDGPGCLIPLPGALLRPRTILISSAAETGRSF GPIPREDGCRTDGPGCLIPLPGALLRPRTILISSAAETGRSF GPIPREDGCRTDGPGCLIPLPGALLRPRTILISSAAETGRSF SLOKYSADTYKGKOGOAKEEKARELFLKAVEEEQNGALYER RRAMQLVPDIEFKITYTRSPDGDCVGNSYIEDNDDDSKMA YFQQQLTFGESVLKLCOPELESSQIHISVLPMEVLMYIFR SDLDLRSLEQLSLVCRGFYICARDPEIWALACLKVWGRSC PYTSWREMFLERPRVRFDGVYISKTTYIRQGGSGLDGFYR VEYYRYIRFFPDGHVMMLTTPEEPQSIVPRLRTR GPRNKKRGWRRLAQEFIGLEVDGFLERPTSVDPALR GPRNKKRGWRRLAQEFIGLEVDGFLEDVALQERTSGGLLS EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLRVDLILE VPAPKDVLAHQVPNAKKLRRKEQLWELLAKGGELPREVVRR LLNPSATRAKPGPQDTVERFFYDLWASDNPLDRFLVGODE QTKKKGVRRPARLHTKFSQAPAVEVAPAGASYNPSFEDHQ AAHEVELQRQKEAEKLERQLADPATEGAATQESTFOELCE ESDCEGEPGGGEPGGGERGDEAVCFTFARLATTEKKTEQORR VHELRVQOAALRAARLRHQELFRLRGIKQVALRAELARI RQARREAEADKPRRLGGRLKYQAPATDLOVGLSSELTDSLRTL NILRDRFKSFQRRNNIEFRAKFKKKYWLVEKRAFRE: ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRT LLKDSSARPAGKGATIGTKVGYKKLFVLDDREAHNEVEPI DFYIHESVQRHGHGRELFQYMLQKERVEPHQLALDRFSQKI LLKHYMLETTVPQVNNFVIFFGFFAHQHPPAPSSKRTHS AVDPTPAPAPRKLPFKARBGIKPYSSSDREPLKVAVEPP RAPRRATPPAHPPPRSSSLGNSPERGPLKPFVD AVDPTPAPAPRKLPFKTBGDIKPTSTELDSNM AVDPTPAPAPRKLPFKREGDIKPYSSSDREPLKVAVEPP RAPRRATPPAHPPPRSSSLGNSPERGPLRFFTD ARVDLCQQGNANATAFFRGHGCTANDANTKYNSRAAQMYRK LGGAALARHGTDLWIDMNSSAVPNHSPEKKDSDFFTEHTQP DAPATEPSGTQQPAPSTESSGLLAGPEHGPNTDLGTSPKAS KSSIIGKKKPAPARKGLGAKKGLGAKKGLGAOKVSSOSFETIERDAO	
GPLPKEDGCETTGGPQLLEPGALLRERTILESAABTGGRS OHPSSGGCRGGTSBSSSAAGAAEAECCHSDTVRE ENESPAETDLQAQLQMFRAQWMFELAPGVSSSNLENRPCG SLQKTSADTKGKQEQAKEEKARELFLKAVEEQNGALYEA RRAMQULPDIEFKITYTRSPDGGGVGNSYIEDNDDDSKMA YFQQQLTFQESVLKLQOPELESSQIHISVLPMEVLMYIFR SDLDLRSLEQLSLVCRGFYICARDPEIWRLACLKVWGGRG PYTSWREMFLERPRYFDGVYISKTTYIRQGEQSLDGFYR VEYYRYIRPFPDGHVMMLTTEEEPQSIVPRLRTR 6471 1750 299 FFFDKMAAGGSGVGGKRSSKSDADSGFLGIRPTSVDPALR GPRINKRGWRRLAQEPLGLEVDQFLEDVRLQERTSGGLIS EKLFFVDTGSKEEKSLTKKRTKVQKKSLLLKKPLRVDLILE LINPSATRAKPGPQDTVERPFYDLWASDNPLDRPLVGQDE CKKKGVKRPARLHTKFSQAPAVEVAPAGASYMPSFEDHQ QTKKKGVKRPARLHTKFSQAPAVEVAPAGASYMPSFEDHQ AAHSVELQRQKEAEKLERQLAIPATEQAATQESTFQELCE ESDGGGEPQGGEGPEAGDAEVCPTPARLATTEKKTEQORR VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARI, RQARREABADKPRRLGELKYQAPDIDVQLSSELTDSLRTL, NILKDRYKSFQRRNMIEPPERAKFKKKYKVKLVEKRAFRE. 6472 3 897 SCGSDRAQWAMEPPFDVDALFPERITVLDQHLRPPARRPGF ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRI ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHMEVEPI DFYIHESVQRIGHGRELFQYMLQKERVEPHQLAIDRFSQKI LIKHYNLETTVPQVNNFVIFEGFFAHQRPPAPSLRATRHS AVDPTPAAPARKLPPKRAEGDIKFYSSDREPLKVAVEPPW RAPRRATPPAHPPPRSSSLGNSPERGPLRFFVG NPSWASITYGVFLGIDCSGVHRELGVILLSFIRSTELDSNNN LEKCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYRRK LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQR DAPATEPSGTQQPAPSTESSGLAQPERGPNTDLLGTSPKAS KSSIIGKKKPAAAKKGLGAKKGLGAKKGLGAROXVSSOSFSTERDAO	APPS
OHPSSGRCRGTESPSSAAGRPASMAEAEDCHSDTVRA ENSSPAETDLQAQLQMFRAQMMFELAPGVSSSNLENRPCR SLQKTSADTKGKORQAKEEKARELFLKAVEEEQNGALYER RRAMQLVPDIEFKTTYTRSPDGDGVGNSYIEDNDDDSKMA YFQQQLTFQESVLKLCOPELESSQIHISVLPMEVLWAYIR SDLDLRSLEQLSLVCRGFYICARDPEIWRLACLKVWGRSC PYTSWREMFLERPRVRFDGVYISKTTYIRQGEQSLDGFYR VEYYRYIRPFPDGHVMMLTTEEPQSIVPRLRTR 6471 1750 299 FFFDKMAAGGSGVGKRSSKSDADGFGLGRPTSVDPALR GPRNKKRGWRLAQEPLGLEVDQFLEVDLQLERTSGGLLS EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKFLEVDLILE VPAPKDVLAHQVPNAKKLRKEQLWEKLAKQBELPREVRR LLNPSATRAKPGPQDTVERPFYDLWASDNPLDRPLVGQDE QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYMPSFEDHQ AAHSVELQRQKEAEKLERQLALPATEQAATQESTFQELCE ESDGEGEPGGGEGPEAGDAEVCPTPARLATTEKKTEQORR VHRLRVQQAALRARLHKPSQAPAVEVAPAGASYMPSFEDHQ AAHSVELQRQKEAEKLERQLALPATEQAATQESTFQELCE ESDGEGPGGGEGPEAGDAEVCPTPARLATTEKKTEQORR VHRLRVQQAALRARLHQELFRLKGIKAQVALRLAELARI RQARREAEADKPRRLGRKYQAPDIDVQLSSELTDSLRTLI NILRDRFKSFQRRNMIEPRERAKFKRKVKVLVUKKRAFRE; ARVADLQQQIMTIIDELGKASAKQNLSAPITSASRMQSNRI LLKDSSARPAGKGAIIGFIKVGYKLFVLDDREAMINEVEPI DFYIHESVQRHGHGRELFQYMLQKERVEFHQLAIDRFSQKI LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATRHS AVDPTPAPARKLPPKREGGIKFYSSDREFLKVAVEPPW RAPRRATPPAHPPPRSSSLGNSPERGPLRPVVP SSAVEFWEGEKMAAEPNKTEIQTLFKHLRAVPTNKACPDC NPSWASITYGVFLCIDCSGVHRSLGVHLSPIRSTELDSMM LRCMQVGGNANATAFFRQGGCTANDANTKYNSRAAQMYREK LGSAALARHGTDLWIDNMSAVPNHSPEKKDSDFFTEHTQP DAPATEPSGTQQPAPSTESSGLAQPERGPNTDLLGTSPKAS KSSIIGKKKRPAAKKGLGAKKGLGAKKGLGAKOKSSSSFETERDA	דחמנ
SNESPABTDLQAQLQMFRAQMMFELAPGVSSSNLENRPQER SLQKTSADTKGKQEQAKEEKARELFLKAVEEEQNGALYEB RRAMQLVPDIEFKITTTRSPDGDGGGGNSYIEDNDDDSKMA YFQQQUTFQESVLKLQPELESSQIHISVLPMEVLMYIFR SDLDLRSLEQLSLVCRGFYLCARDPEIWRLACLKYWGRSC PYTSWREMFLERPRVRFDGVYISKTYYIRQGEQSLDGFYR VEYYRYIRFPPDGHVMMLTTPEEPQSIVPRLRTR VEYYRYIRFPPDGHVMMLTTPEEPQSIVPRLRTR GPRNKKRGWRRLAQEPIGLEVDQPLEDVRLQERTSGCLLSS EKLFFVDTGSKEKGITKKRTKVQKKSLLLKKPLRVDLILE VPAPKDVLAHQVPNAKKLRRKEQLWEKLAKQGELPREVRR LLNPSATRAKPGPQDTVERPFYDLWASDNPLDRFLVGQDE QTKKKGVKRFARLTHKPSQAPAVEVAPAGASYNPSFEDHQ QTKKKGVKRFARLTHKPSQAPAVEVAPAGASYNPSFEDHQ AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCE ESDGEGEGQGGGEGEAGDAEVCFTPARLATTEKKTEQORN VPHLRVQQAALRAARLHQELFRLIGIKAQVALRLELLARI RQARREAEADKPRRLGRLKYQAPDIDVQLSSELTDSLRTLI NILKDRFKSFQRRMMIEPRERAKFKRKYKVKLVEKRAFRE: ACQAREAEADKPRRLGRLKYQAPDIDVQLSSELTDSLRTLI NILKDSARPAGKGAIIGFIKVGYKKLFVLDDREAHMEVEPI DFYTHESVQRHGHGREFFGVMLQKERVEPHQLAIDRPSQKI LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSRATRHEVEPI DFYTHESVQRHGHGREFFGVMLQKERVEPHQLAIDRPSQKI AVDPTPAAPARKLPPKRREGDIKPYSSSDREPLKVAVEPP RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP SSAVEFVWEGEKMAAEENKTEIQTLFKKLRAVFTMKACFDC NPSWASITYGVFLCIDCSGVHRSLGVHLSPIRSTELDSNUM LRCMQVGGNANATAFFROHGCTANDANTKYNSRAAQMYREK LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTOP DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKAS KSSIIGKKKPAAAAKKGLGAKGLGAOKVSSOSFSREEPDAO	שממר
SLOKTSADTKOKOGOAKEEKARELFLKAVEEGOMAALYEA RAMQLVPDI EFKITYTRSPDGDGVGNSYIEDNDDDSKMA YFQQQLTFQESVLKLCQPELESSQIHISVLPMEVLMYIFR SDLDLRSLEQLSLVCRGFYYCARDPEIWRLACLKVWGRSC PYTSWREMFLERPRVRFDGVYISATTYIRQEGSLDGFYR VEYYRYIRFFFDGHVMMLTTPEEPQSIVPRLRTR VEYYRYIRFFFDGHVMMLTTPEEPQSIVPRLRTR GFRNKKRGWRLAGSPIGEVDQFLEDVRLQERTSGGLLS EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLEVDLILE EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLEVDLILE VPAPKDVLAHQVPNAKKLRKEGQLWEKLAKQGSLPREVRR LLNPSATRAKPGPQDTVERPFYDLWASDNPLDRPLVGQDE QTKKKGVKRPARLHTKPSQAPAVEVAPAGASINPSFEDHQ AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCE ESDGFGEFGGGGGFBAGDABVCPTPARLATTEKKTEQORR VHRLRVQQAALRAARLRIGELFRLRGIKQAQVALRLABLARI RQARREABADKPRRLGRIKYQAPDIDVQLSSELTDSLRTLI NILKDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAFRE: ARVDLQQIMTI IDELGKASAKAQNLSAPITSASRMQSNRT LLKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHHEVEPI DFYTHESVQRHGHGRELFGYMLQKERVEPHQLAIDRPSQKI LNKHYNLETTVPQVNNFVIFGFFAHQHPPAPSSKATRHE AVDPTPAAPARKLPPKRREGDIKPYSSSDREFLKVAVEPPW RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP SSAVEFWEGKMAAEENKTEIQTLFKRLRAVPTNKACPDG NPSWASITYGVFLCIDCSGVHRSLGVHLSPIRSTELDSNUM LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREK LGSAALARHGTDLWIDNMSSAVPNHS PEKKDSDFFTEHTQP DAATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKAS KSSIIGKKKPAAAAKKGLGAKGLGAOKVSSOSFSREEPDAO	מסמ
RRAMQLUPDIEFKITYTRSPDGGSVGNSYIEDNDDDSKMA YFQQQLTFQESVLKLCQPELESSQIHISVLPMEVLMYIFGDLDLRSLEQLSLVCRGFYICARDPEIWRLACLKVWGRSC PYTSWREMFLERPRVRFDGVYISKTTYIRQGEQSLDGFYR VEYYRYIRFFPDGHVMMLTTPEEPQSIVPRLETR FFFDKMAAGGSGVGGKRSSKSDADSGFLGRFTSVDPALR GPRNKKRGWRRLAQBPLGLEVDQFLEDVRLOERTSGGLLS EKLFFDDTGSKEKGLTKKRTKVQKKSLLLKKPLRVDLILE VPAPKDVLAHQVPNAKKLRRKEQLWEKLAKQGELPREVRR LLNPSATRAKPGPQDTVERPFYDLWASDNPLDRPLVRGDE QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQ AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCE ESDGEGEPGQGEGPEAGDAEVCPTPARLATTEKKTEQQRR RQARREAEADKPRRLGRLKYQAPDIDVQLSSELTDSLRTLI NILRDRFKSFQRRNNIEPRERAKFRKYKVKLVEKRAFRE- RQARREAEADKPRRLGRLKYQAPDIDVQLSSELTDSLRTLI NILRDRFKSFQRRNNIEPRERAKFRKYKVKLVEKRAFRE- ARVDLQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRR ILKDSSAPPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPI DFYIHESVQRHGHGRELFQYMLQKERVEPHQLAIDRPSQKI LNKHYNLETTVPQVNNFV1FEGFFAHQHRPPAPSLRATRHS AVDPTPAAPARKLPPKRAEGDIKPYSSSDREPLKVAVEPPW RAPRRATTPAHPPPRSSSLGNSPERGPLRPFVP 6473 22 912 SSAVEFVWEGEKMAAEPNKTEIQTLFKRLRAVPTNKACFDC NSEWASITYGVFLCIDCSGVHRSLGVHLSPIRSTELDSNWN LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREK LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQP DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLLGTSPKAS KSSIIGKKKPAAAKKGLGAKCGLGAKCGLGACKCSCOSFERLERDAG	עמעו
SDLDLRSLEQLSLVCRGFYICARDPEIWRLACLKVWGRSC PYTSWREMFLERPRVRFDGVYISKTTYIRQGEQSLDGFYR VEYYRYIRFPDGHVMMLTTPEEPQSIVPRLRTR FFFDKMAAGGSGVGGKRSSKSDADSGFLGLRPTSVDPALR GPRNKRGWRRLAQBPLGLEVDQFLEDVRLQERTSGGLLS EKLFFVDTGSKEGITKKRTKVQKKSLLLKKPLRVDLILE VPAPKDVLAHQVPNAKKLRRKEQLWEKLAKGGELPREVRR LLNPSATRAKPGPQDTVERPFYDLWASDNPLDRPLVGQDE QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQ AAHEVELQRQKEABKLERQLALPATEQAATQESTFQELCE ESDGEGEPQGEGPEAGDAEVCPTPARLATTEKKTEQORR VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARI RQARREAEADKPRRLGRLKYQAPDIDVQLSSELTDSLRTLI NILBRPKFSFQRRNMIEPRERAKFKRKYKVKLVEKRAFRE: ARVOLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRT ILKDSSARPAGKGAIIGFIKVGVKKLFVLDDREAINEVEPP DFYTHESVQRHGHGRELFQYMLQKERVEPHQLAIDRPSQKI LNRHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATRHE AVDPTPAAPARKLPPKRAEGDIKPYSSSDREPLKVAVEPPW RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP SAVEFVWEGEKMAAEPNKTEIQTLFKRLRAVFTNKACFDC NPEWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSNWM LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREK LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQP DAFATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKAS KSSIIGKKKPAAAKKGLGAKKGLGAOKVSSOSFSEIERDAO KSSIIGKKKPAAAKKGLGAKKGLGAOKVSSOSFSEIERDAO	OT T.C.
6471 1750 299 FFFDKMARGSGVGKRSKSDADSGFLGKPTSVDPALR GPRNKKRGWRRLAQEPLGLEVDQFLEDVRLQERTSGGLLS GPRNKKRGWRRLAQEPLGLEVDQFLEDVRLQERTSGGLLS EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLRVDLILE VPAPKDVLAHQVPNAKKLRRKEQLWEKLAKQGELPREVRR LLNPSATRAKPGPQDTVERPFYDLWASDNPLDRPLVGQDE QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQ AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCE ESDGEGEPGQGEGPEAGDAEVCPTPARLATTEKKTEQORR VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRALAELARI RQARREAEADKPRRLGRLKYQAPDIDVQLSSELTDSLRTLI NILRDRFKSFQRRNMIEPRERAKFKRYKVKLVEKRAFRE GA72 3 897 SCGSDRAQWAMEFPFDVDALFPERITVLDQHLRPPARRPGT ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRH LLKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPI DFYIHESVQRHGHGRELFQYMLQKERVEPHQLAIDRPSQKI LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATRHS AVDFTPAAPARKLJPKRARGDIKPYSSSDREFLKVAVEPPW RAPRRATPPAHPPPRSSSLGNSPERGPLRFFVP SSAVEFVWEGEKMAAEPNXTEIQTLFKRLRAVPTNKACFDC NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSMMN LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREK LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQP DAFFATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKAS KSSIIGKKFRAAKKGLGAKKGLGAOKVSSOSFSELERDAO	IVV S
6471 1750 299 FFFDKMAAGGSGVGKRSKSDADGFLGLRFTSVDPALR GFRNKKRGWRRLAQEPLGLEVDQFLEDVRLQERTSGGLLS EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLRVDLILE VPAPKDVLAHQVPNAKKLRRKEQLWEKLAKQGELPREVRR LLNPSATRAKPGPQDTVBRPFYDLWASDNPLDRPLVGQDE QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQ QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQ AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCE ESDGEGEFGQGEGPEAGDAEVCPTPARLATTEKKTEQQRR VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARI RQARREAEADKPRRLGRIKYQAPDIDVQLSSELTDSLRTLJ NILRDRPKSFQRRNMIEPRERAKFKRKYKVKLVEKRAFRE: ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRI ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPI DFYIHESVQRHGHGRELFQYMLQKERVEPPQLAIDRPSQKI LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATRHS AVVDFTPAAPARKLPPKRAEGDIKPYSSSDREFLKVAVEPPW RAPRRATPPAHPPPRSSLGNSPERGPLRFVP 6473 22 912 SSAVEFVWEGEKMAAEPNKTEIQTLFKRLRAVFTNKACFDC NPSWASITYGVFLCIDCSGVHRSLGVHLSPIRSTELDSNWN LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREK LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQP DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKAS KSSIIGKKKPAAAKKGLGAKGLGAOKYSOSFSEIEROAO	KLV
FFFDKMAAGGSGVGGKRSSKSDADSGFLGLRPTSVDPALR GPRNKKRGWRRLAQEPLGLEVDQFLEDVRLQERTSGGLLS EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLRVDLILE VPAPKDVLAHQVPNAKKLRKEQLWEKLAKQGELPREVRR LLNPSATRAKPGPQDTVERPFYDLWASDNPLDRPLVGQDE QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQ AAHEVELQRQKEAEKLERQLALPATEQAATQESSTFQELCE ESDGEGEPGQGEGPEAGDABVCPTPARLATTEKKTEQQRR VHRLRVQQAALRAARLHRQELFRLRGIKAQVALRLAELARI RQARREAEADKPRRLGRLKYQAPDIDVQLSSELTDSLRTLJ NILRDRFKSFQRRNMIEPRERAKFKKYKVKLVEKRAFRE: ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNR ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPI DFYIHESVQRHGHGRELFQYMLQKERVEPHQLAIDRPSQKI LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATRHS AVDPTPAAPARKLPPKRAEGDIKPYSSSDREPLKVAVEPPW RAPRRATPPAHPPPRSSSLGNSPERGPLRFVP SSAVEFVWEGEKMAAEPNKTEIQTLFKRLRAVPTNKACFDC NPSWASITYGVFLCIDCSGVHRSLGVHLSPIRSTELDSNWN LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREK LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQP DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKAS KSSIIGKKKPAAAKKGLGAKGLGAOKYSOSFSEIRFOAA	QHW
GPRNKKRGWRLLAGEPLGEVDQFLEDVRLQERTSGGLLS EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLERVDLILLE EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLERVDLILLE VPAPKDVLAHQVPNAKKLRRKEQLWEKLAKQGELPREVRR LLNPSATRAKPGPQDTVERPFYDLWASDNPLDRPLVGQDE QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQ AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCE ESDGEGEPGQGEGPEAGDAEVCPTPARLATTEKKTEQQRR; VHRLRVQQAALRAARLEHQELFRLEGIKAQVALRLAELARI RQARREAEADKPRRLGRLKYQAPDIDVQLSSELTDSLRTLJ NILRDRFKSFQRRNMIBPRERAKFKRKYKVKLVEKRAFRE: AVADLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNNL LIKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPI DFYIHESVQRHGHGRELFQYMLQKERVEFHQLAIDRPSQKI LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATRHS AVDPTPAAPARKLPPKRAEGDIKPYSSSDREFLKVAVEPPW RAPRRATPPAHPPPRSSLGNSPERGPLRPFVP SSAVEFVWEGEKMAAEPNKTEIQTLFKRLEAVPTNKACFDC NPSWASITYGVFLCIDCSGVHRSLGVHLSPIRSTELDENWN LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREK LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQP DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKAS KSSIIGKKKPAAAKKGLGAKGLGAOKYSOSFSEIRPOAO	
EKLFFVDTGSKEKGLTKKETKVOKKSLLLKKPLRVDLILE VPAPKDVLAHQVPNAKKLRRKEQLWEKLAKQGSLPREVRR LLNPSATRAKPGPQDTVERPFYDLWASDNPLDRPLVGQDE QTKKKGVKRPARLHTKFSQAPAVEVAPAGASYNPSFEDHQ AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCE ESDGEGEPGQGEGPEAGDABVCPTPARLATTEKKTEQQRR VHRLRVQQAALRAARLENQELFRLEGIKAQVALRLAELARI RQARREAEADKPRRLGRIKYQAPDIDVQLSSELTDSLRTLJ NILRDFRSFGQRRNMIBPRERAKFKRKYKVKLVEKRAFRE: ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRI ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDGHLRPPARREGT ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRI ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPI DFYIHESVQRHGHGELFQYMLQKERVEPHQLAIDRPSQKI LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATIRHS AVDFTPAAPARKLPPKRAEGDIKPYSSSDREFLKVAVEPPW RAPRRATPPAHPPRSSSLGNSPERGPLRPFVP SSAVEFVWEGEKMAAEPNKTEIQTLFKRLRAVFTNKACFDC NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSNWN LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREK LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQAB DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKAS KSSIIGKKKPAAAKKGLGAKGLGAOKYSSOSFSEIRFOAD	RRR
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ID	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
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GLVQEAAQPQGSTSETPWNTAIPLPSCWDQSFLTNITFLKVLLW	[-	723	
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L DADTGTLAREDELAKEDEKATA DATTGTLAREDELAKEDEK DATTGTLAREDE DATTG			}	
			_ L	DADPOPLARDELGTWALEATEXMMAAGLEGEREKEGERSWAR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
-	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			VFNPGCEAIQGTLTAEQLERELQLRPLAGR
6484	201	965	QLAVKTKMSGLRPGTQVDPEIELFVKAGSDGESIGNCPFCQRLF
		1	MILWLKGVKFNVTTVDMTRKPEELKDLAPGTNPPFLVYNKELKT
i	İ	ĺ	DFIKIEEFLEQTLAPPRYPHLSPKYKESFDVGCNLFAKFSAYIK
1			NTQKEANKNPEKSLLKEFKRLDDYLNTPLLDEIDPDSAEEPPVS
1	1		RRLFLDGDQLTLADCSLLPKLNIIKVAAKKYRDFDIPAEFSGVW
!	1		RYLHNAYAREETHTCPEDKEIENTYANVAKQKS
6485	6	1091	FYDLVRAVEFLPCPDSQKLEKECQSSEBSMGSNSMRSILEEDEE
	•	1031	DEPENDENT VERDECERVONT FRANCISCO
j	1		DEEPPRVLLYHEPRSFEVGMLVWHKHKKYPFWPAVVKSVRQRDK
			KASVLYIEGHMNPKMKGFTVSLKSLKHFDCKEKQTLLNQAREDF
			NQDIGWCVSLITDYRVRLGCGSFAGSFLBYYAADISYPVRKSIQ
1	1		QDVLGTKLPQLSKGSPEEPVVGCPLGQRQPCRKMLPDRSRAARD
	1		RANQKLVEYIGKAKGAESHLRAILKSRKPSRWLQTFLSSSQYVT
İ			CVETYLEDEGQLDLVVKYLQGVYQEVGAKVLQRTNGDRIRFILD
	}		VLLPEATICAISAGDEVDYKTAEEKYIKGPSLSYREKEIFDNQL LEERNRRRR
6486	10	581	
1		301	LVLQAGGAHLSPSRVTQGIYYMLAFSEMPKPPDYSELSDSLTLA GGTGRFSGPLHRAWRMMNFRQRMGWIGVGLYLLASAAAFYYVFE
}			ISETYNRLALEHIQQHPEEPLEGTTWTHSLKAQLLSLPFWVWTV
ł			IFLVPYLQMFLFLYSCTRADPKTVGYCIIPICLAVICNRHQAFV
			KASNQISRLQLIDT
6487	352	863	SFLKPLRGKMSVTLHTDVGDIKIEVFCERTPKTCENFLALCASN
1	1	****	YYNGCIFHRNIKGFMVQTGDPTGTGRGGNSIWGKKFEDEYSEYL
			KHNVRGVVSMANNGPNTNGSQFFITYGKQPHLDMKYTVFGKVID
İ			GLETLDELEKLPVNEKTYRPLNDVHIKDITIHANPFAQ
6488	878	241	TALQEFGTSGPPLSLRFALPSGTGRFKPLPGARGPSWPPSPRVP
1 1			MEPPNLYPVKLYVYDLSKGLARRLSPIMLGKQLEGIWHTSIVVH
1 1			KDEFFFGSGGISSCPPGGTLLGPPDSVVDVGSTEVTEEIFLEYL
			SSLGESLFRGEAYNLFEHNCNTFSNEVAQFLTGRKIPSYITDLP
1 1			SEVLSTPFGQALRPLLDSIQIQPPGGSSVGRPNGQS
6489	1457	375	KVAKMATALSEEELDNEDYYSLLNVRREASSEELKAAYRRLCML
1 1			YHPDKHRDPELKSQAERLFNLVHQAYEVLSDPQTRAIYDIYGKR
1 1			GLEMEGWEVVERRRTPAEIREEFERLQREREERRLQQRTNPKGT
1	į		ISVGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL
1	1		TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG
1			DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTTVLAR
] [l		NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP
1	ļ		TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR
1		İ	SKRRTGGG
6490	3	1183	HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARS IAADH
		}	KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT
1			HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG
1 1			QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE
] I			APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD
		ļ	DSSPNAMAKVQIFEYNENTRKYAKARTLMTVTDPVHDIAFAPNL
	í	j	GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD
		ļ	NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL
1		1	KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS
6491	3	1183	HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH
1 1	1		KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT
] [ľ	HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG
1 . I	1	j	QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE
	}	į	APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD
	İ	ľ	DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL
1 I		ļ	GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD
	ļ	ł	NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL
			THE TOTAL THE TOTAL THE TANK T

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	A=Alanine, C=Cysteine, D=Aspartic hold =-
	location	1	Glutamic Acid, F=Phenvlalanine, G-Glygine
1	corresponding	to first	H=Hlstidine, I=Isoleucine K=Tweine
	to first		L=Leucine, M=Methionine, N=Asparagine,
ł	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
1	residue of	residue of	S=Serine, T=Threonine, V=Valine,
ł	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
j	sequence	sequence	Codon, /=possible nucleotide deletion
	Deductive		\=possible nucleotide insertion\
6492	34	0.500	KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS
1	1	2573	IPFLKSCCCCLFDFPPPPLDOVOEEECEVEPVTFUCTDVDEDV
1	1	1	FUSVAFGESQSEDEQFENDLETDPPNWOOTVSREVILLGLYDCET
ł	1		KRQEVINELFYTERAHVRTLKVLDOVFYORVSREGIT.Spset.by
[1		IFSNLEDILQLHIGLNEOMKAVRKRNETSVIDOTGEDLITWESG
i			PGEEKLKHAAATFCSNQPFALEMIKSROKKDSRFOTEVODDESN
Į.	İ		PUCKRLQLKDIIPTQMQRLTKYPLLLDNIATYTEWPTEPEYUUV
	ł		AADHCRQILNYVNQAVKEAENKORLEDYORRI.DTSSI.KI.SEVDM
			VEEDKNLDLTKRKMIHEGPLVWKVNRDKTIDLYTLLEDILYLL
1			QKQDDRLVLRCHSKILASTADSKHTFSPVTKI,STVT.VPOVATON
1			KALFVISMSDNGAQIYELVAOTVSEKTVWODI.ICPMAASUKFOS
1	l i		TKPIPLPQSTPGEGDNDEEDPSKLKEEOHGISVTGLOSDDEDLO
}	!		LESTLISSKPQSHSLSTSGKSEVRDLFVAEROFAKEOHTDCTT.v
ł	1		EVGEDYQIAIPDSHLPVSEERWALDALRNIGLIKOLLVOOLGLT
1] ;		EKSVQEDWQHFPRYRTASQGPQTDSVIONSENIKAVHSGFGHMD
1	1 1		FRIGIGDIATCYSPRTSTESFAPRDSVGLAPODSOASNIT.VMDu
	i i		MIMITPEMPTMEPEGGLDDSGEHFFDAREAHSDENDSEGDGAVNK
	1		EEKDVNLRISGNYLILDGYDPVOESSTDEEVASSITIOPMTGTP
Į.	!		AVESTHQQQHSPQNTHSDGAISPFTPEFLVOORWGAMEVSCERT
İ	1		QSPSSCADSQSQIMEYIHKIEADLEHLKKVEESYTILCQRLAGS
6493			ALTUKHSDKS
0493	557	1147	TPARMAYQGSSTSDCMSKTLDSASAHFAASAVVSAPVPSRSEVA
1			KEQNIGHNNINGVVQPSGTSKTLYSTNMALSSSPGTSAVOLVDr
1			VGHTTTNHLIPALCTSSPOTLPMNNSCLTNAUHT MMUSYATEDIAT
}	1	į	VHINTRTSAPSPTALKLATVAASMDRVPKVTPSSAISSTARENH
6494	2425		EPERLGLNGIAETTVAMEVT
"""	2425	1052	AVAGGARPCSTPSSPHRRCRRHRPRPLPRPPAAIMSASAVYVLD
			LKGKVLICRNYRGDVDMSEVEHFMPILMEKEERGMI.SDILAUGG
1			VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKUMOVESEVEVET
1 1		j	EEESIRDNFVIIYELLDELMDFGYPQTTDSKILQEYITQEGHKL
1 1	!		ETGAPRPPATVTNAVSWRSEGIKYRKNEVFLDVTRSVNLLVSAN
1	i	1	GNVLRSEIVGSIKMRVFLSGMPELRLGLNDKVLFDNTGRGKSKS
1 1	į.		VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLNTHVK
	1		PLIWIESVIEKHSHSRIEYMIKAKSQFKRRSTANNVEIHIPVPN
j j	j	į	DADSPKFKTTVGSVKWVPENSEIVWSIKSFPGGKEYLMRAHFGL
1		1	PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL PWVRYITQNGDYQLRTQ
6495	2425	1052	AVACCARDOCONDOCANIDACTOR
	i		AVAGGARPCSTPSSPHRRCRRHRPRPLPRPPAAIMSASAVYVLD
' I	ļ		LKGKVLICRNYRGDVDMSEVBHFMPILMEKEEEGMLSPILAHGG VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVQVFSEYFKEL
Ì	1		EEESIRDNFVIIYELLDELMDFGYPQTTDSKILQEYITQEGHKL
	i	1	ETGAPRPPATVTNAVSWRSEGIKYRKNEVFLDVIESVNLLVSAN
' 1	1		GNVLRSEIVGSIKMRVFLSGMPELRLGLNDKVLFDNTGRGKSKS
		1	VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLNTHVK
- 1		Į.	PLIWIESVIEKHSHSRIEYMIKAKSQFKRRSTANNVEIHIPVPN
1	1	i :	DADSPKFKTTVGSVKWVPENSEIVWSIKSFPGGKEYLMRAHFGL
	j		PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL
		-	PWVRYITQNGDYQLRTO
6496	247	559	LRAVSLLPLQLVLPEYSIHSLFCIMFLCAQEWLTLGLNVPLLFY
l l		1	HFWRYFHCPADSSELAYDPPVVMNADTLSYCQKEAWCKLAFYLL
	_	13	SFFYYLYCMIYTLVSS
6497	1053	352	ANTOI CPI, CPPPUT UPDOGA KNOWGO
j		1,	ANTOICRLCPRRHLHPPCGAKMGNGTEEDYNFVFKVVLIGESGV
l		1,	SKTNLLSRFTRNEFSHDSRTTIGVEFSTRTVMLGTAAVKAQIWD
ļ	İ	;	MAGLERYRAITSAYYRGAVGALLVFDLTKHQTYAVVERWLKELY
		2	DHAEATIVVMLVGNKSDLSQAREVPTEEARMFAENNGLLFLETS
			ALDSTNVBLAFETVLKEIFAKVSKQRQNSIRTNAITLGSAQAGQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
I	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- }	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	4	\=possible nucleotide insertion)
	 		EPGPGEKRACCISL
6498	2636	272	
		212	SLRLCPWGTHLAGPTTMRLSSLLALLRPALPLILGLSLGCSLSL
1	1		LRVSWICGEGEDPCVEAVGERGGPQNPDSRARLDQSDEDFKPRI
1			VPYYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTL
1	1		AVAVNRTVAHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLM
Ī	1		SETLRHLHTHFGADYDWFFIMQDDTYVQAPRLAALAGHLSINQD
	1		LYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
ì	· I		DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPE
			KEGSSAFLSAFAVHPVSEGTLMYRLHKRFSALELERAYSEIEQL
1	1		QAQIRNLTVLTPEGEAGLSWPVGLPAPFTFHSRFEVLGWDYFTE
	i		QHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRF
			QKQRLLNGYRRFDPARGMEYTLDLLLECVTQRGHRRALARRVSL
1	1		LRPLSRVEILPMPYVTEATRVQLVLPLLVAEAAAAPAFLEAFAA
Ì	1		NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAAELERRY
1	1		PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPG
1	1		PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPGPPGAGP
}	1 1	•	DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAARARLAG
	1		ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRD
6499	3	2040	CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQANST
1		2040	SCSADTRPSGQAWPTVGLRAAAGAFRTGSPLALGPETPQVACLP
		İ	GHPPVRPQVSGGPGAMPDPAAHLPFFYGSISRAEAEEHLKLAGM
}			ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNGTYAIAG
1	1 1		GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPOPGVFDC
I	1		LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIATTAHERM
ı	i i		PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYALSLIYG
1	! !		KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKADGLIYC
1	l i		LKEACPNSSASNASGAAPTLPAHPSTLTHPQRRIDTLNSDGYT
			PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLFLKRDNL LIADIELGCGNFGSVRQGVYRMRKKQIDVAIKVLKQGTEKADTE
	i	1	EMMREAQIMHQLDNPYIVRLIGVCQAEALMLVMEMAGGGPLHKF
	ı		LVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLL
1			VNRHYAKISDFGLSKALGADDSYYTARSAGKWPLKWYAPECINF
	Į.		RKFSSRSDVWSYGVTMWEALSYGQKPYKKMKGPEVMAFIEQGKR
1	į		MECPPECPPELYALMSDCWIYKWEDRPDFLTVEQRMRACYYSLA
			SKVEGPPGSTQKAEAACA
6500	1773	726	TGPTHASADAWGLVRSVTBWCANVRGNPCAAALSCPQAVLDAGK
			MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHL
1	1	ľ	QAPNKEDILKISEDERMELSKSFRVYCIILVKPKDVSLWAAVKE
		}	TWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRKAYKYAFDK
]	. [Ī	YRDQYNWFFLARPTTFALIENLKYFLLKKDPSQPFYLGHTIKSG
	1		DLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWKISED
1 1	ļ	ł	KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN
			QVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFO
6501	1	570	LVGMSGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGE
[]	ľ		IHSRLLDHRPVIQGETRYFVKEFEEKRGLREMRVLENLKNMIHE
l l			TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREOERKKI
j	1		HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ
			YAEMEKDLAKFSTF
6502	213	1650	AGYKPDPWAGRNRTAVLPDVSVFHREDVGWNRSWLQQSYQAVKE
		1	KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS
		1	SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT
i	j	1	AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK
	1	1	KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHOLEO.
1	Į.	1	EQARRDALKQRAEQSISEEPGWEEEEEBLMGISPISPKEAKVPV
1			AKISTFPEGEPGPQSPCEENLVTSVEPPAEVTPSESSESISLVT
			QIANPATAPEARVLPKDLSQKLLEASLEEQGLAVDVGETGPSPP

SEQ	Predicted	Predicted end	Amino acid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
[amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Ston
	sequence	sequence	Codon, /=possible nucleotide deletion
 	Bequence	ļ	\=possible nucleotide insertion)
Ì		1	IHSKPLTPAGHTGGPEPRPFARVETLREEAPTDLRVFELNSDSG
			KSTPSNNGKKGSSTDISEDWEKDFDLDMTEEEVQMALSKVDASG
6503	213	1650	EVSGPGGSEGSEPNGPGCESSPQPAQLSPQEGPCSCLR
}	j		AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE
		ĺ	KSSEALEFMKRDLTEPTQVVQHDTACTIAATASVVKEKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT
			AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK
1			KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ
1			EQARRDALKORAEQSISEEPGWEEEEBLLMGISPISPKEAKVPV
ı			AKISTFFEGEPGPQSPCEENLVTSVEPPAEVTPSESSESISLVT
ļ			QIANPATAPEARVLPKDLSQKLLEASLEEOGLAVDVGETGDSDD
Ĭ			INSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFELNSDSG
1			KSTPSNNGKKGSSTDISEDWEKDFDLDMTREEVOMALSKUDASC
6504			EVSGPGGSEGSEPNGPGCESSPOPAOLSPOEGPCSCLP
0304	2131	1294	GKVCLVAHWVCLSILSPPPAGMKTPNAOEAEGOOTRAAAGRATC
			SANMTKKKVSQKKQRGRPSSQPCRNIVGCRISHGWKEGDEDTTO
			WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
1 1			DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA
1 1			PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE
1 1			REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF DDDFHIYVYDLVKKS
6505	2131	1294	
1	Ĭ		GKVCLVAHWVCLSILSPPPAGMKTPNAQEAEGQQTRAAAGRATG SANMTKKKVSQKXQRGRPSSOPCRNIVGCRISHGWKEGDEPITQ
	Ĭ		WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
1			DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA
1	1		PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSBSPPTE
1 1	1		REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF
6506			DDDFHIYVYDLVKKS
6506	1	1350	EVSPPTSCCLTVAVADPGVSEGFRGFGAGCEMPGRGRCPDCGST
1 1			ELVEDSHYSQSQLVCSDCGCVVTEGVLTTTFSDEGNI.prvTvqp
1 1			STGENEQVSRSQQRGLRRVRDLCRVLOLPPTFRDTAVAVVOOAV
1			RHSGIRAARLQKKEVLVGCCVLITCRQHNWPLTMGAICTLLYAD
1 1	1		LDVFSSTYMQIVKLLGLDVPSLCLAELVKTYCSSFKLFQASPSV
1 1			PAKYVEDKEKMLSRTMQLVELANETWLVTGRHPLPVITAATFLA
1 1			WQSLQPADRLSCSLARFCKLANVDLFYPASSRLQELLAVLLRMA EQLAWLRVLRLDKRSVVKHIGDLLQHRQSLVRSAFRDGTAEVET
1 1	1		REKEPPGWGQGGGGEVGNNSLGLPQGKRPASPALLLPPCMLKS
1 1			PKRICPVPPVSTVTGDENISDSEIEQYLRTPQEVRDFQRAQAAR
			QAATSVPNPP
6507	1878	929	RSHASRLPELPSGCLVLQVQELVQMSGMEATVTIPIWQNKPHGA
]		ł	ARSVVRRIGTNLPLKPCARASFETLPNISD;CLRDVPDVDTLAD
		i	IAWIAADEEETYARVRSDTRPLRHTWKPSPLIVMORNASVPNID
			GSEERLLALKKPALPALSRTTELODELSHIRSOTAKTVAADAAC
			ASLTPDFLSPGSSNVSSPLPCFGSSFHSTTSFVISDITRETEUR
		J	VPELPSVPLLCSASPECCKPEHKAACSSSEEDDCVSLSKASSEA
		1	DMMGILKDFHRMKQSQDLNRSLLKEEDPAVLISEVLRRKFALKE
6508	862		EDISRKGN
1		376	WEARKRPORWPSERREVRVPPPHLQRGRSGLEPGTFRKMAAARP
			SIGRVLPGSSVLFLCDMQEKFRHNIAYFPQIVSVAARMLKNTTL
		1	DLLDRGLQVHVVVDACSSRSQVDRLVALARMRQSGAFLSTSEGL
6509	2	1053	ILQLVGDAVHPQFKEIQKLIKEPAPDSGLLGLFQGQNSLLH
	1		FVWNPRGGRKRRRQAAVTQAATRASGTPSPRDGTMTQGKLSVAN KAPGTEGQQQVHGEKKEAPAVPSAPPSYEEATSGEGMKAGAFPP
1			APTAVPLHPSWAYVDPSSSSYDNGFPTGDHELFTTPSWDDQKV
i	j	11	RRVFVRKVYTILLIQLLVTLAVVALFTFCDPVKDYVQANPGWYW
			ASYAVFFATYLTLACCSGPRRHFPWNLILLTVFTLSMAYLTGML
			THE THE PERSON OF THE PERSON O

SEQ	1 5 11		
	Predicted	Predicted end	
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamia Arid R DE DE ASPAREIC Acid, E=
[location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
- 1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
- 1	to first		L=Leucine, M=Methionine, N=Asparagine,
	amino acid	amino acid	P=Proline, O=Glutamine, D=Arginine
	amilio acid	residue of	S=Serine, T=Threonine, V=V=line
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ì	sequence	1 -	\-resible mucleotide deletion,
			\=possible nucleotide insertion)
-	. i	ŀ	SSYYNTTSVLLCLGITALVCLSVTVFSFQTKFDFTSCQGVLFVL
í		!	MILLE FOGULLATILIPFOYVPWI.HAVVAAI.GAGVETT. DI AT DEC
<u> </u>		}	LLMGNRRHSLSPEEYIFGALNIYLDIIYIFTPFLQLFGTNRE
6510	37	1156	PCALDGCPQRGAVHPLLSSAMGLLAFLKTQFVLHLLVGFVFVVS
ł	ı		GLVINEYOLOGU AT ATTEMPT OF THE TOP OF THE LIVERY OF THE LI
	1		GLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLVMLLEWW
	[}	SCIECTLF TDQATVERFGKBHAVIILNHNFETDELCGUTMCEDE
ſ	1	ł	GVLGSSKVLAKKELLYVPLIGNTWYFLEIVFCKRKWFFDDDWM
	1	ĺ	EGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSMEVAAAKGLPVL
- [i	KYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGIL
1	ŀ	ļ	YGKKYEADMCUPPEDI EDYDI PRUDA DOWNERSKANPSLLGIL
1			YGKKYEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIY
ĺ	j i		NOKGMFFGEQFKPARRPWTLLNFLSWATILLSPLFSFVLGVFAS
6511	2541	140=	GSPLLILTFLGFVGAGNGHCR
1	2247	1425	GEEQPLAAAPTECLEQVIGGAGDPGTWASFPSPLPGPAPLKGGK
1	1 1		TMATNFSDIVKQGYVKMKSRKLGIYRRCWLVFRKSSSKGPQRLE
Ĭ	1		KYPDEKSVCLRGCPKVTEISNVKCVTRLPKETKRQAVAIIFTDD
Į.	[SARTFTCDSELEAEEWYKTLSVECLGSRLNDISLGEPDLLAPGV
į.			OCEOTOPPANIEL L DON'T DIRECTES KENDISLGEPOLLAPGV
}	1		QCEQTDRFNVFLLPCPNLDVYGECKLQITHENIYLWDIHNPRVK
ł	1		UVSWPLCSLKKYGRDATRFTFRAGRMCDAGEGI.VTFOTOFGPOT
			1 1QRVHSATLAIAEOEKRVLLEMEKNVRIJNKGTEUVGVDGTDTTT
1	1		MDPRSAYWHHITGSQNIAEASSYAGEGYGAAOASSETDII.NPFT
6512			LUKPKPSQGDSSEAKTPSO
6512	159	807	FGKKSTWFPLSRSLRVASGRSCKLGHGGYTGSGPGFGEPRDSGA
ľ	l i		EVPSGSGRATGCERGGVRGARQGRAPGSSIWRKEPRMVCTRKTK
	1		TIVSTCUTI.COMPATION INC.
	1		TLVSTCVILSGMTNIICLLYVGWVTNYIASVYVRGQEPAPDKKL
1]	i	EEDKGDTLKIIERLDHLENVIKQHIQEAPAKPEEAEAEPFTDSS
6513	2		LPARWGQELSPEGRRVALKOFOYYGYNAVI.chpt.hbb
1 -5225	1 2 1	756	FVSPEPGFSLAQLNLIWOLTDTKOLVHSFAEGODOGGAVANDTA
	}		DE PUBLIAQUINASEREORVRVADEGSETCEVS TEDEGGAAVELOU
1		ł	AAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQ
1			GVPLTGNVTTSOMANEQGLFDVHSILRVVLGANGTYSCLVRNPV
1	1		LOODAUSSUTTEDODGODGODGOTTOVASTERVVLGANGTYSCLVRNPV
1			LQQDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSF
İ	İ	l l	SPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALF
1	1	i	PULLAQGNASLRLQRVRVADEGSFTCFVSTPDFGGAAVGTOVAA
	1		PISKPSMILEPNKDLRPGDTVTITCSSYOGVPPAFVFWODGOGV
1 1		i	PLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQ
	i i	İ	QDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSFSP
		!	EPGFSLAQLNLIWQLTDTRQLVHSFTEGR
6514	985	302	VGTDCRTTSCARTHODY
[]	1	. –	VGIPGPTISSAAEMEDLLDLDEELRYSLATSRAKMGRRAQQESA
1 !	ł	ſ	QAENHLINGKNESLTLTGETSSAKLPRCROGGWAGDSWKACKERD
1 1	1	1	KASEBIEDFRLRPQSLNGSDYGGDIPIIPDLEEVOEFDEVI OVA
		1	APPSIQIARVMTYRDLDNDLMKYSATOTI,DGFTDI,VI,I,TPVR, ND
1 1	1	.l	EHEVRERNPSWQDDVGWDWDHLFTEVSSEVLTEWDPLQTEKEDP
i	_	']	AGQARHT
6515	1345		
, ,	- 1		GRVGSRRRGAAVPGGCGAGSTQLEVSASASCGALGSADMNPIVV
j i	1		VIGGGAGPISKURKERVHOGMVRAATVGYGTIRECCGAUDAUDG
, 1	ı		AVVALEDDPEFNAGCGSVLNTNGEVEMDASTMDGKDLGAGAMER
j I	j	·	VQCIANPIKLARLVMEKTPHCFLTDQGAAQFAAAMGVPEIPGEK
[l	· .	LVTERNKKRLEKEKHEKGAQKTDCQKNLGTVGAVALDCKGNVAY
]	į į		ATSTCOT CARACTER STORE OF THE CONTROL OF THE CONTRO
{	1	· [:	ATSTGGIVNKMVGRVGDSPCLGAGGYADNDIGAVSTTGHGESIL
	1	1.	KVNLARLTLFHIEQGKTVEEAADLSLGYMKSRVKGLGGT.TVVCK
6516			IGDWVAKWTSTSMPWAAAKDGKLHFGIDPDDTTITDI.P
0270	1	1402	FRRLRYLGQDATAAARDLRTRGLQGYCPSATARQQVLVSALQQL
	f	1 7	KGRRSEHRNENQEMPYSTNKELILGIMVGTAGISLLLLWYHKVR
1	ı	1;	COCIAMKI DEET OF CHIEFICATION OF THE CONTROL OF THE COLUMN
i		1:	KPGIAMKLPEFLSLGNTFNSITLQDEIHDDQGTTVIFQERQLQI
	ł	[]	LEKLNELLTNMEELKEEIRFLKEAIPKLEEYIQDELGGKITVHK
	<u></u>]	(SPQHRARKRRLPTIQSSATSNSSEEAESEGGYITANTDTEEQS
		-	

	SEC	Q Predicted	Dwords -t - 3	
	ID		Predicted end	
	NO:		location	I Warranting, CECVSERING Deliconnection and a
		location	corresponding	Giucamic Acid, Febbanulalanian a al
		corresponding	to first	""" "" " " " " " " "
	i	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
		residue of	amino acid	W=Trimtonhan V=Tri
	l	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		sequence		\=possible nucleotide insertion)
	Į.			FPVPKAFNTRVEELNLDVLLQKVDHLRMSESGKSESFELLRDHK
	1	j		EXFRDEIEFMWRFARAYGDMYELSTNTQEKKHYANIGKTLSERA
			Í	TARGERINGICHLWIAVLCGYVSEREGIOMETHYGIY TURNING I
	l			1 AND PERFELITIES AND AND PRINCIPLE OF THE PROPERTY OF THE PRO
		ļ	ł	YEAR OF DEALER COUNTY TO THE TOTAL TO THE TOTAL TOTAL TOTAL TO THE TOTAL
	6517	3		I ALLOGE IV I REDKEAOKEMOK IMTGI.VD
			1414	GRVWGGSSSLNAMVYVRGHAEDVERWORDCARCHDVALLE
ı		1	1	AANGABLGASKYRGADGPLRVSPGKTNUDLUGADI DAMOOR GIID
		İ		1 DISSINGFOURGEGMENTIHEGROWGAACAUT WAXT COURSE TO 1
				EARLING KVLFEGTRAVGVEYVKNGOGUDAVACVDUTI GOGT TIT
- 1				SEVERILE GLICANDELKKI GT PUNCUI, DOUGONT OPER TELES
- 1				ACTRPITLHSAQKPLRKVCIGLEWLWKFTGEGATAHLETGGFIR
				SQPGVPHPDIQFHFLPSQVIDHGRVPTQQEAYQVHVGPMRGTSV
- 1				GWLKLRSANPQDHPVIQPNYLSTETDIEDFRLCVKLTREIFAQE ALAPFRGKELQPGSHIQSDKEIDAFVRAKADSAYHPSCTCKMGQ
- 1		1		PSDPTAVVDPQTRVLGVENLRVVDASIMPSMVSGNLNAPTIMIA
ŀ	6518			EKAADIIKGQPALWDKDVPVYKPRTLATQR
- 1	6218	242	1098	PAWNPGSEPRTRVRPRARSEDT, DDDDDDDDDDDDDDDD
- 1			1	ATTACARRAPPPPSTMGDAGSRRSKADST.DDDCDGGDttagagreen
				1 ACCRETADE VAROPDIDISAPSTERISACENT. PORREMONNAME 1
				A T T T S P S Q Q P D P T E D N V T S P S K E E C C D C T D T A UTC T T T D D T S C
- 1				1 0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
- 1		i .) NEED VOCALIGACIO VECMINET. DECUNOTED UMO DO DO SER I
	6519	3	1113	I MIVADDRAVGRSCORIGEGES
			1113	ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS
				I CANAL A CARALER VNGEGGGGGGGGGGGGT AND A NANA COLUMN
		Į.		I TO THE PURPOPOSION ASSESSES ASSESSED TO THE PROPERTY OF THE
i				VPPTLLHAQPHHLLLPAAAAASANAKSRRPKEKREKERRRHGL GGAREAGGASPEFNGEUNDLDDAY
-		1		GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKKHK VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKHK
- [
ı				MADDING TOSALPENSKEPROST KEDDIJOMNII POJ DOM BOSSO - 1
-	6520	 3		""" NEW TOOMS VINCTO
-		1 3 1	1113	ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS
				ANN VALEDANAPER VNGRGGSGCNSDOLODDAADGDAGGGGGGGGGGGGGGGGGGGGGGGGGGGG
		}		"DEPT COMPOSSIONS FOR SACTATION CARROLL COMPOSITION OF THE SACTATION OF TH
i		1		*** THUMAQPARLLLIPAAAAASANAYCDDDYDYDDYDDYDD
1				OUT DAGGESTEINGEVKPI PROKTKOKTVEDOVEVENDENTERS I
1		1 1		ATTACA TO CONCE ANT DIVERSE OF MALE AND A LANGUAGE CONTRACTOR OF THE PROPERTY
		1		ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG
 		<u> </u>		KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ
1 .	6521	184	1798	KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP
1		J		IRRTVNSTRETPPKSKLAEGEEKPEPDISSEESVSTVEEQENE TPPATSSEAFORYGERENE
1		1		TPPATSSEAEQPKGEPENEEKEENKSSEETKKDEKDQSKEKEKK
1		}	,	TAME A COMMITTION OF THE PROPERTY OF THE PROPE
				PUNSUAS V VALRKY LIHKYPSLEI. ERROUVI. I. VONT VERT MEGALET
				AQVAGAGGGFVVVOXSRKTPOKGRNPKNPGGAIDDEDOLEGE -
	1		F .	DVDPDAFIRDCEPKEASYSLIRKYVSOVVDVI.DVDTDDAFF
			1 .	DURAY DRUGULEOLIUKGASGTFOI, KKSGEKDI, I. GGGI MINAR TT. G
	1	ĺ	1 4	ALAMMSPKICSTIALKKYVLENHPGTNSNYOMULI VVIII OVOR
1	}		1 '	MGWIEQISGKGFSGTFOLCFPYYDSDGVI.FDKVFDDDGDDDD
l	ſ	1	1 2	DEDESSEEDSEDEEPPPKRRLOKKTPAKEDGKAAGUKODGGKD
L		1	1 2	FKVSAAQRGKARPLPKKAPPKAKTPAKKTPDSSTUTEVDSSGGS
6	522	1042		MPATSARRE
				KWLRPSPRSHRTPESGRVLSLFRLPPPGMALSGSTPAPCWEED

SEQ	Predicted	Predicted end	Amino poid compet
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
· I	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ſ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 -	\=possible nucleotide insertion)
			ECLDYYGMLSLHRMFEVVGGQLTECELELLAFLLDEAFGAAGGL
		ĺ	SRARSGLKLLLELERRGQCDESNLRLLGQLLRVLARHDLLPHLA
	1		RKRRRPVSPERYSYGTSSSSKRTEGSCRRRRQSSSSANSQQGSP
			PTKRQRRSRGRPSGGARRRRRGPQPHPSSSQSPPDLPLKAK
6523	2	1097	ASCOTRRTAALDSGERIAGRRSPIALAMASNFNDIVKQGYVKI
1	}		RSRKLGIFRRCWLVFKKASSKGPRRLEKPPDEKAAYFRNFHKVT
	I		ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEEWC
1			KHLCMECLGTRLNDISLGEPDLLAAGVQREQNERFNVYLMPTPN
			LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST
i			WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEQHER
1			LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRQNSVGE
			IYSLQGNHENRHSDLTGKSCKTSENRFLEENAPLVMYGITHHLF
			MDTSTCKVVHDLE
6524	2	1097	ASCQTRRRTAALDSGERIAGRRSPIALAMASNFNDIVKQGYVKI
	1		RSRKLGIFRRCWLVFKKASSKGPRRLEKFPDEKAAYFRNFHKVT
			ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEEWC
1			KHLCMECLGTRLNDISLGEPDLLAAGVQREONERFNVYLMPTPN
]	1		LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST
į			WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEOHER
	i		LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRONSVGR
			IYSLQGNHENRHSDLTGKSCKTSENRFLBENAPLVMYGITHHLP
6525			MDTSTCKVVHDLE
0523	1	1859	GESPFSEEESIEFNPSSSGRSARTVSSNSFCSDDTGWPSSQSVS
	l 1		PVKTPSDAGNSPIGFCPGSDEGFTRKKCTIGMVGEGSIOSSRYK
1 .			KESKSGLVKPGSEADFSSSSSTGSISAPEVHMSTAGSKPSSSSP
1	}		NRGPHGRSNGASSHKPGSSPSSPREKDLLSMLCRNQLSPVNIHP
1			SYAPSSPSSSNSGSYKGSDCSPIMRRSGRYMSCGENHGVRPPNP
ľ			EQYLTPLQQKEVTVRHLKTKLKESERRLHERESEIVELKSQLAR
1	i		MREDWIEEECHRVEAQLALKEARKEIKQLKQVIETMRSSLADKD
			KGIQKYFVDINIQNKKLESLLQSMEMAHSGSLRDELCLDFPCDS
[]	'		PEKSLTLNPPLDTMADGLSLEEQVTGEGADRELLVGDSIANSTD
1		Ì	LFDEIVTATTTESGDLELVHSTPGANVLELLPIVMGQEEGSVVV ERAVQTDVVPYSPAISELIQSVLQKLQDPCPSSLASPDESEPDS
]		i	MESFPESLSALVVDLTPRNPNSAILLSPVETPYANVDAEVHANR
			LMRELDFAACVEERLDGVIPLARGGVVRQYWSSSFLVDLLAVAA
, ,			PVVPTVLWAFSTQRGGTDPVYNIGALLRGCCVVALHSLRRTAFR
			IKT
6526	2	2034	SGRAGEPEEWRGRQIIDSKETWIPFNSEDSQQLEEAYSSGKGCN
 		,	GRVVPTDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGDKD
1 1	1		NKYVPYSESFSQVLEETYMLAVTLDEWKKKLESPNREIIILHNP
i i	1	1	KLMVHYQPVAGSDDWGSTPMEQGRPRTVKRGVENISVDIHCGEP
	1		LQIDHLVFVVHGIGPACDLRFRSIVOCVNDFRSVSLNILOTURV
j	į	1	KAQENQQIGRVEFLPVNWHSPLHSTGVDVDLORITLPSINBLRH
1.1	1	1	FINDTILDVFFYNSPTYCQTIVDTVASEMNRIYTLFLORNDDRK
] '	1		GGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDOGD
		İ	TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLOETGID
		ļ	LGPRKKILNYFSTRKNSMGIKRPAPOPASGANIPKESEFCSSSN
j			TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFT,TVPGI
[[į.	KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMIJ
			PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTPADV
		1	PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKERVLDINV
			GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV
6527			LKEIYQTQGIFLDQPLQ
9327	1	922	GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCQRGDLS
	ĺ		FIFNGDAAPSESFVVLDNEQKVYQRIHHEESEMETEEEVDILMS
			SDIYSATLSTKSISFTRAQTGWLFREDKTERVGNFLADFYLVNG

SEQ	Predicted	Predicted end	Amino acid coment
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
J	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ļ			LVLESRKRREHLSEEDILRNKAIMESLSKGGNIMEONFEDIEDO
ł			SLTPPPQNTITWEEYISAENGKAPHLGRELVCKESKKTFKATTA
1			MSQEFPLGIELLLNVLEVVAPFKHFNKLREFVOMKLPPGFDVKI.
6528	<u> </u>		DIPVFPTITATVTFQEFRYDEFDGSIFTIPDDYKEDPSRFPDI.
0528	1	1073	LTGPAAAEPRCAADAGMKRALGRRKGVWLRLRKILFCVLGLVTA
İ			IPFLIKLCPGIQAKLIFLNFVRVPYFIDLKKPODOGLNHTCNVV
}			LQPEEDVTIGVWHTVPAVWWKNAQGKDOMWYEDALASSHPTTI.v
]		LHGNAGTRGODHRVELYKVLSSLGYHVVTFDYRGWGDSVGTPSE
			RGMTYDALHVFDWIKARSGDNPVYIWGHSLGTGVATNLVRRLCE
i	1		RETPPDALILES?FTNIREEAKSHPFSVIYRYFPGFDWFFLDPI
1	İ		TSSGIKFANDENVKHISCPLLILHAEDDPVVPFQLGRKLYSIAA
	[PARSFRDFKVQFVPFHSDLGYRHKYIYKSPELPRILREFLGKSE PEHQH
6529	363	2215	
ľ	ļ		THIRYNKIGVVKTMSCGNEFVETLKKIGYPKADNINGEDFDWLF EGVEDESFLKWFCGNVNEQNVLSERELEAFSILQKSGKPILEGA
1	•		ALDBALKTCKTSDLKTPRLDDKELEKLEDEVQTLLKLKNLKIQR
			RNKCQLMASVTSHKSLRLNAKEEEATKKLKQSQGILNAMITKIS
			NELQALTDEVTQLMMFFRHSNLGQGTNPLVFLSQFSLEKYLSQE
ł			EQSTAALTLYTKKQFFQGIHEVVESSNESQFFNFLKIQTPSICD
1			NQEILEERRLEMARLQLAYICAQHQLIHLKASNSSMKSSIKWAE
1			ESLHSLTSKAVDKENLDAKISSLTSEIMKLEKEVTQIKDRSLPA
1	1		VVRENAQLINMPVVKGDFDLQIAKQDYYTAROELVINOLIKOKA
!			SFELLQLSYEIELRKHRDIYRQLENLVOELSOSNMMLYKOLEMI.
	}		TDPSVSQQINPRNTIDTKDYSTHRLYOVLEGENKKKEI,FI,THGN (
j l			LEEVAEKLKQNISLVQDQLAVSAQEHSFFLSKRNKDVDMI,CDTI.
1 1			YQGGNQLLLSDQELTEQFHKVESQLNKLNHLLTDILADVKTKRK
1 1			TLANNKLHOMEREFYVYFLKDEDYLKDIVENLETQSKIKAVSLE
6530	128	2986	D CANUMAN TROOPERS
1		2500	GAAHHGAIVQVHPLLPGSSTIMIHDLCLVFPAPAKAVVYVSDIQ ELYIRVVDKVEIGKTVKAYVRVLDLHKKPFLAKYFPFMDLKLRA
1 1			ASPIITLVALDEALDNYTITFLIRGVAIGQTSLTASVTNKAGQR
1 1			INSAPQQIEVFPPFRLMPRKVTLLIGATMQVTSEGGPQPQSNIL
1 1			FSISNESVALVSAAGLVQGLAIGNGTVSGLVQAVDAETGKVVII
			SQDLVQVEVLLLRAVRIRAPIMRMRTGTQMPIYVTGITNHQNPF
1 1	1		SFGNAVPGLTFHWSVTKRDVLDLRGRHHEASIRLPSQYNFAMNV
1		j	LGRVKGRTGLRAVVKAVDPTSGOLYGLARELSDRTOVOVERKLO
1	1	i	LLNPEIEAEQILMSPNSYIKLOTNRDGAASLSYRVIDGPEKUDU
]	ļ		VHVDEKGFLASGSMIGTSTIEVIAQEPFGANOTIIVAVKVSPVS
	1	}	YLRVSMSPVLHTQNKEALVAVPLGMTVTFTVHFHDNSGDVPHAH
1 1		İ	SSVLNFATNRDDFVQIGKGPTNNTCVVRTVSVGLTLLRVWDAKH
		i	PGLSDFMPLPVLQAISPELSGAMVVGDVLCLATVLTSLEGLSGT
		ł	WSSSANSILHIDPKTGVAVARAVGSVTVYYEVAGHLRTYKEVVV
			SVPQRIMARHLHPIQTSFQEATASKVIVAVGDRSSNLRGECTPT
			QREVIQALHPETLISCQSQFKPAVFDFPSQDVFTVEPQFDTALG
	1		QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA
		1	EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSFGWPSFITYTVGVLDPAAGSQGPLSTTLTFSSP
1			VTNQAIAIPVTVAFVVDRRGPGPYGASLFQHFLDSYQVMFFTLF
		l l	ALLAGTAVMIIAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS
		1	SPTSPNALPPARKASPPSGLWSPAYASH
6531	845	1425	PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS
1			SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFAEYWYQA
ļ			QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL
i	ĺ	ļ :	NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS
			SGLLVLPQAGLLTPHPS
6532	2		AAGPPSEVVNQDSLFPEPEPGPAPQVLLGPQGPGL1KGVAPPTL
			T. T. Z.

SEQ	Predicted	Predicted end	1 Amino
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
i i	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
ı	residue of	amino acid	W-Trustonban V Sussaine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l l	sequence	Judacuco	Codon, /=possible nucleotide deletion,
		 	\=possible nucleotide insertion)
1	1	1	ITDSTGTHLVLTVTNKNAHSPGLSRGSPQQPSSQPGSPAPAPSA
1			QMDLEHPLQPLFGTPTSLLKKEPPGYEEAMSQQPKQQENGSSSQ
ı	ľ	ł	QMDDLFDILIQSGEISADFKEPPSLPGKEKPSPKTVCWSPLAAQ
1	Į.		PSPSAELPQAAPPPPGSPSLPGRLEDFLESSTGLPLLTSGHDGP
į			EPLSLIDDLHSQMLSSTAILDHPPSPMDTSELHFVPEPSSTMGL
1	j	,	DLADGHLDSMDWLELSSGGPVLSLAPLSTTAPSLFSTDFLDGHD
6533	1798		LQLHWDSCL
1	1/30	373	STISWLARVEPPRRSSGVGAARLRFPGGSRPLRARACVLALAVL
	I I		ALLERNNADSMSAHSMLCERIAIAKELIKRAESLSRSRKGGIEG
Į.	1		GAKLCSKLKAELKFLQKVEAGKVAIKESHLOSTNLTHLRATUES
1			AENLEEVVSVLHVFGYTDTLGEKOTLVVDVVANGGHTWVKATGR
1			KAEALHNIWLGRGQYGDKSIIEQAEDFLOASHOOPVOYSNPHIT
ŀ			FAFYNSVSSPMAEKLKEMGISVRGDIVAVNALLDHPEELOPSES
			ESDDEGPELLQVTRVDRENILASVAFPTEIKVDVCKRVNLDITT
			LITYVSALSYGGCHFIFKEKVLTEQAEQERKEQVLPQLEAFMKD
1			KELFACESAVKDFQSILDTLGGPGERERATVLIKRINVVPDODS
1			ERALRLVASSKINSRSLTIFGTGDTLKAITMTANSGFVRAANNQ
6534	47		GVKFSVFIHQPRALTESKEALATPLPKDYTTDSEH
1000	1 1	596	KATRFISAAFVVLNKQGVSPAKLPHTSWSWSLQTLSFLFSGDLA
			EKSLQCFPCSAMLLELIPLLGIHFVLRTARAQSVTQPDIHITVS
1			EGASLELRCNYSYGATPYLFWMERTVEEAFILLVCLKPWRVASS
1			LEKKEKEDESFOLLLGSRYNVLKAHCLLPLIRWLTSGDSLLSAQ
6535	250		PHCPQGL
0535	250	964	LIKTFFRDVAIQRDLLPKEKNLETLLTLAFLEIDKAFSSHARLS
0555	250	964	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKDMKT.
0555	230	964	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGOPHVNGRLAMTRSIGD
0333	250	964	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSOEIW
0333	250	964	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAMGKYKN
6536	242		ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA
		1174	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVITDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVFTGS
			ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLQWSLEGHOLGVVSVDISHTLDTA
			ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKMRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSOVLATGTHV
			ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGTLFKOEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLCWSLEGHQLGVVSVDISHTLPIAASSS LDDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGATDGI
			ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSOLLVTASDDGYIK
			ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWUNVAFCPDDTHFVSSSSDKSVKVW
			ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC
		1174	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI
6536	242		ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGTLFKOEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTPSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI NRFNPPPTQGPDFSLVYRPDVDPEVAKDKASFRNYTSGPILDRV
6536	242	1174	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGTLFKOEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLCWSLEGHQLGVVSVDISHTLPIAASSS LDDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI NRFNPPPTGGPDPSLVYRPDVDFEVAKDKASFRNYTSGPLLDRV FTTYKLMHTHQTVDFVSSKHAQFGGFSYKKMTVWEAVDLLDGLV
6536	242	1174	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKNEDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQVIATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI NRFNPPPTQGPDPSLVYRPDVDFEVAKDKASFRNYTSGPLLDRV FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV
6536	242	921	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQVLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI NRFNPPPTQGPDFSLVYRPDVDFEVAKDKASFRNYTSGPLLDRV FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV LALFGEPQWAVVGDTFFVGGCRPQASVVFCDSTFODNPDLODPRV
6536	242	921	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQVLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI NRFNPPPTQGPDFSLVYRPDVDFEVAKDKASFRNYTSGPLLDRV FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV LALFGEPQWAVVGDTFPYGCRPQASVVFCDSTFQDNPDLQDPRY STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG
6536	242	921	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDDAHIRLWDLERGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI NRFNPPPTQGPDFSLVYRPDVDPEVAKDKASFRNYTSGPLLDRV FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV LALFGEPQWAVVGDTFPVGCRPQASVVFCDSTFQDNPDLQDPRY STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR
6536 6537	1638	921	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGTLFKOEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLGWSLEGHQLGVVSVDISHTLPIAASSS LDDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI NRFNPPPTGGPDPSLVYRPDVDPEVAKDKASFRNYTSGPLLDRV FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV LALFGEPQWAVVGDTFPVGCRPQASVVFCDSTFQDNPDLQDPRY STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR
6536 6537	1638	921	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGGDHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI NRFNPPPTQGFDPSLVYRPDVDFEVAKDKASFRNYTSGPLLDRV FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV LALFGEPQWAVVGDTFPVGCRPQASVVFCDSTFQDNPDLQDPRY STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVWEYDETMEKYIPVLMAQAKIYWNLENYDMV
6536 6537	1638	921	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGGPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQVIATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI NRFNPPPTQGPDPSLVYRPDVDFEVAKDKASFRNYTSGPLLDRV FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV DESDPDVDFPNSFHAFGTAEGIRKAHPDKDWFHLVGLLHDLGKV LALFGEPQWAVVGDTFPVGCRPQASVVFCDSTFQDNPDLQDPRY STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV EKIFRKSVEFCNDHDVWKLNVAHVLFMOENKYKEAIGFYEPTUK
6536 6537	1638	921	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQVLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI NRFNPPPTQGPDPSLVYRPDVDFEVAKDKASFRNYTSGPLLDRV FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV LALFGEPQWAVVGDTFFVGCRPQASVVFCDSTFQDNPDLQDPRY STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYYMV KHYDNILNVSAIVLANLCVSYIMTSONEKAERLMRKIEKEFEROL
6536 6537	1638	921	ADATLLTSGTTATVALLEDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS LDDAHRLWDLERGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTPSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI NRFNPPPTQGPDFSLVYRPDVDPEVAKDKASFRNYTSGPLLDRV FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV DESDPDVDFPNSFHAFGTAEGIRKAHPDKDWFHLVGLLHDLGKV LALFGEPQWAVVGDTFPVGCRPQASVVFCDSTFQDNPDLQDPRY STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV EKIFRKSVEFCNDHDVWKLNVAHVUFMQENKYKEAIGFYEPIVK KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL SYDDPNRKMYHLCIVNLVIGTLYCAKGNYEFGISRVIKSLEPVN
6536 6537	1638	921	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGTLFKOEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI MRFNPPPTQGPDFSLVYRPDVDPEVAKDKASFRNYTSGPLLDRV FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV LALFGEPQWAVVGDTFFVGCRPQASVVFCDSTFQDNPDLQDPRY STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYMV EKIFRKSVEFCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPIVK KHYDNILNVSAIVLANLCVSYINTSQNEKAEELMRKIEKEEEQL SYDDPNRKMYHLCIVNLVIGTLYCAKGNYBFGISRVIKSLEPYN KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIOECVOFLGHC
6536 6537	1638	921	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGTLFKOEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI MRFNPPPTQGPDFSLVYRPDVDPEVAKDKASFRNYTSGPLLDRV FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV LALFGEPQWAVVGDTFFVGCRPQASVVFCDSTFQDNPDLQDPRY STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYMV EKIFRKSVEFCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPIVK KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL SYDDPNRKMYHLCIVNLVIGTLYCAKGNYBFGISRVIKSLEPYN KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIQECVQFLGHC ELYGTNIPAVIEQPLEEERMHVGKNTVTDESRQLKALIYEIIGW
6536 6537	242 1638 3345	921	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGGPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKMEDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI NRFNPPPTQGFDPSLVYRPDVDFEVAKDKASFRNYTSGPLLDRV FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV LALFGEPQWAVVGDTFPVGCRPQASVVFCDSTFQDNPDLQDPRY STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVWEYDETMEKYIPVLMAQAKIYWNLENYPMV EKIFRKSVEFCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPTVK KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL SYDDPNRKMYHLCIVNLVIGTLYCAKGNYBFGISRVIKSLEPYN KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIQECVQFLGHC ELYGTNIPAVIEQFLEEERMHVGKNTVTDESRQLKALIYEIIGW NK
6536	242 1638 3345	921 2412	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGGPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI NRFNPPPTQGPDFSLVYRPDVDFEVAKDKASFRNYTSGPLLDRV FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV LALFGEPQWAVVGDTFPVGCRPQASVVFCDSTFQDNPDLQDPRY STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV EKIFRKSVEFCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPTUK KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL SYDDPNRKMYHLCIVNLVIGTLYCAKGNYBFGISRVIKSLEPYN KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIQECVQFLGHC ELYGTNIPAVIEQPLEEERMHVGKNTVTDESRQLKALIYEIIGW NK FLGAASPHPHFSSLAPHPDQPEFTPVQDELEAMELWGPGV
6536 6537 6538	242 1638 3345	921 921 2412	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVUTGS LDDLVKVWKWRDERLDLQWSLEGHQLGVVVDISHTLPIAASSS LDDAHIRLWDLERGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTPSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI NRFNPPPTQGPDPSLVYRPDVDPEVAKDKASFRNYTSGPLLDRV FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV DESDPDVDFPNSFHAFGTAEGIRKAHPDKDWFHLVGLLHDLGKV LALFGEPQWAVVGDTFPVGCRPQASVVFCDSTFQDNPDLQDPRY STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV KKIFRKSVEFCNDHDVWKLNVAHVLFWQENKYKEAIGFYEPTVK KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL SYDDPNRKMYHLCIVNLVIGTLYCAKGNYBFGISRVIKSLEPYN KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIQECVQFLGHC ELYGTNIPAVIEQPLEEERMHVGKNTVTDESRQLKALIYEIIGW NK FLGAASPHPHFSSLAPHPDQPEFTPVQDELEAMELWGPGV LERLWLLLLRRPEDAMAECPTLGEAVTDHPDRLWAWEKFYVLDR
6536 6537 6538	242 1638 3345	921 921 2412	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGGPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSFSRSFASSGRWA SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI NRFNPPPTQGPDFSLVYRPDVDFEVAKDKASFRNYTSGPLLDRV FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV LALFGEPQWAVVGDTFPVGCRPQASVVFCDSTFQDNPDLQDPRY STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV EKIFRKSVEFCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPTUK KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL SYDDPNRKMYHLCIVNLVIGTLYCAKGNYBFGISRVIKSLEPYN KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIQECVQFLGHC ELYGTNIPAVIEQPLEEERMHVGKNTVTDESRQLKALIYEIIGW NK FLGAASPHPHFSSLAPHPDQPEFTPVQDELEAMELWGPGV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
••••	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
İ		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6541	1165	536	RTLVQRRILMLLRKPARGRDLRGRGRGTPRGGRKGLLPTPDEFP
1		i	RFEGGRKPDSWDGNREPGPGHEHFRDTPRPDHPPHDGHSPASRE
1			RSSSLQGMDMASLPPRKRPWHDGPGTSBHREMEAPGGPSEDRGG
1			KGRGGPGPAQRVPKSGRSSSLDGEHHDGYHRDEPFGGPPGSGTP
	1		SRGGRSGSNWGRGSNMNSGPPRRGASRGGGRGR
6542	3	3775	SWPRGRGETGGHPGALRTRTMQKSVRYNEGHALYLAFLARKEGT
j			KRGFLSKKTAEASRWHEKWFALYQNVLFYFEGEQSCRPAGMYLL
	l i		EGCSCERTPAPPRAGAGQGGVRDALDKQYYFTVLFGHEGQKPLE
	į		LRCEEEQDGKEWMEAIHQASYADILIEREVLMQKYIHLVQIVET
ł			EKIAANQLRHQLEDQDTEIERLKSEIIALNKTKERMRPYQSNQE
1	ŀ		DEDPDIKKIKKVQSFMRGWLCRRKWKTIVQDYICSPHAESMRKR
1	ĺ		NQIVFTMVEAESEYVHQLYILVNGFLRPLRMAASSKKPPISHDD
			VSSIFLNSETIMFLHEIFHQGLKARIANWPTLILADLFDILLPM
1			LNIYQEFVRNHQYSLQVLANCKQNRDFDKLLKQYEANPACEGRM
	l i		LETFLTYPMFQIPRYIITLHELLAHTPHEHVERKSLEFAKSKLE
1			
			ELSRVMHDEVSDTENIRKNIAIERMIVEGCDILLDTSQTFIRQG
J]	-	SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLFTKHFLICTRS
1			SGGKLHLLKTGGVLSLIDCTLIEEPDASDDDSKGSGQVFGHLDF
1 .			KIVVEPPDRAAFTVVLLAPSRQEKAAWMSDISQCVDNIRCNGLM
			TIVFEENSKVTVPHMIKSDARLHKDDTDICFSKTLNSCKVPQIR
1		1	YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVLGKLSD
į į	i i		IYKRPFTSIPVRSLELFFATSQNNRGEHLVDGKSPRLCRKFSSP
			PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSSPTTTTQS
1	,		PAASPPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNPRVDLCNK
[LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPSTPRHLR
	:		YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPPGFNNTÉRTC
			DKEFIIRRTATNRVLNVLRHWVSKHAQDFELNNELKMNVLNLLE
1			EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDIIQMTDC
			MKAECFESLSAMELAEQITLLDHVIFRSIPYEEFLGQGWMKLDK
			NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIEKWVAV
			ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKQTKALMD
	1		KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAFIEEGT
1			PNFTEEGLVNFSKMRMISHIIREIRQFQQTSYRIDHQPKVAQYL
L			LDKDLIIDEDTLYELSLKIEPRLPA
6543	1857	950	FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCTHPLDL
			LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASLCRQMT
			YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLAGGFVG
]			TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEGLRRLF
			SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIFTHFVA
]		•	SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVETAKLGP
			LAFYKGLVPAGIRLIPHTVLTFVFLEQLRKNFGIKVPS
6544	630	79	PSPCFIRSRLDGQPWMAGLEAWLSQNFSLHQPQSRVRVRRASIS
[[1		EPSDTDPEPRTLNPSPAGWFVQQHPBLELMSSFRERFGRNWLQY
1	[RSHLEPSGNPLPATPTTSAPSAPPASSOGPDTAPRPSPPOREAR
] !	ļ		GPQESPQKMSEEVRAEPQEEEEEKEGKEEKEGEMAPLPRAHLG
1 1			EGKQKECP .
6545	176	560	
"""	1,0	360	PPHSHAALLPAAMTPLLTLTLVVLMGLPLAQALDCHVCAYNGDN
}	į		CFNPMRCPAMVAYCMTTRTYYTPTRMKVSKSCVPRCFETVYDGY
6546			SKHASTTSCCQYDLCNGTGLATPATLALAPILLATLWGLL
0546	1657	364	HLLNGLDEVAAFFVADLGAIVRKHFCFLKCLPRVRPFYAVKCNS
]]	ļ		SPGVLKVLAQLGLGFSCANKAEMELVQHIGIPASKIICANPCKQ
	j	Į.	IAQIKYAAKHGIQLLSFDNEMELAKVVKSHPSAKMVLCIATDDS
	1		HSLSCLSLKFGVSLKSCRHLLENAKKHHVEVVGVSFHIGSGCPD
			PQAYAQSIADARLVFEMGTELGHKMHVLDLGGGFPGTEGAKVRF
}			EEIASVINSALDLYFPEGCGVDIFAELGRYYVTSAFTVAVSIIA
<u> </u>			KKEVLLDQPGREEENGSTSKTİVYHLDEGVYGIFNSVLFDNICP
			

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	\A-Alanine, C=Cvsteine
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
- 1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ł	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
- !	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
į.	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	sequence		Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
		 	TPILOREPEON vogernoon
1			TPILQKKPSTEQPLYSSSLWGPAVDGCDCVAEGLWLPQLHVGDW
			LVFDNMGAYTVGMGSPFWGTQACHITYAMSRVAWEALRRQLMAA EQEDDVEGVCKPLSCGWEITDTLCVGPVFTPASIM
6547	1	541	LHSKYLADAL CSORCMMRCGRARGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
ĺ			LHSKYLAPALCSQPGMMRCCRRRCCCRQPPHALRPLLLLPLVLL PPLAAAAAGPNRCDTIYQGFAECLIRLGDSMGRGGELETICRSW
Ì			NDFHACASQVLSGCPEEAAAVWESLQQEARQAPRPMNLHTLCGA
			PVHVRERGTGSETNQETLRATAPALPMAPAPPLLAAALALAYLL
<u> </u>			RPLA
6548	2	219	FVSRLSVRDVRFPTFLGGHGADAMHTDPDYSAAYVPIETDAEDG
L	1		IKGCGITFTLGKGTEVGELKILSRFQNA
6549	73	1490	ETGRVCEDARPACGSRSRRRRKEAAPGIPTPSPSSSSPTSSRPA
1			ARAFSKAPARLSRPRAREEPPDPGRRYIQBEIIQARKHKLIKMC
]		SSVAAKLWFLTDRRIREDYPQKEILRALKAKCCEEELDFRAVVM
			DEVVLTIEQGNLGLRINGELITAYPQVVVVRVPTPWVQSDSDIT
i	i		VLRHLEKMGCRLMNRPQAILNCVNKFWTFQELAGHGVPLPDTFS
			YGGHENFAKMIDEAEVLEFPMVVKNTRGHRGKAVFLARDKHHLA
ı	l i		DESHLIRHEAPYLFQKYVKESHGRDVRVIVVGGRVVGTMIRGET
1	į		DGRMQSNCSLGGVGMMCSLSEOGKOLAIOVSNILGMDVCGIDII
i .			MKDUGSFCVCEANANVGPIAFDKACNIDVAGITADVAASITDSC
			RLTRRMSLLSVVSTASETSEPELGPPASTAVDNMSASSSSVDSD
6550	2202		PESTERELLTKLPGGLFNMNOLLANEIKLLVD
0550	2293	922	FRVSRDGAPDCGIEQMGLAMEHGGSYARAGGSSPGCWVVLDVEE
1 ' 1	1		LFVSLIQFLILGLVLFMVYGNVHVSTESNLOATERDARGIVGO
1			LUGGITASQSNLTKELNFTTRAKDATMOMWI.NADDDI.DD TAYA CED
1 1			QCQGDRVIYTNNQRYMAAIILSEKOCRDOFKDMNKSCDALLEMT
1 1			NORVETLEVELAKERTICTKDKRSVLINKRVAREOLVECTVPDE
1			LQHQERQLAKEQLQKVQALCLPLDKDKFEMDI.RNT.WpDgttbbe
1			LUNLGINLYHPLGSELASIRRACDHMPSIMSSKVEELADGIDAD
]			IERVARENSDLOROKLEAQOGLRASQEAKQKVEKEAQAREAKLQ
1 1	ĺ		AECSROTOLALEEKAVLRKERDNLAKELEEKKREAEQLRMELAI
1 1			RNSALDTCIKTKSQPMMPVSRPMGPVPNPQPIDPASLEEFKRKI
6551	157	748	LESQRPPAGIPVAPSSG
	1	. /	IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE
	1		ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN
l i	1		ASLPRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER
			EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKEEASR
6552	157	748	IQPPDPRMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE
! !	ĺ	-	ADTVDLNWCVISDMEVIBLNKCTSGQSFEVILKPPSFDGVPEFN
		!	ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER
}		i	EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ
			EKDKHAEEVRKNKELKEEASR
6553	2	1807	FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD
1		1	BYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV
- 1	1		RPRLBLMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD
	İ	İ	LGVLGSFIHREBYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS
- 1	}		LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG
1	j		SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS
• [1	YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEBLYAEIRDKN
			FNAVGSVLSKKAKI ISAAFEERHNAKTVGEI KOFVSOLDUMOD D
ļ		Į	RGSLANHTSIAELIKDVTTSEDFFDKLTVEOFFMSGIDTDVANNI
[YIEDCIAQKHSLIKVLRLVCLOSVCNSGLKOKVLDVVVPPTLOT
j		f	IGYEHILTLHNLEKAGLLKPOTGGRNNYPTTRKTI.PLUMODUNE
ļ		1 '	QNPTDISYVYSGYAPLSVRLAOLLSRPGWRSIEEVIDTI.DCDWF
1	ŀ	1 -	EERQPLPTGLQKKROPGENRVTLTFFT.GGVTFAETADLDFLCOL
			EDGGTEYVIATTKLMNGTSWIEALMEKPF
	,		

SEQ	Predicted	l Drodies-3	
ID	beginning	Predicted end nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid E-
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ı	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Trophon V-Trophon V-Trophon V-Trophon V-Trophon V-Trophon V-Trophon V-Trophon V-Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
j	sequence		\=possible nucleotide insertion)
6554	119	1244	FEMGSQVSVESGALHVVIVGGGFGGIAAASQLQALNVPFMLVDM
İ		"	KDSFHHNVAALRASVETGFAKKTFISYSVTFKDNFRQGLVVGID
1			LKNOMVLLQGGEALPFSHLILATGSTGPFPGKFNEVSSQQAAIQ
ŀ	1		AYEDMVRQVQRSRFIVVVGGGSAGVEMAAEIKTEYPEKEVTLIH
1			SQVALADKELLPSVRQEVKEILLRKGVQLLLSERVSNLEELPLN
1		1	BYREYIKVQTDKGTEVATNLVILCTGIKINSSAYRKAFESRLAS
			SGALRVNEHLQVEGHSNVYAIGDCADVRTPKMAYLAGLHANIAV
1			ANIVNSVKQRPLQAYKPGALTFLLSMGRNDGVGOTSGFYVGRIM
			VRLTKSRDLFVSTSWKTMRQSPP
6555	1552	498	IHMALLRKINQVLLFLLIVTLCVILYKKVHKGTVPKNDADDESE
ĺ			TPEELEEEIPVVICAAAGRMGATMAAINSIYSNTDANII.FYVVC
			LRNTLTRIRKWIEHSKLREINFKIVEFNPMGLKGKIRPDSSRPE
J			LLQPLNFVRFYLPLLIHQHEKVIYLDDDVIVOGDTOELYDTTT.A
-			LGHAAAFSDDCDLPSAQDINRLVGLONTYMGYLDYRKKATKDIG
			ISPSTCSFNPGVIVANMTEWKHORITKOLEKWMOKNVEENLYSS
1	{		SLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHFL
6556	241	1449	QEAKLLHWNGRHKPWDFPSVHNDLWESWFVPDPAGIFKLNHHS
1	***	1449	ASLCKGCFFVTHVLVIILPSLQSFPTFGFLLDIDGVLVRGHRVI
1			PAALKAFRLVNSQGQLRVPVVFVTNAGNILQHSKAQELSALLG
1			CEVDADQVILSHSPMKLFSEYHEKRMLVSGQGPVMENAQGLGFR
1			NVVTVDELRMAFPLLDMVDLERRLKTTPLPRNDFPRIEGVLLLG
			EPVRWETSLQLIMDVLLSNGSPGAGLATPPYPHLPVLASNMDLL WMAEAKMPRFGHGTFLLCLETIYQKVTGKELRYEGLMGKPSILT
			YQYAEDLIRRQAERRGWAAPIRKLYAVGDNPMSDVYGANLFHQY
1			LQKATHDGAPELGAGGTRQQQPSASQSCISILVCTGVYNPRNPQ
			STEPVLGGGEPPFHGHRDLCFSPGLMEASHVVNDVNEAVQLVFR
			KEGWALE
6557	2598	1534	RMCGRTSCHLPRDVLTRACAYQDRRGQQRLPEWRDPDKYCPSYN
1 1			KSPQSNSPVLLSRLHFEKDADSSERIIAPMRWGLVPSWFKESDP
1	1		SKLQFNTTNCRSDTVMEKRSFKVPLGKGRRCVVLADGFYEWORC
}	i		QGTNQRQPYFIYFPQIKTEKSGSIGAADSPENWEKVWDNWRLLT
1 1			MAGIFDCWEPPEGGDVLYSYTIITVDSCKGLSDIHHRMPAILDG
			EEAVSKWLDFGEVSTQEALKLIHPTENITFHAVSSVVNNSRNNT
1	ľ		PECLAPVDLVVKKELRASGSSQRMLQWLATKSPKKEDSKTPQKE
] [1		ESDVPQWSSQFLQKSPLPTKRGTAGLLEQWLKREKEEEPVAKRP YSO
6558	21	1138	
1 !	·		FHGRRRGGRKMELGSCLEGGREAAEEEGEPEVKKRRLLCVEFAS VASCDAAVAQCFLAENDWEMERALNSYPEPPVEESALERRPETI
i i	Ţ.		SEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWNID
[İ		GLDLNNLSERARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSS
j	1		NYELITGHEEGYFTAIMLKKSRVKLKSQEIIPFPSTKMMRNLLC
[1		VHVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQEAPES
			ATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWD
	}		TOMNSNLGITAACKLRFDRIFFRAAAEEGHIIPRSLDLLGLEKL
			DCGRFPSDHWGLLCNLDIIL
6559	3	364	GPELSGLPTRPKKLKANOTPIAMDCCASRSCSVPTGPATTTCSS
1		İ	DKSCRCGVCLPSTCPHTVWLLEPTCCDNCPPPCHIPOPCVPTCF
656			LLNSCQPTPGLETLNLTTFTQPCCEPCLPRGC
6560	3	1435	TATSGGIWLRRKWRCHWPRPLPQSCVGTEGGLOVRDTSSRIAKG
1		j	GVDHTKMSLHGASGGHERSRDRRRSSDRSRDSSHERTESOLTPC
1	1		IRNVTSPTRQHHVEREKDHSSSRPSSPRPOKASPNGSISSAGNS
]		SRNSSQSSSDGSCKTAGEMVFVYENAKEGARNIRTSERVTLIVD
[j		NTRFVVDPSIFTAQPNTMLGRMFGSGREHNFTRPNEKGEYEVAR
l	j	f	GIGSTVFRAILDYYKTGIIRCPDGISIPELREACDYLCISFEYS
- 1	İ	1	TIKCRDLSALMHELSNDGARROFEFYLEEMILPLMVASAOSGER
L			ECHIVVLTDDDVVDWDEEYPPQMGEEYSQIIYSTKLYRFFKYIE

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	M=AldRine, C=CVSteine, D=longrid late n
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ł	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
ł			NRDVAKSVLKERGLKKIRLGIEGYPTYKEKVKKRPGGRPEVIYN
	1		YVQRPFIRMSWEKEEGKSRHVDFQCVKSKSITNLAAAAADIPQD
6561			QUVVMRPTPQVDELDILPIHPPSGNSDI,DPDAONDMI.
6267	3	1086	PGRRFRRKESSSSRWFPADCLLGLRGPASSLLSDFDSWDGWG
J			PCPMAATDLSFMYRWFKNCNLVGNISEKVVETTGCDGGROWT
- [!	AKQUVURGMQVLAACFTEEGSOKLORDTSVRIOTTII.DVIIIVORG
j	j	1	LAAAQWVRDKVGEQGLWALVNNAGVGI.PSCPNEWI.TVDDETVVI
			INVNLVGLIBVTLHMLPMVKRARGRVVNMSSSCGPVAVICCCVC
	1		VSKEGVEAFSDSIRRELYYFGVKVCIIEPGNVRTATI.GVENTER
		[KMKKLWERLPQETRDSYGEDYFRIYTDKI,KNIMOVAFDDUDDUT
1	1		NSMEHAIVSRSPRIRYNPGLDAKLLYIPLAKLPTPVTDFILSRY
6562	1	1562	LPRPADSV
		1302	MSTLYDIRAHKAQLLRFFASSDSNKALEQRRTLHTPKLEHLDRV
			LYEWFLGKRSEGVPVSGPMLIEKAKDFYEQMQLTEPCVFSGGWL
ļ			WRFKARHGIKKLDASSEKQSADHQAAEQFCAFFRSLAAEHGLSA
			EQVYNADETGLFWRCLPNPTPEGGAVPGPKQGKDRLTVLMCANA TGSHRLKPLAIGKCSGPRAFKGIQHLFVAYKAQGNAWVDKEIFS
			DWFHHIFVPSVREHFRTIGLPEDSKAVLLLDSSRAHPQEAELVS
j	1	•	SNVFTIFLPASVASLVQPMEQGIRRDFMRNFINPPVPLQGPHAR
İ	ĺ		INMNDATESVACAWNAVPSHVFRRAWRKI.WDSVAFAFGGGGGDDD
			LEAECEPVKPHNKSFAHILELVKEGSSCPGOLDODOD A GWOULD C
			REAEGGRPPAATSPAEVVWSSEKTPKADODGDGDDGEGERVAND
			WAAVAFDAVLRFAEROPCFSAOEVGOLRALDAVPPROCOURDED
6563	1319	2694	GALGAVVKVEALQEGPGGCGATAOSPI,PCSSTACDN
		2024	LARPAQPVLLREPEGAGPPVPAGHLVHHLQGGHLRERAHPDLEA
1			HEHPLPCDQMFWRQMGGHLRMVEANSRGVVWGIGYDHTAWVYTG
1		i	GYGGGCFQGLASSTSNIYTQSDVKCVHIYENQRWNPVTGYTSRG LPTDRYMWSDASGLQECTKAGTKPPSLQWAWVSDWPVDFSVPGG
-			TDQEGWQYASDFPASYHGSKTMKDFVRRRCWARKCKLVTSGPWL
			EVPPIALRDVSIIPESPGAEGSGHSIALWAVSDKGDVLCRLGVS
1			BUNPAGSSWLHVGTDOPFASISIGACYOVWAVARDGEA PURCON
]		ł	1PSQPAGDCWYHIPSPPRORLKOVSAGOTSVVALDPNONT MYDO
] [İ	GITPSIPQGSSWEHVSNNVCRVSVGPLDOVWVTANKUOGGUGI C
1 1	i	i	RGTVCHKIGVQPHEPKGHGWDYGIGGGWDHISVPANDTPADDGG
6564	1	075	SUEQEPSAPPEAHGPVCC
1	-	975	APGSCALWSYCGRGWSRAMRGCQLLGLRSSWPGDLLSARLLSQE
1 1		;	RRAAETHFGFETVSEEEKGGKVYOVFESVAKKVDVMMDMMCT.CT
1 1			HRVWKDLLLWKMHPLPGTQLLDVAGGTGDIAFRFLNYVQSQHQR
1 1		1	KQKRQLRAQQNLSWEEIAKEYQNEEDSLGGSRVVVCDINKEMLK
1			VGKQKALAQGYRAGLAWVLGDAEELPFDDDKFDIYTIAFGIRNV THIDQALQEAHRVLKPGGRFLCLEFSQVNNPLISRLYDLYSFQV
1		İ	IPVLGEVIAGDWKSYQYLVESIRRFPSQEEFKDMIEDAGFHKVT
1			YESLTSGIVAIHSGFKI,
6565	1464	999	RSAVANGLTKRRMGLKLNGRYISLILAVQIAYLVQAVRAAGKCD
1	i	4 .	AVERGE BUCLERLEDSMANYPOCHDDKTNTKTRICTPVWpDptrocm
	1	1	VTALTDCQEGAKDMWDKLRKESKNLNIOGSLFELCGSGNGAACS
6566	3		LLPATPVLLVSLSAALATWLSF
	3	1385	KYESAQPGGTQPEPGLGARMAIHKALVMCLGLPLFLFPGAMAGG
		1 2	HVPPGCSQGLNPLYYNLCDRSGAWGIVLEAVAGAGTVTTFTVTTTT
!		1 -	LLVASLPFVQDTKKRSLLGTOVFFLI.GTI.GI.FCI.VFACUEVDDD
		1 2	STCASRRFLFGVLFAICFSCLAAHVFALNFLARKNHGDDGWUTD
ļ j		1.3	IVALLETIVEVIINTEWLIITLVRGSGEGGPOGNSSAGWAYASD
1	1	1;	CAIANMDFVMALIYVMLLLLGAFLGAWPALCGRYKRWRKHGVFV
İ		1	LLTTATSVAIWVVWIVMYTYGNKQHNSPTWDDPTLAIALAANAW
		16	AFVLFYVIPEVSQVTKSSPBQSYQGDMYPTRGVGYETILKEQKG SMFVENKAFSMDEPVAAKRPVSPYSGYNGQLLTSVYQPTEMAL
		<u></u>	

.

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	Seserine, reinreonine, vevaline,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
ļ	Degazine		\=possible nucleotide insertion)
			MHKVPSEGAYDIILPRATANSQVMGSANSTLRAEDMYSAQSHQA
6567	125		ATPPKDGKNSQVFRNPYVWD
1 030,	123	863	TKRSNLKAYACSIHHIRTMSYVFVNDSSQTNVPLLQACIDGDFN
			YSKRLLESGFDPNIRDSRGRTGLHLAAARGNVDICQLLHKFGAD
			LLATDYQGNTALHLCGHVDTIQFLVSNGLKIDICNHQGATPLVL
1			AKRRGVNKDVIRLLESLEEQEVKGFNRGTHSKLETMQTAESESA
1			MESHSLLNPNLQQGEGVLSSFRTTWQEFVEDLGFWRVLLLIFVI
6568			ALLSLGIAYYVSGVLPFVENQPBLVH
0300	3	1183	HASDRLLVLPDNYSHPSQASANLQGPSRTTELFHPTLASISSPM
f			LEGAELYFNVDHGYLEGLVRGCKASLLTQQDYINLVQCETLEDL
			KIHLQTTDYGNFLANHTNPLTVSKIDTEMRKRLCGEFEYFRNHS
}			LEPLSTFLTYMTCSYMIDNVILLMNGALQKKSVKEILGKCHPLG
			RFTEMEAVNIAETPSDLFNAILIETPLAPFFQDCMSENALDELN
ì		•	IELLRNKLYKSYLEAFYKFCKNHGDVTAEVMCPILEFEADRRAF
			IITLNSFGTELSKEDRETLYPTFGKLYPEGLRLLAQAEDFDQMK
1			NVADHYGVYKPLFEAVGGSGGKTLEDVFYEREVQMNVLAFNRQF
6560			HYGVFYAYVKLKEQEIRNIVWIAECISQRHRTKINSYIPIL
6569	205	1532	RRRGPQRLGHGRPTPLLCRWRTAGPSHWEKQARAFQGLRPVDPR
			RMSWLFPLTKSASSSAAGSPGGLTSLQQQKQRLIESLRNSHSSI
1			AEIQKDVEYRLPFTINNLTININILLPPQFPQEKPVISVYPPIR
Į l	1		HHLMDKQGVYVTSPLVNNFTMHSDLGKIIQSLLDEFWKNPPVLA
	i		PTSTAFPYLYSNPSGMSPYASQGFPFLPPYPPQEANRSITSLSV
1 1			ADTVSSSTTSHTTAKPAAPSFGVLSNLPLPIPTVDASIPTSQNG
]			FGYKMPDVPDAFPELSELSVSQLTDMNEQEEVLLEOFLTLPOLK
1 1			QIITDKDDLVKSIEELARKNLLLEPSLEAKRQTVLDKYELLTQM
1			KSTFEKKMOROHELSESCSASALQARLKVAAHEAEEESDNIAED
			FLEGKMEIDDFLSSFMEKRTICHCRRAKEEKLQQAIAMHSQFHA
6570	300		PL PL
"3"	330	1304	ARLPRLTFLREGFLYVLLSHWVFVGAPRPPASDSWKKGLVPSAP
	i		PASRKMGSKALPAPIPLHPSLQLTNYSFLQAVNTFPATVDHLQG
!!!	1		LYGLSAVQTMHMNHWTLGYPNVHEITRSTITEMAAAQGI,VDARF
ļ i	Ī		PFPALPFTTHLFHPKQGAIAHVLPALHKDRPRFDFANLAVAATQ
i	j		EDPPKMGDLSKLSPGLGSPISGLSKLTPDRKPSRGRLPSKTKKE
1 1			FICKFCGRHFTKSYNLLIHERTHTDERPYTCDICHKAFRRQDHL
			RDHRYIHSKEKPFKCQECGKGFCQSRTLAVHKTLHMQTSSPTAA
6571	169		SSAAKCSGETVICGGT
55,4	103	656	APDMNRKKLQKLTDTLTKNCKHLFRGFDXDNDGCVNVLEWIHGL
	į		SLFLRGSLEEKMKYCFEVFDLNGDGFISKEEMFHMLKNSLLKQP
			SEEDPDEGIKDLVEITLKKMDHDHDGKLSFADYBLAVREETLLL
6572	49	1646	EAFGPCLPDPKSQMEFEAQVFKDPNEFNDM
	**	1040	TPERAQPGALLGAAGCCVCGGRWWPRSHERGYFSSAKMGSKRRN
1			LSCSERHQKLVDBNYCKKLHVQALKNVNSQIRNQMVQNENDNRV
			QRKQFLRLLQNEQFELDMEEAIQKAEENKRLKELQLKQEEKLAM
		ĺ	BLAKLKHESLKDEKMRQQVRENSIELRELEKKLKAAYMNKERAA
[ļ	QIAEKDAIKYEQMKRDAEIAKTMMEEHKRIIKEENAAEDKRNKA
			KAQYYLDLEKQLEEQEKKKQEAYEQLLKEKLMIDEIVRKIYEED
1	!		QLEKQQKLEKMNAMRRYIBEFQKEQALWRKKKREEMEEENRKII
	ļ		EFANMQQQREEDRMAKVQENEEKRLQLQNALTQKLEEMLRQRED
	İ	j	LEQVRQELYQEEQAEIYKSKLKEEAEKKLRKQKEMKQDFEEQMA
' 1		1	LKELVLQAAKEEEENFRKTMLAKFAEDDRIELMNAQKQRMKQLE
1	1	İ	HRRAVEKLIEERRQQFLADKQRELEEWQLQQRRQGFINAIIEEE
	1		RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI
6573	777	255	CEEK
95/3	767	275	GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK
1		•	LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL
			TRKLSQRPTVEELRERKILIRFSDYVEVADAQDYDRRADKPWTR

<u> </u>			
SEQ	Predicted	Predicted end	Amino acid gegment control
ID	beginning	nucleotide	
ю:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	n=nistidine, I=Isoleucine K-liceine
i i	to first		L=Leucine, M=Methionine, N=Asparagine,
- 1	amino acid	amino acid	Parroline, Q=Glutamine, R=Arginine
ì		residue of	S=Serine, T=Threonine, V=Valine
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	Î	\=possible nucleotide insertion)
			LTAADKVSRGECWRVGGRTVCWVSLGSPLGSV
6574	204	1159	LESSYPHENOUSHINGSTONE
)	}		LESSVPVSVGVFWACGVSWTGAAGLQDGALSDTMARNAEKAMTA
- 1	1		LARFRQAQLEEGKVKERRPFLASECTELPKAEKWRRQIIGEISK
	1	F	AVAULQNAGLGEFRIRDLNDEINKLLREKGHWEUDTER GCDDV
- 1		ł	GRVGPKMLDHEGKEVPGNRGYKYFGAAKDI,PGVREI,FEKEDI,DD
i	Į.	i	PRETRAELMKAIDFEYYGYLDEDDGVIVPLEOEVEKKLPAELUR
	1	Í	AWAREARLARGEKEEEEEEEEINIYAVTEEEGDEEGGOEVO
- 1		ļ	GDDSQQKFIAHVPVPSQQEIEEALVRRKKMELLQKYASETLQAQ
			SEEARRLLGY
6575	117	820	SPALASQSGGITEEKMLEPQENGVIDLPDYEHVEDETFPPFPPP
1	1		ASPEDONARGED DESCRIPTION OF THE PROPERTY OF THE
ŀ	}		ASPERQDGEGTEPDEESGNGAPVPVPPKRTVKRNIPKLDAQRLI
1			SERGLPALRHVFDKAKFKGKGHEAEDLKMLIRHMEHWAHRLFPK
1	į i		DOFEDFIDROEYLGSKKEVOTCLKRIRIDIDILHEDEVENDER
1	1		AENNEHDVTSTELDPFLTNLSESEMFASELSISLTEEOOOPIED
6576	1	1022	NAQUALERRQAKLP
1	1 - 1	1060	PEPQALVGQKRGALRLLVARLVLTVSAPAEVRRRVLRPVLSWMD
i	1		RETRALADSHFRGLGVDVPGVGOAPGRVAFVSEPGAFGVADETE
j			GFLLPNLPCVFSSAFTOGWGSRRRWVTPAGPPDFDUI.I.prvcpv
1	1 1	•	VVPVANCGVQEYNSNPKEHMTLRDYITYWKEYIQAGYSSPRGCL
1	!		YLKDWHLCRDFPVEDVFTLPVYFSSDWLNEFWDALDVDDYRFVY
1	1		AGPAGSWSPFHADIFRSFSWSVNVCGRKKWLLFPPGOEEALRDR
)	1 1		HGNLPYDVTSPALCDTHLHPRNQLAGPPLEITQEAGEMVFVPSG
ľ	1 1		WHHQVHNLVMCCFSCPLSGAFLQEDGSTTSPLSQPELGWNGVAH
			G G G G G G G G G G G G G G G G G G G
6577	2271	987	SDRMASDDFDIVIEAMLEAPYKKEEDEQQRKEVKKDYPSNTTSS
1	1		TSNSGNETSGSSTTCETONDORDEDORKEVKKDYPSNTTSS
	1		TSNSGNETSGSSTIGETSNRSRDRDRYRRRNSRSRSPGRQCRHR
i	1 1	ĺ	SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF
ļ	1		REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV
1]		GRANDARI I SDRNSRRSKGI AYVEFCETOSVPI A TGLTGODI I G
	1 1		VPIIVQASQAEKNRLAAMANNI,OKGNGGPMPT,VVGGC.UENTDDD
f	j i	1	MERGIFEFFGKIONIVLMKDSDTGRSKGYGFTTFSDSECARDAT
1	}		EQUING F ELAGRAMRVGHVTERLDGGTDITFPDGDOFIDI.Ggagg
	! !	1	REQLIMAKLAEGAGIQLPSTAAAAAAAAAAAAAAI.OLNGAVELGA
6578	777		LNPAALTALSPALNLASQCLOLSSLFTPOTM
1 -2,2	377	1489	PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKDELLDA
į i			LQIALVVSLYWVTSISMVFLNKYIJ,DSPSI,DT.DTDTFUTEVCOT
, ,			VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG
[ļ	MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA
ļ l	i	j	LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI
1 1	·	i	YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLLGELQALRDF
1 1	1		AOLGEN PROGRAMME GOT PORT TO THE PUBLIC GELQAL RDF
!		1	AQLGSAHFWGMMTLGGLFGFAIGYVTGLQIKFTSPLTHNVSGTA
		1	KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK
6579	2	222	KTPEEPSPKDSEKSAMGV
		711	RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT
	l	I -	I IMGKDKYENEDLIKHGWPEDIWFHUDKI.SSAUUVI.DI UVOENA
1	ľ	1	EDIPKEVLMDCAHLVKANSIOGCKMNNVNVVVTDWGNI VVTDD
1		1.	DVGQIGFHRQKDVKIVTVEKKVNEILNRI.FKTKVFDFDDIAABE
	ì	1	ECRDREERNEKKAQIQEMKKREKEEMKKKREMDELRSYSSLMKV
			ENMSSNQDGNDSDEFM
6580	62	1571	LVALKNWKPKGTNIPAPQSPVFGEAVSGVYMMTKVLGMAPVLGP
	i] ;	RPPQEQVGPLMVKVEEKEEKGKYLPSLEMFRQRFRQFGYHDTPG
ł	[1 i	PREALSQLRVLCCEWLRPEIHTKEQILELLVLEQFLTILPQBLQ
İ	İ	;	MANOERCHESTERMENT I BEN ANDER THE VERSET TITLE OF THE PROPERTY
ſ		1.	AWQEHCPESAEEAVTLLEDLERELDEPGHQVSTPPNEQKPVWE
i	į	12	KISSSGTAKESPSSMQPQPLETSHKYESWGPLYIQESGEEQEFA
	-	1,2	DPRKVRDCRLSTQHEESADEQKGSEAEGLKGDIISVIIANKPE
			SLERQCVNLENEKGTKPPLQEAGSKKGRESVPTKPTPGERRYI

10 beginning nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence corresponding to first amino acid residue of amino acid amino acid sequence corresponding to first amino acid amino acid amino acid sequence corresponding to first amino acid amino acid amino acid sequence corresponding to first amino acid amino acid sequence corresponding to first amino acid amino aci	SEQ	Predicted	Predicted end	Amino agid gogge
Corresponding to first amino acid amino acid residue of amino acid amino acid amino acid amino acid amino acid acid acid acid acid acid acid acid	ID			
corresponding to first amino acid serious control of the control of the control of the control of the control of amino acid amino acid amino acid amino acid sequence control of amino acid sequence control of amino acid sequence control of the control of amino acid sequence control of the control of the control of amino acid sequence control of the c	NO:	nucleotide		Clutania Acid R Plant Baspartic Acid, E=
to first amino acid residue of amino acid am	1			Glucamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of saino acid amino acid amino acid amino acid amino acid sequence amino acid sequence amino acid sequence acid se	1	corresponding		haristidine, laisoleucine, Kalysine,
amino acid residue of amino acid amino approximation acid amino approximation acid amino approximation acid amino approximation acid amino amino approximation acid amino amino approximation acid amino amino approximation acid amino a	ľ	to first		Debeddine, Mamethionine, NaAsparagine,
residue of amino acid sequence	1			S-Carine, U=Glutamine, R=Arginine,
amino acid sequence Sequence	i			S=Serine, T=Threonine, V=Valine,
Sequence C-possible muclectice deletion.	1			w=tryptopnan, Y=Tyrosine, X=Unknown, *=Stop
CARCGRAP SISSILITERINETIERER PYCTROCKAR SHISSINIT HIATHUNDRYDOCKOGKAR GROSSILLEKIORMHTE BAPYOCKO KARSOKGSLIKHRITHERER PYCTROCKAR SHOULD TORK PYKCKECKAR SHISSIN SHIP SHIP SHOULD TORK PYKCKECKAR SHISSIN SHIP SHIP SHIP SHIP SHIP SHIP SHIP SHIP	- 1		acdamice	Codon, /=possible nucleotide deletion,
ARPSIGGS LICHPRITHCEPTY CLORGOSPIGALS HORD. ARPSIGGS LICHPRITHCEPTY CLORGOSPIGALS HORD. TGKKPYKCKEGGRAFMHSSKPMHERRITTGERPWCHHICGKTPY SKSNLSKRIGGRAFMHSSKPMHERRITTGERPWCHHICGKTPY SKSNLSKRIGGRAFMHSSKPMHERRITTGERPWCHHICGKTPY FYFIKHGLSTPMASNITAS LAQARKUVEQUKWENITAR KVSKA ADLANYCCHARAEDPLITVPASNIPPREKKFCAIL (FITKHGSPVSVPLISEUURKELESLLENEGOVIPTSSETT OPHITYSTULVAR FRILDEDSHIDGLILITSENGVUDLISSETT OPHITYSTULVAR FRILDEDSHIDGLILITSENGVUDLISSET LICH OPHITYSTULVAR FRILDEDSHIDGLILITSENGVUDLISSET LICH OPHITYSTULVAR FRILDENDSGULVER FRILDRICH AND SASTELGT SSMHFSPRSISIF OPHITYSTULVAR FRILDRICH AND SASTELGT SSMHFSPRSISIF ILPLSLVSLGREN TO IRAPPINE TALFRS PDSSHIRST LICHLANCEAU RISSELGRICUVLPS PT ALFRS PDSSHATSCPCHILINRCEAU RSPS PLGRICUVLPS PT ALFRS PDSSHATSCPCHILINRCEAU RSPS PLGRICUVLPS PT ALFRS PDSSHATSCPCHILINRCEAU RSPS PLGRICUVLPS PT ALFRS PDSSHATSCPCHILINRCEAU RSPS PLGRICUVLPS PT ALFRS PDSSHATSCPCHILINRCEAU RSPS PLGRICUVLPS PT ALFRS PDSSHATSCPCHILINRCEAU RSPS PLGRICUVLPS PT ALFRS PDSSHATSCPCHILINRCEAU RSPS PLGRICUVLPS PT ALFRS PDSSHATSCPCHILINRCEAU RSPS PLGRICUVLPS PT ALFRS PDSSHATSCPCHILINRCEAU RSPS PLGRICUVLPS PT ALFRS PDSSHATSCPCHILINRCEAU RSPS PLGRICUVLPS PT ALFRS PDSSHATSCPCHILINRCEAU RSPS PLGRICUVLPS PT ALFRS PDSSHATSCPCHILINRCEAU RSPS PLGRICUVLPS PT ALFRS PDSSHATSCPCHILINRCEAU RSPS PLGRICUVLPS PT ALFRS PT ALS STRIPTS SCHOOL SERVER PROBLEMS PROBLEMS PROBLEMS RSPS PLGRICUVLPS PT ALFRS PROBLEMS PROBLEMS PROBLEMS RSPS PLGRICUVLPS PT ALFRS PROBLEMS PROBLEMS PROBLEMS RSPS PLGRICUVLPS PLGRICUM PROBLEMS PROBLEMS PROBLEMS PROBLEMS RSPS PLGRICUM PROBLEMS PROBLEMS PROBLEMS PROBLEMS RSPS PLGRICUM PROBLEMS		 	 -	(=possible nucleotide insertion)
AASSGGSLIKHYR HTGEKPYCCUSGCKSFSGRAGLSSHQLI TGKEYPKCKEGGRAFMISSPRMICHER HTGEVPCHICHGKYF SKSNISKIQRVHTGEGEAP 476 RYPIKRUSSPYMASSNYTSSTAQARKUVQUKMEANTDRIKVSK AADLAMYCCHARAKEDPLITPVPASSNYFRKKFFCALI 6582 1428 718 718 718 718 718 718 718 7		ł		CAECGRAFSNSSNLTKHRRTHTGEKPYVCTKCGKAFSHSSNLTL
6581 228 476 RVELKOLSSTYNKSKECKARNISSKYNKHRIHTEEKPWECHHOGKTPK RVELKOLSSTYNKSKIAARKULVOLKMEANIDRIKKSKI AADLANYCSHAKEPPLLTVPASNIPTEKKSFETAIL 6582 1428 718 CFITKTHESPYSVYLSFULKKEELESLLENEGOVITSSFIT OPELATOR OF HITWITUNING PREPLYVSKRIPTSSFIT OPELATOR OPELATOR OF HITWITUNING PREPLYVSKRIPTSSETS OPERATOR O	ſ	1		HIRTHLVDRPYDCKCGKAFGQSSDLLKHQRMHTEEAPYQCKDCG
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41 RIPSMISGRIRMCTWRPATALMSASLRIGITSSMHPSPRSISIE LSMMLSPLPSNTRGLSPTALFRSPDSHATSCPRIHLMERCRALL RSPSPLGRLQVLPRSPLHVETHMSGREVIGLQVQRSRSGTGPAG SQAGSGAVQGGMCIP PDPMAALGPSSQNVTEYVVRVPKNTIKKYNIMAPNAADKVNFAT WNQARLERDLENKKIYQEBEMPSGAGSBFNRKLREEARRKKYG CPDGAFFAPVHMYNTFULARRITLITABEABEEWERRINVLHH FSIMQGRILKDODDEDEBEKERGRRKASLBIHTHULRDDLENS SDASDASGEBGRYPKAKKKAPLAKGGRKKKKKKGSVTENTSYYIFTQ CPDGAFFAPVHMYNTFULARRITLITABEABEEWERRINVLHH FSIMQGRILKDODDEDEBEKERGRRKASLBIHTHULRDDLENS SDASDASGEBGRYPKAKKKAPLAKGGRKKKKKKGSUDEAFPES DDGDPEGGEVPYMANGGSSSGEPBSKAKAPQQEEGPKUDEQS BSESSEBERPBEDEKREEBEKKERDERKPSGGSSKONSFOTFSAB GSSTSSTIRAABSKLRGGRVSEMPAARKIRUTGFQSLSGKST TOLSSEGTIVNLAQILKRINPERRMINDKHHFSLKE GPINISRTDDFVGGDPFABASCSVITHSHTHATMTYKLLIKKFOTKK TOLSSEGTIVNLAQILKRINPERRMINDKHHFSLKE GFINISRTDDFVGGDPFABASCSVITHSHTHATMSRDADFADDMQ HKKEQRAAQKADVLITGAGNPVGDELNUTTVGRGFGLLVQDVVT TDEMAHPGRBRIPERVHAKGAGAFGFFEVTHDITTXYSKAKVFE HIGKKTFIAVFSTVAGSGSSADTVEDPRGFAVKFYTEGMNDL VUNNTPIPFIRDFILPPSFIHSGKNNPOTHENFALKFYTEGMNDL VUNNTPIPFIRDFILPPSFIHSGKNNPOTHENFALKFYTEGMNDL VUNNTPIPFIRDFILPPSFIHSGKNNPOTHENFALKFYTEGMNDL VUNNTPIPFIRDFILPPSFIHSGKNNPOTHENPDTHRKR PSHLYGVSFLFANDLANGVSGFFFKLVNAMSBAVVCK FHYKTDGSIKNLSVEDAARLSQEDPDYGIRDLFNA LATGKYPSW TFYJOWATFNCASTFPNPFOLITKVWPHKDYFLIPVGKLVLNRN PVNYFAEVSGIAFDESNPPPGIHSSPDKMGGREFALVNRAPVNVLNE GQRRGLGENISPSTAMPVGGTPADNKKRKSSKLINETTGGGQESSGL NLGKKLSVERDVMLEELSLLTNRGSKMFLIRGMVGKFTVVNLNE EQRRILCENIAGHLKDAQIFTQKKAVKNTTEVHPDYGSHIQALL DKNAMSKPNNAHTHYQGGSHLAAREKKN. DVSNSSSMHFFKKLFVYGGGGAGGSTYSKSKNGRGSGAGG GGSAGGYGSDQOHHLGSGSGAGTGGPAQQAGRGGAAGTAGVGE GSSAGGYGSDQOHHLGSGSGAGTGGPAQQAGRGGAAGTAGVGE TGSGDQAGGEKHTTYVKTYISPWERMSKRGSGAGG GSSAGGYGSDQOHHLGSGSGAGGTGGPAQAGRGGAAGTAGVGE TGSGDQAGGEKHTTYFTYTSPEMMGETISPKMVGKSPKGMRPALITY HOYGLNKLCENTFPRFEDMGETIKHFVVCHVDAPRQQVGASGTITT HOYGLWKLCENTFPRFEDMGETIKHFVVCHVDAPRQQVGASGTT LFPULVSGLVLVNIDDNGKSWIDMATKLSGTSTT.DPUTVISH LFSQEELVNNTELVQSKYGQGKUFLGALTYGCENSAMPTLABG LFPULVSGLVLVNIDDNGKSWIDMATKLSGTSTT.DPUTVISH LFSQEELVNNTELVQSKYGQUGKUTGALDLEFNSMTSRDLD INRPGTVNNAKTIRCPVMLVVGDNARPABEGGVCCNSKLDFTTB]			DEACHTH CHARLES TO THE TOTAL T
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189 1750 PLEMALGESQNVTEYUVRVPKNTTKKYNIMAFNAADKVNFAT WNQARLERDLENKKI YBEEMPESGASESFURKLREBARKKYG IVLKEFREBOPWLLRVMGKSGKFKFKGIKKGGVTENTSYYIFTO CPGAFEAPPVINWYNFTPLARHRTLTAEBABEEWERRNKVLNH FSIMOQRRLKDQDQDEDEEKEKKRASELRIHDLENDLEMS SDASDASGEGGRVPKAKKKAPLAKGGRKKKKKKSDDEAFES DDGDFEGGVDYMSDGSSSSGEPESKKAPQQESGPKGVBGS ESSEESEEKPEEDKEFEEKEFEEKAPTOEKKRRKDSSEESDSSE ESDIDSEASSAFFMAKKTPPKREKFSGSSRGNSRGOTFSAE GGSTSSTLRAASKLEGCKRVSEMPAAKKRLDTGPGSLGKST TOLSSEQTVNVLAGILKRLMPERRMINDKHFSLKE GFIRNSRIDDFVGGDPVAEFBAVKRILKDTGPGSLGKST TOLSSEQTVNVLAGILKRLMPERRMINDKHFSLKE HIGKKTPIAVRFSTVAGEGSGAVTSVDPRGFBLVODVF TUDEMAHDRERIPERVUHAKGAGAFGFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGEGSGATTFKDATAGSTFFLOWNUDFVSLR PESLHQVSFFLSNSGIFDGRHNNOYGSBTFFLWANADGRAVCK UNNYP1FFIRDPILPSFIHSQKRNPQTHLKDEMWDFMSLR PESLHQVSFFLSNSGIFDGRHNNOYGSBTFFLWANADGRAVYCK FHYKTDGIKNLSVEDAARLSOEDPDYGIRDLFNAIAGSKYVSK TFY1QVMTFKQAETFPNPPDLTKWPHKDYFLIPVGKLVLNRN PVNYFAEVEQIAPDFSMMPGIEASPDKMLGRIFAYYDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMODNGGADNYYNNLNE EQRRKLCENIZAGHKKAQIF 19CKWWHKDYFLIPVGKLVLNRN PVNYFAEVEGIAFDFSMMTANDDNTOVRAFYVNVLNE EQRRKLCENIZAGHKKAQIFTFYNKRKSSKLIMBLTGGGGRSGL NLGKKLSVPDWHLEELSLITMRGSKMFKLROWSEFFIVENHP DVFSDSSMDHFGKFLFTVGGGLGTAGGGFSYSKSNGRGGSQAGG GGSAGGYGSDQOHHLGSGSGAGGTGGAGAGGGAAGAGAAGA SGSAGGYGSDQOHHLGSGSGAGGTGGAGAGGGAAGAGAAGA SGSAGGYGSDQOHHLGSGSAGGTGGGGSYSKSNGRGSQAGG GGSAGGGEKHITVFKTY1SPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRTPGMPKX FRYSGGRHEGERDERFORDERFTYPGENDEITTYHTYTSPREDMGEITKHFVVCHVDAPGGQOVGASGF PGGYGPPSMEQLAMMLPSVVQHFGFKVVIGIGGAGAYVLAKFA LIFPDLVEGLUNIDLDPGKGWTHAARKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSVRQQIGNVNQAALQLEWNNYNSRRIDLD INRPGTVNNKTLRCPVNLVDGDRAARAGAGAGGAAGAAGAALDAD LFSGELVNNTELVQSVRQQIGNVNQAALQLEWNNYNSRRIDLD INRPGTVNNLTLRCPVNLVDGDRAARLGGLTSTLPDTVLSH LFSGEELVNNTELVQSVRQQIGNVNGAALQLEWNNYNSRRIDLD INRPGTVNNLTLRCPVNLVVDGNAARAGAGAGAGAGAAGAALADAD	i i			**SPSPLGKLQVLPRSPLHVHTHNSGKEVLGLQVQRSRSGTGPAC
WNQARLERJLSNIKIYQEEEMPESGAGSIFRIKLRERARKXYG IVLKERPPEDQPHLIEVNOKSGRKFRGIKKGYTENTSYYIFIQ CPEGAFEAPPYHNWYNFTPLARRETLTAEBAEEEWERNKVLING FSIMQQRILKDQDQDEDEEKEKGGRKKKKKGDIDEAFEDS SDASDAGGEGGRVFKAKKAPLAKGGRKFKKKKKGDDEAFEDS DDGDFEGGEVDYMSDGSSSSGEPBSKAKAPQGEDFWSVDKOS DSSESSEERFPPEEKKEAPPPQEKKRKKKKGDDEAFEDS EDDDDFEGGEVDYMSDGSSSSGEPBSKAKAPQGEEDFWSDVDKOS DSSESSEERFPPEEKKEAPPPQEKKRKKKKGSDEAFEDS GGSTSSTLRAAASKLEQGKRVSEMPAARKLRLDTOPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRXTLRKPMTKDLLKKFQTKK TOLISSEQTVUVLAQTLKKINDFRKMINDKWHFSLKE GFIRNSTDDFVGGDFRAEASCSVLHSKPHANADSRDPASDQMQ HKKEQRAAQKADVLTTGAGNPUGDKLNVITUGPRGPLLVQDVVF TIDEMAHFDRRRIPERVUTAKGAGAFGYFEVYHDITKKYSKAKVFE HIGKKTFTAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL VUNNTPIPFIRDFLIGVRDPHUTLKYPMWVDFWSLR PESLHQVSFLFSDRGIPDGHRMNQYGSHTFKLWNANGEAVYCK PHYKTDQGIKNLSVYBDARRLSQEDPDGVIRDLHNA IATGKYPSW TFY1QVMTFRQAETFPKNPFDLTKWPHKNYPLLVPGKVLVINRN PVNTFAEVEQTAFTPSNPPDLTKWPHKNYPLLPVGKVLVINRN PVNTFAEVEQTAFTPSNPPDLTKWPHKNYPLLPVGKVLVINRN PVNTFAEVEQTAFTPSNPPDLTKWPHKNYPLLPVGKVLVINRN PVNTFAEVEQTAFTPSNPPDLTKWPHKNYPLLPVGKVLVINRN PVNTFAEVEQTAFTPSNPPDLTKWPHKNYPLLPVGKVLVINRN PVNTFAEVEQTAFTPSNPPGLTKSPRHWQDNGGGAPNYPNSF GAPBQPSALEHSIQYSGEVRRYNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFTQKGKVNFTEVHPDVSGHTQALL DKYNAERFKABIHTFVQSGSHAAREKANL 6586 32 804 PLFEQPAESTSTMFVSGTFAENKKRSSKLIMBLTGGGGESSGL NLKKKLSVPRDVMLEELSLLTNRGSKMFKLRGNRVEKFTYENHP DVFSDSMDHFQKFLPTVGGQLGTAGGGFTSKSNGRGGSQAGG SGSAGQYGSDQQHHLSGSGSAGGTGGPAGQARGGAAGTAGVGE TGSGDAGGGSKHITVFKYTJSWERAMGVPDQQKMELGILLL GSSAGGYGSDQCHHLSGSGSAGGTGGPAGGARGGAAGTAGVGE TGSGDAGGGRKHITVFKYTJSWERAMGVPDQQKMELGILLL FREVELUKHLUVUNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH HDVGLMHKLCFNTFFMFEDMGELTKHFVVTADPGQQGASQF PGGYPFSMEQLAAMLPSVVOHEGFKYTGIGGGAAYVLAKFA LIFPDLVEGLUVUNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LIFPGLVENAKTLRCVWLVVGDNAPAEBGVVECNSKLDPTTTT FRAMDSGGLLPQVTQSKUTFAFKYFUGOMGRASHLAPA LIFPGLVTDAAACHTARPSVOTAGARGGAAVLAKFA LIFPGLVVRNAKTLRCVWLVVGDNAPABEGGVVECNSKLDPTTTT FRAMDSGGLEPQVTQTSKUTFAFKYFUGOMGRASHDAPLAPA	6584	189	1750	SQAGSGAVQGGNWCIP
CPGAPEAFPVNIMYNFTLARRATCIAEBAEEMERNKVLNH FSIMQORILKDQDQDEDEEEKKRGRKKKKGSUTENTSYYIFTO CPDGAPEAFPVNIMYNFTLARRATCIAEBAEEMERNKVLNH FSIMQORILKDQDQDEDEEEKKRGRKKKKGSDEAFEDS SDASAGEEGGRVFKAKKKAPLAKGGKKKKKKGDDEAFEDS DDGDEGGGEVDVMSDGSSSSGEPBSKAKAPQGESPKOVEGOS DSSEESEERPPEEDKEFEEEKKAPTPQEKKRKKGSDEAFEDS ESDIDSEASSAFFMAKKKTPPKREKKPSGGSSRGNSRFOTFSAE GGSTSSTLRAAASKLEQGKRVSEMPAAKKLRDTOPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKK TOLISSEQTVUNUAQILKRLNPERKMINDKMIFSLKE GPIRNSRIDDFVGGDPRAEASCSVLHSKFHANADSRDPASDOMQ HWKEQRAAQKADVLITGAGNPVGDELNVITVGPRSPLLVQDVVF TDEMAHFDRER PLEVVIAKGAGAFGYFEVTHDITKYSKAKVF HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGRWDL VGNNTPIPFIRDPILFPSFIHIGVRINPQTHLKDPDWWDFMSLR PESSHQVSFIFLESDRGIPPGHRHMNYQSHTFKLVNANGEAVYCK PHYKTQQGIKALSVEDARLSQEDPDYGIRDLFNAIATGKYPSW TFYLQVMTFNQAETPFNPPDITKVWHKDYPLIPVGKLVLNARN PVNYFAEVEQTAFPPSNMPPGILASPDKMTQGRLFAVPOTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPBGQPSALLHSIQYSGEVARFNTANDDNVTQVRAFYVNVLINE EQRKRLCENIAGHLKDAQIFIQKAVNNFTEVHDYVSGHIQALL DKYMAEKPKNAIHTFVQSGSHLAAREKANL DKYMAEKPKNAIHTFVQSGSHLAAREKANL DKYMAEKPKNAIHTFVQSGGHLARGGGFSYSKSNGRGGSQAGG GSGSAGGYGSDOGHLLGSGSGAGGTGGFSGAGGAGGAGTAGVGB TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKABLPKKSFNRTAMPYGGTEKASKMTTROMPKV TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKABLPKKSFNRTAMPYGGTEKASKMTTROMPKV TGSGDQAGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKABLPKKSFNRTAMPYGGTEKASKMTTROMPKV LIFPDLVEGLUVUNIDPNNGKSTDMAATKLSGLTSTLPDTVUSH LIFPGLVELUVUNIDPNNGKSTDMAATKLSGLTSTLPDTVUSH LIFPGLVELUVUNIDPNNGKSTDMAATKLSGLTSTLPDTVUSH LIFPGLVENAKTLRCEVMLVVQDNAPAEDGOVECNSKLDPTTTT FLKMADSGGLPQVTQSKUTGPFKYPLOGMWRMSASMTBLADQ			1750	PEPPEAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFAT
CERGAFEAFPVHNWYNTTPLARHATLITAERABEEMERRINKVLIMH FSISIMOGRIKIKOODODEDEEMEKKRGRKKKKUSDIDEAFEDS SDASDASGEEGGRVPKAKKKAPLAKGGRKKKKKUSDDEAFEDS DDGDFEGGEVDYWSDGSSSSGEPESKAKAPQOEGEPKGVDEOS DESEBSEBERPPEDKEEREKKAPTPOEKKRKKSSEESDSSE EGDIDSEASSAFMAKKKTPPKRERKPEGGSSGRONSREGTESABE GGSTSTIRAAASKLEGGKEVSEMPAKRIKILDTGPOESKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKK TOLSSEQTVNVLAQILKRLNPERRMINDKHFSLKE GFIRNSRIDDFVGGDFRAEASCSVLHSKFHAMADSRDPASDOMO HWKEGRAAQKADVLTTGARPHVOEKDHVITVGPRGPLLVQDVVF TDEMAHFORERIPERVVHAKGAGAFGYFEVTHINITKYSKAKVFFE HIGKKTPIAVRFSTVAGEGGSADTVRDPRGFAVKFYTEDGRWDL VGNNTPIPFIRDPILPPSFIHSQKRIPGYHLKDPDWMDFWSLR PHYKTDQGIKNLSVEDARALSGEDPYGIRDLEMA LATGKYPSW TFYXIQVMTFNCAETFFPNFDLIKWPHKDYPLIPVGKLVLINRN PVNYFAEVEGIAFDFSNMPGIKASPDWKLQGRLFAYPDTHRH LGPNYLHIPVNCPYRARVANYGGPPCMGPMCNGGGAPNYYPNSF GAPEQOPSALEHSIQYSGEVRRFNTANDDNYTQVRAFYVNVLINE EQRRKLCENIAGHLKDAQIFIGKKKKSKLINELTGGGGESGL NLGKKISVPRDVMLEELSLLTMRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGGIFAGGGFSYSKRGRGGSQAGG GGSAGGTGGDAGGAGGAGGAGGAGGAGG SGSAGGYGSDQGHLIGSGSGAGGTGGPAGGAGGGGAAGTAGVGB TGSGDQAGGEKHTVFKTYISPMERAMGVDPQQKMELGIDLLA VGAKAELPKYKSFNRTAMPYGGYEKASKRMTPQMKV TGSGDQAGGEKHTVFKTYISPMERAMGVDPQQXMELGIDLLA VGAKAELPKYKSFNRTAMPYGGYEKASKRMTPGMKV TGSGDQAGGEKHTVFKTYISPMERAMGVDPQQXMELGIDLLA VGAKAELPKYKSFNRTAMPYGGYEKASKRMTPGMKV LIFPDLVEGLVLVNIDDNGKWIDWARKLSGLTSTLPDTVLSH HDVGLNHKLCFNTFFNFEDMGEITKHFVVCHVDAPGQQVGASGF PQGYOFPSMEQLAMMPSVVQHFGFKYVIGGGAGAVVLAKFA LIFPDLVEGLVLVNIDDNGKWIDWARKLSGLTSTLPDTVLSH LFSGELVNNTELVQSVRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNNAKTIRGEVMLVVGNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQCVTQPGKLAFAFKYFLOGMAWPSASKHFILAPG FLKMADSGGLPQCVTQPGKLAFAFKYFLOGMAWPSASKHFILAPG FLKMADSGGLPQCVTQPGKLAFAFKYFLOGMAWPSASKHFILAPG FLKMADSGGLPQCVTQPGKLAFAFKYFLOGMAWPSASKHFILAPG FLKMADSGGLPQCVTQPGKLAFAFKYFLOGMAWPSASKHFILAPG FLKMADSGGLPQCVTQPGKLAFAFKYFLOGMAWPSASKHFILAPG FLKMADSGGLPQCVTQPGKLAFAFKYFLOGMAWPSASKHFILAPG FLKMADSGGLPQCVTQPGKLAFAFKYFLOGMAWPSASKHFILAPG FLKMADSGGLPQCVTQPGKLAFAFKYFLOGMAWPSASKHFILAPG FLKMADSGGLPQCVTQPGKLAFAFKYFLOGMAWPSASKHFILAPG FLKMADSGGLAFAFTLAFG FLKMADSGGLAFTTTTT	1 1			WNQARLERDLSNKKIYQEEEMPESGAGSEFNRKLREEARRKKYG
SDADASGEGGRUPVAKKAPLAKGGKKKKKKGSDDEAFEDS SDADASGEGGRUPVAKKAKAPLAKGGKKKKKKGSDDEAFEDS DDGDFEQGEDGRUPVANDGSSSSQEPESKAKAPQGEEGPKGVDEQS DSSESEERKPPEDKKEEEEKKAPTPOEKKRRKDSSESDSSE ESDIDSEASSAFFMAKKKTPKREKEPGGSRGNSRRGTPSAE GGSTSSTLRAAASKLEQGKRVSEMPAAKRLRLDTGPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRAVITRKEMTTKDLLKKFQTKK TGLSSEQTVNVLAQILKRIMPERRMINDKHIFSLKE 6585 3 1678 GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ HWKEQRAAQKADVLTTGAGNPVGGDKINVITVGPRGPLLVQDVVF TDEMAHFDRERIPERVHAKGAGAFGFFEVTHDITKVSKAVFFE HIGKKTPIAVRSTVAGEGGSADTVRDPRGPAVKFYTEDGNWDL VGNNTPIPFIRDPILFPSFHISQKRNPQTHLIKDPDMVWDFWSLR PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLWANAGEAYFCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TFYLQVMTPAQAETFPHDTKVWPHKOYPLIPVGKLVLNRN PVNYFAEVEQIAFDPSNMPPGITKASPRMDNVTQVRAFYVNVLNE EQRRILCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALI LGPNYLHIPVNCPYRARVANYQRDGPMCMDNGGGAPNYYPNSF GAPRQOPSALHESIGYSGRYPRTANDDNVTQVRAFYVNVLNE EQRRILCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALI NKKKLSVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFGVSGSGAGGTGGPAGQAGRGGAAGTAGVGE SGSAGGYGSDQHLLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE SGSAGGYGSDQHLLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMPQMBKV TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMPGMBKV HDVGLHHKLCFNTFFNFEDMQEITKHFVVCHVDAFGQOVGASQF PGGYOFPSMEQLAAMLPSVVQHFGFKYVIGGVAGAAVYLAKFA LIFPDLVEGLVINNIDNGKWIDWARKLGGLTSTLPDTVLSH LFSQEBLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVVNNAKTLRCEVMLVVGNAPAEDGVVCENSKLDPTTTT FLKMADSGGLAPQTYDGKKUFDAFRKYFLGGMAYMSASRMDILAPG FLKMADSGGLAPQTYDGKKUFDAFRKYFLGGMAYMSASRMDILAPG FLKMADSGGLAPQTYDGKKUFDAFRKYFLGGMAYMSASRMDILAPG FLKMADSGGLAPQTYDGKKUFDAFRKYFLGGMAYMSASRMDILAPG FLKMADSGGLAPQTYDGKKUFDAFRKYFLGGMAYMSASRMDILAPG FLKMADSGGLAPQTYDGKKUFDAFRKYFLGGMAYMSASRMDILAPG FLKMADSGGLAPQTYDGKKUFDAFRKYFLGGMAYMSASRMDILAPG FLKMADSGGLAPQTYDGKKUFDAFRKYFLGGMAYMSASRMDILAPG FLKMADSGGLAPQTYDGKKUFDAFRKYFLGGMAYMSASRMBILAPG FLKMADSGGLAPQTYDGKKUFDAFRKYFLGGMAYMSASRMBILAPG FLKMADSGGLAPQTYDGKKUFDAFRKYFLGGMAYMSAGRAFTLAPG FLKMADSGGLAPQTYDGAFRAFRYFLAGGMAYMSAG				CDCABEARPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTQ
SSASDASGEEGGRVPKARKKAPLAKGGRKKKKKKGSDDEAFEDS DDGDFSGEVDYMSDGSSSSQEEPESEKARAPQQEGPKGVDEQS DSSESSEEEKPPEEDKEEEEKKAPTPQEKKRKKDSSEESDSSE ESDIDSEASSAFPHAKKKTPPKRERKPSGGSGRONSRPGTPSAE GGSTSSTLRAAASKLEQCKUVSEMPAKRLRLDTGPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKK TGLSSEQTUNVLAQILKRLINPERRWINDKMHFSLKE GPIRNSRIDDFVGGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ HWKEQRAAQKADVIJTGAGNPVGDKINVITVOPRGPLLVQDVVF TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL VGNNTPIPFIRDPILPPSFHISQRRNPQTHLKDPDMVWDFWSLR PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGBAVYCK FHYKTQGIKNLSVEDAARLSOEDPDYGIRDLFNA LATGKYPSW TFYLQVMTFRQAETFPFNPFDLITKVWPHKDYPLIPVGKLVLNRN PVNYFAEVEQIAFDPSOMPPGILASPDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANVQRDGPMCMQDNQGAPNYYPNSF CAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRRKLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYMAEKFKNALHTFUGSHLASPGSHLAREKANL KYMAEKFKNALHTFUGSHLASPGSGALGGTGGGGGSGSGL NLGKKISVPRDVMLEELISLITNGSKMFKLRGMRVEKFIYENHP DVFSDSSMDHFCKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSQQOHLLGSGSGAGGTGGPAGQAGRGGAACTAGVGE TGSGDQAGGECKHITVFKYYISPWERMGUDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV HDVGLNHKLCFNTFPNFDDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVGHFGFKYVIGIGGAGAYVLAKFA LIFPDLVEGLVUNIDPNKGRIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELUQSYRQQICNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPWALVVQGNLQFFWNMYNSRRDLD INRPGTVPNAKTLRCPGKJUNDAAFEBGVVECNSKLDDFTTT FLKMADSGGLPQVTQPGKLITEAFKYFLOMGYVENSAMDFILAPQ				CPDGAFEAFPVHNWYNFTPLARHRTLTAEBAEEEWERRNKVLNH
DUGP#SQEVDYMSDGSSSQEPESKARAPQQEEGPKQVDEQS DESEESEEERPPEEDKEEEEKKAPTPQEKKRKUSSEESDSSE ESDIDSEASSAFFMAKKKTPPKEEKKPSGGSSRGNSRPGTPSAE GGSTSSTLRAAAGKLEQCKRVSEMPAAKKLRLDTGPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTXCLLKKFQTKK TGLSSEQTVNVLAQILKRLNPERKMINDKMFSLKE GFIRMSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ HWKEQRAQKADVITTGAGNPYGGDKINVTVOPRGFLLVQDVVF TDEMAHFDRERIPERVHAKGAGAFGYFEVTHDITXYSKAKVFE HIGKRTPLAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGIMDL VGNNTPIPPIRDPILPPSFHIBGKRNPQTHLKDPDMVWDFWSLR PESHAQVSFLFSDRGIPDGHHMMYGSHTFKLVNANGBAVYCK PHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNALATGKYPSW TFY1QVMTFNQAETFPFNPFDILTKWPHKKDYFLIPPGKLVLNRN PVNTFAEVEQIAFDPSMPPGIEASPDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMONQGAPNYYPNSF GAPEQQPSALEHSIQYSGEVARPHTANDDNVTQVRAFYVNVLNE EQRRLCENIAGHLKDAQIFIQKKAVKNPTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL DKYNAEKPKNAIHTFVQSGSHLAAREKANL PLPEQPASSTSTMPVSGTPAPNKKKSSKLIMELTGGGQESSGL NLGKKLSVPRDVMLEELSLLTNRGSKNFKLMCMEVEKFIYENHP DVFSDSSMDHPQKFLPTVGGQLGTAGGGFSYSKSNGRGGSQAGG SGSAGQVGSDQOHHLGSGSGAGGTGGPAGQAGRGAAGTAGVGE TGSGDQAGGGGKHITVFKTYISPWERAMGUDPQQKMELGIDLLA YGKAKELPKYKSFRITAMPYGGYEKASKMTPQMPKV 6587 75 1117 RRVFSLGKMPECWDGEHDIETFYGLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFPNFEDMQEITKHFVVCHVDAPGQQVGASQF PGGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAFVLAKFA LIFPDLVEGLVLVNI DPNGKGNIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVQGNLDAAPTKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVQGNLDAAPEABGAWVECNSKLUBPTTTT FLKMADSGGLPQVTQPGKILTEFKYFLOGMYYMPSAAMTBLABQ	1 1	ľ		F51MQQRRLKDQDQDEDEEEKEKRGRRKASELRIHDLEDDLEMS
SSESSEERKPPEEDKEEEEKKAPTPOEKKRKKOSSEESDSSE ESDIDESASSAFRMAKKTPPKRERKPSGGSSRGMSRPGTPSAE GGSTSSTLRAAASKLEQGKVSEMPAAKKLEUDTGPOSLSGKST FQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKK TOLSSEQTVAVILAQTLKRLMPERKMINDKMHFSLKE GPIRNSRIDDFVGGDPRAEASCSVLHSKPHANADSEDPASDOMQ HWKEQRAAQKADVLITGAGANPVGDKLMVITVGPRGPLLVQDVVP TDEMAHPDRRIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGIMDL VGNNTPIPFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLR PESLHQVSFLFSDRGIPDGHRMINGYSHTFKLVMANGEAVYCK PHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TFY1QVMTFNQAETFPPMFFDLTKVWPHKDYPLIPVGKLVLNRN PVNYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHR FRYTHIQVMTFNQAETFPPMFFDLTKVWPHKDYPLIPVGKLVLNRN PVNYFAEVEQIAFDPSNMPPGIEASPDKMLQGGAPMYVPNSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKFKNAIHTFVQSGSHLAAREKANL DKYNAEKFKNAIHTFVQSGSHLAAREKANL DKYNAEKFRNDWLEELSLLINRGSKMFKLRQMRVEKFIYEMHP DVFSDSSMDHFKKFIPVGGUGTAGGFSYKSNGRGGSQAGG SGSAGQYGSQQHHLGSGSGAGGTCGPAGQAGKGGAAGTAGVGG SGSAGQYGSQQHHLGSGSGAGGTCGPAGQAGKGGAAGTAGVGG SGSAGQYGSQQHLGSGSGAGGTCGPAGQAGKGGAAGTAGVGG SGSAGQYGSQQHLGSGSGAGGTCGPAGQAGKGGAAGTAGVGG SGSAGQYGSQQHLKYNSFNATMYYGGYEKASKMTPQMFKV HDVGLNHKLCFNTFFMFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA HDVGLNHKLCFNTFFMFEDMQEITKHFVVCHVDAPGQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLUIVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTIRCFVWLVGDNAPAEDGVVCCNSKLDFTTTT FLWAADSGGLPQVTQDGKUTGAFKYFLGGMGFASAMTELAPA	1 1	j		DDCDBBCCBUDGERFEDS
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FESTHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGEAVYCK PHYKTDQGIKNLSVEDAARLSQEDDYGIRDLFNAIATGKYPSW TFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRN PVNYFAEVEQIAFDPSNMPPGIEAS PDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRITANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL DKYNAEKPKNAIHTFVQSGSHLAAREKANL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAQQYGSDQQHLIGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGKKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKITEAFKYFLOGMGYMPSASMTBLAPQ	! [1		VGNNTPIPETEDDII PROBELICOVENIONE VIRGINAVE VIEDGNWDL
FHYKTDGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TFYIQVMTFNQAETFPFNPFDLTKVWPHKDYFLIPVGKLVLINRN PVNYFAEVEQIAFDPSNMPPGIEAS PDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNS F GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL NLGKKISVPRDVMLEELSLLTINGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQOHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAFGQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKITEAFKYFLOGMGYMPSASMTBLAPQ	1			PESLHOVSFILESDEGTEDGEDEWNIGGGETTER
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FVNYFAEVEQIAFDESMMPPGIEASPDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDMQGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYMAEKPKNAIHTFVQSGSHLAAREKANL PLPEQPAESTSTMPVSGTPAPNKKKSSKLIMELTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQARGGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVXQANLQLFFNMYMSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKITEAFKYFLOGMGYMPSASMTBLAPQ	1 1	i		TFYIOVMTFXOAETFPFNPFDLTKUMPHXDXDLTDXOXXXX
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GAPEQQPSALEHSTQYSGEVRRPTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 804 PLPEQPAESTSTMPVSGTFAPNKKRKSSKLIMELTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGSQAGG SGSAGQYGSDQQHLGSGSGAGGTGGPAGQAGGGAAGTAGVGE TGSGDQAGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PGGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLOGMGYMPSASMTBLAPQ	1 1	į		LGPNYLHIPVNCPYRARVANYORDGPMCMODNOGGA DARWANGE
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PLPEQPAESTSTMPVSGTFAPNKKRKSSKLIMELTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGGAGAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PGGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVYGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLOGMGYMPSASMTBLAPQ	L		ĺ	DKYNAEKPKNAIHTFVOSGSHI AAPEKANI.
NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGGAGAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV RRVPSLGXMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PGGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLUVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLOGMGYMPSASMTBLAPQ	6586	32	804	PLPEOPAESTSTMPVSGTPAPNKKEKSSKI, IMPLTCCCORCCO
DVFSDSMDHFOKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQOHHLGSGSGAGTGGPAGQAGRGGAACTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 11117 RRVFSLGXMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PGGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQJIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLOGMGYMPSASMTBLAPQ]]	1		NLGKKISVPRDVMLEFI.SLI.TNPGSKMEVI.POMPVEVETVPVVID
SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGGKHITVFKTYISPWERAMGVDPQQKWELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV FRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLOGMGYMPSASMTBLAPQ	1	Í	j	DVFSDSSMDHFOKFLPTVGGOLGTAGOGFSVSKSNGBCGGOAGG
TGSGLOGAGGECKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTPQMPKV GAKAELPKYKSFNRTAMPYGGYEKASKRMTPQMPKV RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVXQANLQLFWMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLOGMGYMPSASMTBLAPQ	l 1	1	1	SGSAGQYGSDOOHHLGSGSGAGGTGGPAGAAGTAGUGB
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PGGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLOGMGYMPSASMTR1APQ	1	j	İ	HDVGLNHKLCFNTFFNFEDMOEITKHFVVCHVDADGOOVGAGG
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			l i	RTASLTSASSVDGSRPQACTHSESSEGLGQVNHTMEVSC
Statutura Statut		·····		5

	SEQ	Predicted	Predicted end	Amino poid
	ID	beginning	nucleotide	Amino acid segment containing signal peptide
	NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
		location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	i	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	1	sequence	pedaetice	Codon, /=possible nucleotide deletion
	6588	137	F01	\=possible nucleotide insertion\
		1 23/	501	LGLQAQLLELRINNYOLSDELRINGVELTSLEOVVAYI DEBEGG
	Į.			AQRALSKSKRAQEVEVILLSENEMLOAKIHSOEEDEDI.ONGTIMA
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	0505	2	1405	RPWGSAMATFSROEFFOOLLOGCLUPTAOOGLOOTMILLATOLA
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	1			YLVLFLCRHSSHRGVFLSVTILIYLLMGEMHMVDTVTWHKMRGA
	İ	1		QMIVAMKAVSLGFDLDRGEVGTVPSPVEFMGYLYFVGTIVFGPW
	ł			ISFHSYLQAVQGRPLSCRWLQKVARSLALALLCLVLSTCVGPYL
	ŀ	1		FPYFIPLNGDRLLRNKKRKARGTMVRWLRAYESAVSFHFSNYFV
		1		GFLSEATATLAGAGFTEEKDHLEWDLTVSKPLNVELPRSMVEVV
		1		TSWNLPMSYWLNNYVFKNALRLGTFSAVLVTYAASALLHGFSPH
	ı			LAAVLLSLAFITYVEHVLRKRLARILSACVLSKRCPPDCSHOHR
	ł	!		LGLGVRALNLLFGALAIFHLAYLGSLFDVDVDDTTEEQGYGMAY
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	i	1		GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKSTTMEGAMLPNY
				GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY
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				RYLEFYVLESKLTEFHGAFPDAQLPSKRIIGPKNYEFLKSKREE
]		FQEYLQKLLQHPELSNSQLLADFLSPNGGETQFLDKILPDVNLG
ı		j		KIIKSVPGKLMKEKGQHLEPPIMNFINSCESPKPKPSRPELTIL
		į		SPTSENNKKLFNDLFKNNANRAENTERKQNQNYFMEVMTVEGVY
	ı	i		DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDYYLQCKL
	1	i		EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKGAKQTFEEM
I	1	1		MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYVLLDI
ı				VIQELFPELNKVQKEVTSVTSWM
ı	6591	2177	656	VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR
1	1	1	1	GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKSTIMEGAMLPNY
-1	- 1	1		GVAEGEDDFIEEGIVVMEDDSFVEAVSTPNTPRNLAAWKISIPY
1	ì			VDFFEDPSSBRKEKKERIPVFCIDVERNDRRAVGHEPEHWSVYR
-[- 1	l	Į.	RYLEFYVLESKLTEFHGAFPDAQLPSKRIIGPKNYEFLKSKREE
1	1		ł	FQEYLQKLLQHPELSNSQLLADFLSPNGGETQFLDKILPDVNLG
I	ļ	j		KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPKPKPSRPELTIL
1		i		SPTSENNKKLFNDLFKNNANRABNTERKONONYFMEVMTVEGVY
1	1			DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDYYLQCKL
1	1		j	EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKGAKQTFEEM
ı	ì			MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYVLLDI
L			j	VIQELFPELNKVQKEVTSVTSWM
ı	6592	3	1861	APEFLGSTISSGSMIDANLKLLQBAEQRLKAIVAEKFALATKEG
1		1	1:	DLPQVERFFKIFPLLGLHEEGLRKFSEYLCKQVASKAEENLLMV
ı	- 1	ł	j:	LGTDMSDRRAAVIFADTLTLLFEGIARIVETHQPIVETYYGPGR
ı	i i	į.	i :	LYTLIKYLQVECDRQVEKVVDKFIKQRDYHQQFRHVQNNLMRNS
1	ł		!!	TTEKIEPRELDPILTEVTLMNARSELYLRFLKKRISSDFEVGDS
l	1		[]	MASEEVKQEHQKCLDKLLNNCLLSCTMQELIGLYVTMEEYFMRE
	ľ	•		TVNKAVALDTYEKGQLTSSMVDDVFYIVKKCIGRALSSSSIDCL
	1		10	CAMINLATTELESDFRDVLCNKLRMGFPATTFQDIQRGVTSAVN
	- 1	1	l i	IMHSSLOOGKPDTKGIESTDEAKMSFLVTLNNVEVCSENISTLK
1	i	1	1 i	CTLESDCTKLFSQGIGGEQAQAKFDSCLSDLAAVSNKFRDLLQE
1			ا ا	ELTELNSTAIKPOVOPWINSFFSVSHNIEEEEFNDYEANDPWVQ
	I	1	16	PFILNLEQQMAEFKASLSPVIYDSLTGLMTSLVAVELEKVVLKS
	1	į.	1 7	FURLEGLQFDKELRSLIAYLTTVTTWTIRDKFARLSQMATILN
]		l î	ERVTETIDYWGDNGGDI TWDI TON THOUSEN TO THE
			7	ERVTEILDYWGPNSGPLTWRLTPAEVRQVLALRIDFRSEDIKR
	6593	3		
	ļ	ļ		AFSAGSRRRGLALQRGVLGGLGGYCPCCCRRRGRLLVLLLLVR
			n	GGEGGGGRGRGDKRRRRQARRQRRRPEPAEARGGKMADVLSVL
				QYNIQKKEIVVKGDEVIFGEFSWPKNVKTNYVVWGTGKEGQPR

SEQ	Predicted	Predicted end	Drive cold
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
No:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
•	sequence	1	\=possible nucleotide insertion)
			EYYTLDSILFLLNNVHLSHPVYVRRAATENIPVVRRPDRKDLLG
1	İ		YLNGEASTSASIDRSAPLEIGLQRSTQVKRAADEVLAEAKKPRI
		ì	EDEECVRLDKERLAARLEGHKEGIVQTEQIRSLSEAMSVEKIAA
-	ł		IKAKIMAKKRSTIKTDLDDDITALKQRSFVDAEVDVTRDIVSRE
ł	i		RVWRTRTTILQSTGKNFSKNIFAILQSVKAREEGRAPEQRPAPN
1	1	ļ	AAPVDFTLRTKQPIPAAYNRYDQERFKGKEETEGFKIDTMGTYH
1		; 	GMTLKSVTEGASARKTQTPAAQPVPRPVSQARPPPNQKKGSRTP
1			IIIIPAATTSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENETL
			IQRRKDQMQ9GGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFVQ
1	i		GPAWQFKGWPWLLPDGSPVDIFAKIKAFHIKYDEVRIDDNYOKW
			DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF
6594	1	1096	EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNPWSA
1	1		DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIEERYGKDIJ.
1			NLSRKKPCGQSEINTLKRALEVFKQQVDNVAOCHIOLAGSLREE
1			ARKMEEFREKQKLQRKKTELIMDAIHKOKSLOFKKTMDAKKNYE
İ			QKCRDKDEAEQAVSRSANLVNPKQQEKLFVKLATSKTAVEDSDK
	ł		AYMLHIGTLDKVREEWQSEHIKACEAFEAOECERINFFRNALWI.
			HVNQLSQQCVTSDEMYEQVRKSLEMCSIQRDIEYFVNORKTGOI
Í			PPAPIMYENFYSSQKNAVPAGKATGPNLARRGPLPIPKSSPDDP
			NYSLVDDYSLI.YQ
6595	57	781	PLGTMSDSDLGEDEGLLSLAGKRKRRGNLPKESVKILRDWLYLH
			RYNAYPSEQEKLSLSGQTNLSVLQICNWFINARRRIJ.PDMLRKD
!	j j		GKDPNQFTISRRGGKASDVALPRGSSPSVLAVSVPAPTNVLSLS
1	1		VCSMPLHSGQGEKPAAPFPRGELESPKPLVTPGSTLTLLTRAEA
			GSPTGGLFNTPPPTPPEQDKEDFSSFQLLVEVALORAAEMELOK
6596			QQDPSLPLLHTPIPLVSENPQ
0 2 30	2	1026	PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY
			GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP
			PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD
			VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD
			FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV
1 1	1		KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA
1 1			AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN
6597	2	1026	ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH
- 1	- 1	4440	PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY
; I			GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP
ļ l			PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWYEKIRD VLIQKSQMTEPGPDVKKKTEEEDVBCEDDLILACQPESSVKALD
; !	}		FDISETRIEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV
	ļ		KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA
]	į		AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN
L			ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH
6598	1099	419	PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL
[VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE
ļ !		ĺ	LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV
l	1		FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS
			DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD
		}	SKGLQS
6599	164	1593	KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR
	j	_	MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS
	1		DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST
1	ĺ	1	DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE
ļ	1		LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE
1		ļ	VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN
j		1	EAVAAVTEEHKLYDDIDFDIEEFAKDVGAQILLHSHKKDILMH
			RWRYPSLSLHGIEGAFSGSGAKTVIPRKVVGKFSIRLVPNMTPE
			TITAL VOLUMENT TO THE PROPERTY PARTIES

SEQ	Predicted	Predicted end	Amino acid coment contain
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			VVGEQVTSYLTKKFAELRSPNEFKVYMGHGGKPWVSDFSHPHYL
!			AGRRAMKTVFGVEPDLTREGGSIPVTLTFQEATGKNVMLLPVGS
		1	ADDGAHSQNEKLNRYNYIEGTKMLAAYLYBVSQLKD
6600	2	934	PGRLFRVAAMESAGLEQLLRELLLPDTERIRRATEQLQIVLRAP
,		!	AALSALCDLLASAADPQIRQFAAVLTRRRLNTRWRRLAAEQRES
		!	LKSLILTALQRETEHCVSLSLAQLSATIFRKEGLEAWPQLLQLL
	ł		QHSTHSPHSPEREMGLLLLSVVVTSRPEAFQPHHRELLRLLNET
1]		LGEVGSPGLLFYSLRTLTTMAPYLSTEDVPLARMLVPKLIMAMQ
]			TLIPIDEAKACEALEALDELLESEVPVITPYLSEVITECLEVAP
			NVALGNAIRIRILCCLTFLVKVKSKALLKNRLLATLAAHPFPHC
5555			GC
6601	529	1420	PRAAARAPPPAVLRRDRRAATAPGAGEMTLHGPLAQRYFLNHIE
			KITTWQDPRKAMNQPLNHMNLHPAVSSTPVPORSMAVSOPNIJM
			NHQHQQQMAPSTLSQONHPTONPPAGLMSMPNALTTOOOOOKI.
]]			RLQRIQMERERIRMRQEELMROBAALCROLPMEAETLAPVORAV
1			NPPTMTPDMRSITNNSSDPFLNGGPYHSREOSTDSGLGLCCVCV
1 }			PTTPEDFLSNVDEMDTGENAGOTPMNINPCOTREPDFLDCLPCT
6602	127	<u> </u>	NVDLGTLESEDLIPLFNDVESALNKSEPFLTWL
3302	1.2.7	617	LLDFPALPKFVLAQSPKAGKPSTMTSMTQSLREVIKAMTKARNF
			ERVLGKITLVSAAPGKVICEMKVEBEHTNAIGTLHGGLTATLVD
1 1			NISTMALLCTERGAPGVSVDMNITYMSPAKLGEDIVITAHVLKQ
6603	79	660	GKTLAFTSVDLTNKATGKLIAQGRHTKHLGN
-1		000	PVGPSSLAARTGLGHLPFLHRLASSRGLDMDLLQFLAFI,FVLLL SGMGATGTLRTSLDPSLEIYKKMFEVKRREQLLALKNLAQLNDI
1 1	ĺ		HQQYKILDVMLKGLFKVLEDSRTVLTAADVLPDGPFPQDEKLKD
			AFSHVVENTAFFGDVVLRFPRIVHYYFDHNSNWNLLIRWGISFC
			NCTGVFNQGPHSPILSLM
6604	3	688	TSTAQRQGGERMSFRGGGRGGFNRGGGGGFNRGGSSNHFRGGG
1			GGGGGNFRGGGRGGFGRGGGRGGFNKGQDQGPPERVVLLGEFL
	[HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDEIFGQLR
			DFYFSVKLSENMKASSFKKLQKFYIDPYKLLPLORFLPRPPGEK
1 1			GPPRGGGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
			GGFRGRGH
6605	7	848	SGSRRGAMRAAGVGLVDCHCHLSAPDFDRDLDDVLEKAKKANVV
1 1			ALVAVAEHSGEFEKIMQLSERYNGFVLPCLGVHPVOGLPPEDOR
1 1			SVTLKDLDVALPIIENYKDRLLAIGEVGLDFSPRFAGTGROKER
1 1	Ì		QRQVLIRQIQLAKRLNLPVNVHSRSAGRPTINLLOEOGAEKVI.I.
1 1		į	HAFDGRPSVAMEGVRAGYFFSIPPSIIRSGQQKLVKQLPLTSIC
1	į		LETDSPALGPEKQVRNEPWNISISABYIAQVKGISVEEVIEVTT
6606	2	1600	QNALKLFPKLRHLLQK
	•	1682	FVEIRPRAEVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS
1 1			KSLGLIEGYGGRGKGGLPATLSPAEEEKAKGPHEKYGYNSYLSE
1			KISLDRSIPDYRPTKCKELKYSKDLPQISIIFIFVNEALSVILR
1 1	Ì	1	SVHSAVNHTPTHLLKEIILVDDNSDEEELKVPLBEYVHKRYPGL
			VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP
] [VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM
			YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI
	i		GPYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER
[]	ł		RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC
	ļ		LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP
]	ļ		DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG
[1:	RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK
6607	137	986	VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT
	}	},	GISFQGRGGAGPGVPTRTQVFAAMGAVMGTFSSLQTKQRRPSKD
		l :	KIEDELEMIMVCHRPEGLEQLEAQINFIKRELQVLYRGFKNECP
			2 40.141001

SEQ	Predicted	Predicted end	Amino acid
ID	beginning	nucleotide	The second of th
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
-	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tvrosine, X=Unknown +-Ston
1	amino acid	sequence	Codon, /=possible nucleotide deletion
<u> </u>	sequence		\=possible nucleotide insertion\
1			SGVVNEDTFKQIYAQFFPHGDASTYAHYLFNAFDTTOTCGUVEE
1	İ		DEVIALSILLRGTVHEKLRWTFNLYDINKDGYINDERMINIUM
Ì			I I DMMGK YTYPVLKEDTPRQHVDVFFQKMDKNKDGI VTLDEFT.E
6608	224		I SCOEDDNIMKSLOLFONVM
1 0000	224	1140	RPCFSSPTGLCPRLSYPMILLQHAVLPPPKQPSPSPPMSVATRS
1			TGTLQLPPQKPFGQEASLPLAGEEELSKGGEODCALEELCKDLV
			CKLCNVTLNSAQQAQAHYOGKNHGKKI.RNVVAANSCDDDADMON
			VVEPAATPVVPVPPCMGSFKPGGRVILATENDYCKLCDacker
ŀ	1		AVAQAHYQGKNHAKRLRLAEAOSNSFSESSELGORRARKEGNER
i	ł		KMMPNRKNMYTVQNNSGPYFNPRSRORIPRDLAMCUTESCOFVC
6609	1	443	SMCNVGAGEEMEFRQHLESKQHKSKVSEQRYRNEMENLGYV
1	-	743	FRLRCRRFRVAGGRLAGAGLRESRVPAPEORLSALTLLSWSAVT
			PAAEPGNFQLSPAEPRGPLASPVRAAPRAPCPAAEMSELNTKTS
	[PATNQAAGQEEKGKAGNVKKAEEEEEIDIDLTAPETEKAALAIQ
6610	319	881	GKFRRFQKRKKDPSS
		001	GRKSLCNLHIPIRFPLTYPDMYMGMMCTAKKCGIRFQPPAIILI
			YESEIKGKIRQRIMPVRNFSKFSDCTRAAEQLKNNPRHKSYLEQ
			VSLRQLEKLPSPLRGYLSGQSLAETMEQIQRETTIDPEEDLNKL
1 .			DDKELAKRKSIMDELFEKNQKKKDDPNFVYDIEVEFPQDDQLQS CGWDTESADEF
6611	978	212	
1 1			PGCSGAGSRVWWLPALRHLAMGSTESSEGRRVSFGVDEBERVRV
1 1	j		LQGVRLSENVVNRMKEPSSPPPAPTSSTFGLQDGNLRAPHKEST LPRSGSSGGQQPSGMKEGVKRYEQEHAAIQDKLFQVAKREREAA
ļ			TKHSKASLPTGEGSISHEEQKSVRLARELESREAELRRRDTFYK
! !	Ī		EQLERIERKNAEMYKLSSEQFHEAASKMESTIKPRRVEPVCSGL
			QAQILHCYRDRPHEVLLCSDLVKAYQRCVSAAHKG
6612	1724	992	VSTHASALSRTQGQPQRQPRAAASGAGAGTAGGGGSGGAEGSKM
	1		STEAQRVDDSPSTSGGSSDGDQRESVQQEPEREQVQPKKKEGKI
1 1			SSKTAAKLSTSAKRIQKELAEITLDPPPNCSAGPKGDNIYEWRS
i i			TILGPPGSVYEGGVFFLDITFSPDYPFKPDKVFFDTPTVUCNTN
i l			SQGVICLDILKDNWSPALTISKVLLSICSLLTDCNPADDIVGGT
6613			ATQYMTNRAEHDRMARQWTKRYAT
0073	130	748	ELELSSNMPEQSNDYRVAVFGAGGVGKSSLVLRFVKGTERESVY
1	!		PIVEDTYRQVISCDKSICTLOITDTTGSHOFPAMOPLETERGYA
' I	1		FILVYSITSRQSLEELKPIYEOICEIKGDVESTPIMIJCNKCDE
	ĺ		SPSREVQSSEARALARTWKCAFMETSAKLNHNVKELFOELLNLE
6614	3		KRRTVSLQIDGKKSKOOKRKEKLKGKCVIM
	-	1191	SSAABAMRVLVRRCWGPPLAHGARRGRPSPQWRALARLGWEDCR
i	ĺ		DSRVREKPPWRVLFFGTDQFAREALRALHAARENKEEELTDKLE
			VVTMPSPSPKGLPVKQYAVQSQLPVYEWPDVGSGEYDVGWASE
Ī	i	1	GRLLNEALILKFPYGILNVHPSCLPRWRGPAPVIHTVI.3GDTVT
		ļ	GVTIMQIRPKRFDVGPILKQETVPVPPKSTAKELEAVLSRLGAN
1	1		MLISVLKNLPESLSNGRQQPMEGATYAPKISAGTSCIKWEEQTS
1			EQIFRLYRAIGNI I PLQTLWMANTIKLLDLVEVNSSVLADPKLT
	\$		GQALIPGSVIYHKQSQILLVYCKDGWIGVRSVMLKKSLTATDFY
6615	832	35	NGYLHPWYQKNSQAQPSQCRFQTLRLPTKKKQKKTVAMQQCIE
	i		GRVGAGASAMSELPGDVRAFLREHPSLRLQTDARKVRCILIGHE
	İ		LPCKLPELQVYTRGKKYQRLVRASPAPDYAEFEPHIVPSTKNPH
J	ĺ	1	QLFCKLTLRHINKCPEHVLRHTQGRRYQRALCKYEECQKQGVEY
1		ľ	VPACLVHRRRRBDOMDGDGPRPREAFWEPTSSDEGGAASDDSM
1		1	TDLYPPELFTRKDLGSTEDGDGTDDFLTDKEDEKAKPPREKATD
		1.	EGRRETTVYRGLVQKRGKKQLGSLKKKFKSHHRKPKSFSSCKQS
6616	347		LLPPCQGARPLSSPPHASEDNLFLFWNCILCAFPHPSPQPLQYP
			VWPLLLVITQIPAPRHLRNRPFSFSRGGLDSFSGSLSTPSICRS

D	SEQ	Predicted	Predicted end	l Amiros politica
Noi nucleatide corresponding to first corresponding to first amino acid residue of amino acid sequence	ID		nucleotide	
corresponding to first amino acid amino acid created of amino acid created of amino acid created of amino acid sequence amino acid amino acid sequence acid sequence a	NO:	nucleotide		Glutamic Acid, E-Phanel
corresponding to first amino acid amino acid residue of amino acid sequence		location		H=Histiding T-T-22-44
to first amino acid residue of sequence sequence sequence ### April	1	corresponding		LeLeucine M-Mothierine, Kabysine,
amino acid residue of amino acid sequence sequen	1		amino acid	Perroline O-Glubaniae Paradine,
### ### ### ### ### ### ### ### ### ##			residue of	S=Serine. T=Threonine v-vol:
Sequence Oddon, /-possible nucleotide insertion) PRWVWARPPREUTPAUMGISIPININGSTRUPSPPPOSS POPHICHTICGUVS WINGLERFT INDPROGNINGSERILST NUCLEOTIDE INSERTION SERVINGSERILST NUCLEOTIDE INSERTION SERVINGSERILST NUCLEOTIDE SERVINGSERILST NUCLEOTIDE SERVINGSERILST NUCLEOTIDE SERVINGSERILST NUCLEOTIDE SERVINGSERILST NUCLEOTION SERVINGSERILST NUCLEOTIDE SERVINGSERIC CAST SERVINGSERIC CAST SERVINGSERIC CAST SERVINGSERIC CAST SERVINGSERIC CAST SERVINGS NUCLEOTIDE SERVINGSERIC CAST SERVINGS SERVINGSERIC CAST SERVINGSERIC CAST SERVINGS SERVINGS SERVINGS SERVINGS SERVINGS SERVINGS SERVINGS SERVINGS SERVINGS SERV	- 1	residue of	amino acid	W=Trvptophan V=Turosino V=Tu
Apossible nucleotide insertion	1		sequence	Codon, /=possible pucleotide deletion
PAMVKARAPPEKGLUPAVLMGLSLEFLINEDFINLOPSPHKQOPA POPOHECHICOLVDSPHKGLERTIRDPEGGROTAWEEENLSKY KDSETRIUWYLEGVCSKSDFECHRILLSISEELVESWMFHKQOPA PLECOMICOSUM CONTROL STRUKTUROUS CONTROLESPECCHOGOGOGOGOGOGOGOGOGOGOGOGOGOGOGOGOGOGO	L	sequence	_	\=possible nucleotide incertion)
STATISTICS STA				PAWVKMAPWPPKGI, VPAVI, WGI, ST, ET NI, PGP, FW, OPERPOR
ADSETRIAVEVLEGVCS KSDFECHRILLSISSELVES WERFINGOPA PDLEPOMLCSD SILKLCPSGTFFSSCLECTERS PCGGVGCCES EGTRGGGGHCCQGCGLGYFSAERASHINLCSACC GFCARCGGFESSNCLQCKKGRAGHHLKCVDIDECGFEGANCGAN OFCVNTEGSYECDCARACIGCMGAGGGRCKKCSFCFGVOYSKC LDVDECGTEVCFGENKCCERT KGGVRCIACSFCKKCSFCFGVOYSKC LDVDECGTEVCFGENKCCERT KGGVRCIACSFCKKCSFCFGVOYSKC LDVDECGTEVCFGENKCCERT KGGVRCIACSFCKKCMFGTOVCSKC LDVDECGTEVCFGENKCCERT KGGVRCIACSFCKKCMFGTOVCSKC LDVDECGTEVCFGENKCCERT KGGVRCIACSFCKKCMFGTOVCSKC LDVDECGTEVCFGENKCCERT KGGVRCIACSFCKKCMFGTOVCSKC LDVSTATT LISS FCKCCKCKVDELICALGILGSHOCHEVTTA 1 FIGAVAANTOVKLISERSBLVLLGGFKGCK ENKREILALTSELKCEKCKVDELICALGLIGSHOCHEVPTD1STVCS RKKEELALTSELKCEKCKVDELICALGLIGSHOCHEVPTD1STVCS RKKEELALTSELKCEKCKVDELIAKLVKNRTRIDSSAFSLCFC LIGPATFTIL GFGATATI	1			PPQPHPCHTCRGLVDSFNKGLEPTTPDNPCCCNTAWEDDNY CANA
FOLLOWINGSDERIC CORATTERSECLIPCEGGTERPEGGYGGCEG ESTREGGSGESCOCGGCGT SPERENRASHIVCSACE GPCARCSG PESENCLOCKGRALBHIKKUDIDECT FERANGAN OF CONTEST SYECTION AND CONTEST SYETION AND CONTEST SYECTION AND CONTEST SYETION AND CONTEST SYSTEMATICAL AND CONTES			1	KDSETRLVEVLEGVCSKSDFECHDILFICERET VECKWEINGORA
BUTHERSEGICCOGGYTGEACROCGIGTYPEAERNASHILVCSACE GPCARCSGEESSENCLOCKRAPLHIKUTGACE GPCARCSGEESSENCLOCKRAPLHIKUTGACE LDVPECTSTVCTPEGNYCCIONTEGGYRCI CONTROGYRCI COVERO IPESAGFFSENTEBELVULQOMFFGIITCALATLAAKGDLVFTA IPEGAAANTGYNLSERSENSPULEGFIKGE BUTHERSTANTGYNLSERSENSPULEGFIKGE SYLLDTKVCPHRNPLSLPCEFTGESTLOGGSSIPVEKGCLVS LSYHLDTKVCPHWOADUOSSSIPNUSGIKGE RWESLAALFEELKOEGKRUDELIAALVXRTKIIGSABSICCE LGPATTIT. 6618 548 136 DEKVARRAPNSPAFQNDIYPLVSAPRATTAESPHSKVLQNTQCR MYREMISBERSIICLSAAAAGGTGKKQGGGRAMATLDRKVPSEE AFLIKEWSSWIDAAKLHCSONVDLEEAGKGGKSEWHRINKEA KYKGT 6619 246 842 PASSEVLITAAWMFLLINCIVAVSONMGIGKNGDLEFFPLENEFR YCRAMTISSVEGKONLVIMGRKTWFSIP ENKIPLKURINLULIS RELKEPPQGAHFLARSLDDALKLTGPELNIKVUMINIVGGSV YKRAMNHLGHIKLFVTRINDOFESSIPTSPLENYKLINGIVAVGSV YKRAMNHLGHIKLFVTRINDOFESSIPTSPLENYKLINGIVAVGSV YKRAMNHLGHIKLFVTRINDOFESSIPTSPLENYKLINGIVAVGSV YKRAMNHLGHIKLFVTRINDOFESSIPTSPLENYKLINGIVAVGSV YKRAMNHLGHIKLFVTRINDOFESSIPTSPLENYKLINGIVAVGSV YKRAMNHLGHIKLFVTRINDOFESSIPTSPLENYKLINGIVAVGSV YVALVMQIYFGDPGIFQGGGGWMUNDENSHILDIFSSI MSGOGSIBLERTRUPFSAAAACSCROLOLVIVTACLIFRITG VYTALVMQIYFGDPGIFQGGGGWMUNDENSHILDIFSSI DERAPAAPLEGGGGGGWMUNDENSHILDIFSSI DERAPAAPLEGGGGGGWMUNDENSHILDIFSSI DAVAAACLGIVAHSSGGGGGWMUNDENSHILDIFSSI DAVAAACLGIVAHSTBURAACSCROLOLVIVTACLIFRITG VYTALVMGIYFGDPGIFQGGGWWYGTLARACSIGITIASV PAGARLEETLOSSMITKGGLVAVYGGHVALSPPPFHIGPALI SALNILEGFRITSIVSSEGGAHWAVETLIKALALALAGGLDFYVYD STITESMOMILSKVERAYLKGHINDSGAPPFLLPTVARABGLCGTYLA LGANGABGLGGLTVAFTFYBLAFFGREDGCGCGLYLINLV SIPHAAMMG SALNILEGFRITSIVSSEGGAHWAVETLIKALALAGGCGTYLA ALGANGABGLSCLTOVEFTPULAFFFREDGCCGCTYLA ALGANGABGLSCLTOVEFTPULAFFFREDGCCGCTYLA ALGANGABGLSCLTOVEFTPULAFFFREDGCCGTYLA ALGANGABGLSCLTOVEFTPULAFFFREDGCCGCTYLA ALGANGABGLSCLTOVEFTPULAFFFREDGCCGTYLA ALGANGABGLSCLTOVEFTPULAFFFREDGCCGTYLA ALTSCOCKTON SWYGGGGGGGGGWMUNDENGEPPNT SKYNIGAGRRESSBALATEVSFRAMEANMPKREFGRSCRIKVISMON FELPPHAGGLSCLTARGGGLTAVGTVARACGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	1			PDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTFPDCGGYGOGPG
GFCANEGSPEERIOCKEGGMADSHELKCUDIDECTEGANGGAD OFCANTEGSYECRICARGCCEMAGGGERKGESPYQOVGSKC LDVDECETSUCTGERINGCENTEGGYRCICAGGYKGMEGICVKDO IPESAGFFSEMTBELUVLQMFFGIITCATAAKGDLVFTA IFIGAVAAMTGYMLSERSDRVLEGFIKGE WARMAGVSLUELEBELGGEICLGEVFKESLALLQCGHSYCKGCLVS LGYMLDTKVRCPMCWQAVDGSSSLPNVSLAWVIEALERLPGGPPP KYCVHERNPLSIPCERCQENICCELGUGLGSHQHFVYTISTVCS RMKEELAALFSELKCGCKVDELIAGUKTRITIGSAPSICCE LGPATFTIL G618 548 136 BEKVARRAPINSPAFONDIYDLEVASPRATTAESPWSKVLQNTQCR NVFKMTSERSRIPCLSAAAAEGTGKKQCGRAMAATLDRKVPSPE APLIGKWESRYDDAAKLHGONVDLEBAGKEGKSEWMRLINKEA WKYGT FORMTTISSVECKONLVIMGERTYFSIPPEKNEPPLKDRINLINLS FERKEPPGGAHFLARSLDDALKLTERPELAWMINIVGGSV YREAMNHLGHIKLFVTRIMODFSSTPFSRIDLEKYKLLDEPTG FERKEPPGGAHFLARSLDDALKLTERPELAWMINIVGGSV YREAMNHLGHIKLFVTRIMODFSSTPFSRIDLEKYKLLDEPTG BERKEPPGGAHFLARSLDDALKLTERPELAWMINIVGGSV YREAWNHLGHIKKVEVCUERDD NSRVDDFYARARNAENEASGESALGAYSPVDYMSTTSFPRLPE DEPAPAAPALGICATVANHSCHEND MSSVDDFYARARNAENEASGESALGAYSPVDYMSTTSFPRLPE DEPAPAAPALGICATVANHSCHEND MSSVDGSPLRETTKOPFSAAAAECCKONDUTVIVTACLTFRTG VTVALVMQITFEDPGIFQGGAVVTDAARCTSIGIBUSGSSS MGSQDGSPLRETTKOPFSAAAAECCKONDUTVIVTACLTFRTG VTVALVMQITFEDPGIFQGGGAVMUTDARCTSIGIBUSGGSSW DAAVAAALGIATVANHSCHGGGSWMUTDIRRNESKLDTFRES APGALRESTLQRSMETTRGLLVGUVGWKKLHEAHQLYGRLDWS QVIAFAAAVAQCFNVTHALARALAGLLPBYPPHTGPALI SALNILBGFTATISTUSEQALMWASLINDARASCREDPYDT STITSSDOBLSKVAAAYURGHINDSGAPAPYAGGNLTLEWARAQ HEGGVITEBFSTNSALVKRINDSGAPAPYAGGNLTLEWARAQ HEGGVITEBFSTNSALVKRINDSGAPAPYAGGNLTLEWARAQ HEGGVITEBFSTNSALVKRINDSGAPAPYAGGNLTLEWARAQ HERGVITEBFSTSPLENSVONGERFUSPPHTGPALI SALNILBGFTATISTUSECALMWSSLNOPPOSGLTTPSGILLINSOMLDPS WNPTANHSSPLENSVONGERFUSPPHTGPALI AAQULINGPDDFVAMSSLNOPPOSGLTTPSGILLINSOMLDPS WNPTANHSSPLENSVONGERFOLDTANAVSLOPPOSGLTTPSGILLINSOMLDPS WNPTANHSSPLENSVONGERFOLDTANAVSLOPPOSGLTTPSGILLINSOMLDPS WNVIGAGRIRRSPSBALAIEVFRAMICHTUSCHTANAGR KELYTISETTSTULGLGOVERTOSSVOTYHRGHVENDERFOLL GARSGAGETTRGFERFARAMEANMERREEGGSCELTIKVISMGN AFPKKKSTALKYCEKFFVENALTIGIGDYVTAKVHRORG KELYTHAMINICHTSTVYTULNILBKWTN HERPOKLSCOTTRANASCHSPSSALSSSSSSETETEVPOPTPADDOFFUL GRASGAGETTRGFERFARAMEANM	1	1	ļ	EGTRGGSGHCDCOAGYGGEACGOCGIGYFFAFRNASHLVCCACE
UPCONTEGS YECRDCARGLICMAGPGRCKKCSPOYQQUISKC LDVPECTSTVCPGENNQCENTEGGYRCICAGKOMEGICVERO IPESAGFFSENTEDELVVLQQMFFGIITCALANTAAKGDLVFTA IPIGAVAMNTGYNLSERSPRVLEGFIKGE SYHLDTKVCPMGAVDJOSSSLRYVSLARVICALARAGDLVFTA IPIGAVAMNTGYNLSERSPRVLEGFIKGE SYHLDTKVCPMGAVDJOSSSLRYVSLARVICALARDGDFP KVCVHRRNPLSLFCERDGELICGLGGSGQHHPVTPISTVCS RMKEELAALFSELKOEGKVDELICGLGGLIGSHQHHPVTPISTVCS RMKEELAALFSELKOEGKVDELICAGLGGSHQHHPVTPISTVCS RMKEELAALFSELKOEGKVDELICAGLGGSHQHHPVTPISTVCS RMKEELAALFSELKOEGKVDELICAGLGGSHQHHPVTPISTVCS RMKEELAALFSELKOEGKVDELICAGLGGSHQHHPVTPISTVCS RMKEELAALFSELKOEGKVDELICAGLGGSHQHHPVTPISTVCS RVCVHRRNPLSERFRCESAAAAEGTGKKQGEGRAMATLDRKUPSGE LGPATFIF. 6618 548 136 DOKVARERAPMEDAFQUDIYPLVSAPRATTAESPPSKVLQNTQCR NVPRMTSERSRIPCLSAAAAEGTGKKQGEGRAMATLDRKUPSGE APGKRASSMIDAAKHHCSONVDLEEAGKEGGKRSEVMRINKEA WKGGT PASSEVLITAAVMPLLINCIVAVSONMGIGKNDDLERFPLENEFR YFGRMTTISSVECKONLUMGRKTHFSI PSKRIPLKDRINLVLIS RELKEPPQGAHFLARSLDDALKLTGRPELANKVOMI HIVGGSV YKRAMNHLGHLKLFVTRIRMDFESSITFSLERYKLLEAPHDEYBELDEYPLEPPG ILSDVGGKHIKKKPEVCEKDD 3 1879 NSKVDEFVARRRARAENSASGSALGAYSPVDYMSTTSPPFRLDE DEPAPAAPLEGRREDEAFLODPTDDDSFIKSARLOBLTYVTACLIPPRG VYTALVMGITFGDPGIFGOGAVVTDAARCTSIG SEVLSKQGSV DAAVAALGIGAVARHAULKLFVTRINDFPSSHLARSKGGBSSSGSSSSSSSTEPSTPLSSGGSV DAAVAALGIGAVARHAULKSPPPFRIPELSG RPPLFGGSILLERDLLAFVLDULGTSGFAAFVAGGRUTTVTACLIPPRG VYTALVMGITFGDPGIFGOGAVVTDAARCTSIG SEVLSKGGSV DAAVAALGIGAVARHAULKSPVOVYRGHULSSPPPHIGPALI SALINLEGFNITSIVSREGALHWVAETIKLALALAGRIGDEVVD STITESMDDMLSKVBAAYLKGHUNVAETIKLALALAGRIGDEVVD STITESMDDMLSKVBAAYLKGHUNVAETIKLALALAGRIGDEVVD STITESMDDMLSKVBAAYLKGHUNVAETIKLALALAGRIGDEVVD STITESMDDMLSKVBAAYLKGHUNVAETIKLALALAGRIGDEVVD STITESMDDMLSKVBAAYLKGHUNDFGSGALTFFTLDSG WNNRTAMHSAPSLENSVQCKRPLSFYELAKLI.DPD AAATSGLGASSTIRLTSSVCHORPSPYELAKLI.DPD AAATSGLDASSI SELTISTVCHAGGGGAMAATHORGGRAFTLESTVARDFFTLDGGFTLANGGG KFLYTISSTVSTYLGLGSOVENTAAFFSCHETOVPPBABGLGGTYLA LGAANGARGLGGLGTOVPTFTUAFFSFTEBLGGCTYLA LGAANGARGLGCAGAVATHGHUNDFSKUFOVPPDASDCLGTYLA LGAANGARGLGCAGAVATHGHUNDFSKUFOVPPDASDCHAUCHPPBABGLGGMIN FDHAGHBPFYEVRRP SKVKIGGARRASSSSGSSTEPEDVPPDASDC	1		İ	GPCARCSGPEESNCLQCKKGWALHHLKCVDTDECGTEGANCGAD
DUVBECTEVCEGENKCENTEGGYRCICAEGYKMEGICVERGE 1PESAGFFSEWTEBELVULQGWFFGILATILAKKGDLVFTA 1FIGAVAAMTGYWLSERSDRVLEGFIKGR VWMAMQVSLEHEBPLGCPFICLEVYKESIMLGOGBSYCKGCLVS LSYHLDTKVRCCMCQAVGGSSSLPNYSLAWVIEALRIPGDPEP KVCWHRINDLSLFCERGOGLIGGLGGLGSRGHHHHIDGEPEP KVCWHRINDLSLFCERGOGLIGGLGGLGSRGHHHIDGE RMKRELAALFSELKQEQKKVDELIAKUVNRRTIDGSAPSLCPC LGPATTFIT LGPATTFIT LGPATTFIT GERVARRAPNSFAFQNDIYPLVSAFRATTAESPWSKVLQNTQCR NVERMISERSHIPCLSAAAAEGTCKKQQBGRAWATLDRKVPSPE AFIGSKWSSWIDAAKLHCSDNVDLEEAGKGGKGSRGWRINKEA WKYGT FASSEVLTAAVWFLLLINCIVAVSONMGIGKNGDLPRFPFLRNEFR YFQRMTTISSVEGKQNLVIMGRKTWFSIPENRPLKURINLVLLS RELKEPPGGAHFLARSIDDALKLTERFENAKUVMINIVAGSSV YKRAMHLGHLKLFVTRINODFSDTFFSEIDLEKYKLLPEYPG LISDVQSCKHIKVKFFEVCKDD 3 1879 NSRVDDFVARARMARNERSGEBALGAVSFVDYMSTTSFPRLPE DEPAPAAPLGRENDEDAFLGDPDTDPDSFLKSAGLGRBSSSSS MGSSOGSSLRSTIRKDPFSAAAACGGGOLTVIVTACLTFRTG VTVALVMQIYFGDPGIFQGAVVTDARGTSLGHEVSKGGSSV DAAVAAALCLGIVAPHSSGLGGGGWHWKGLHEAHQLYGLPWS OVALPAAAVAQDCFFAVTDLARLARGUHDIRRESHLIDERES APGALRESTLQRSWETKFGILVGVFGMWKGLHEAHQLYGLPWS OVALPAAAVAQDCFFAVTDLARLARGUHDIRRESHLIDERES APGALRESTLQRSWETKFGILVGVFGMWKGLHEAHQLYGLPWS OVALPAAAVAQDCFFAVTDLARLARGUHDSPPBTEPBAL SALNILBGFALTSLVSREGALHWAFTLKTALALARGGDEVTOL SALNILBGFALTSLVSREGALHWAFTLKTALALARGGDEVTOL SALNILBGFALTSLVSREGALHWAFTLKTALALARGGDEVTOL SALNILBGFALTSLVSREGALHWAFTLKTALALARGGDEVTOL SALNILBGFALTSLVSREGALHWAFTLKTALALARGGDEVTOL SALNILBGFALTSLVSREGALHWAFTLKTALALARGGDEVTOL SALNILBGFALTSLVSREGALHWAFTLKTALALARGGDEVTOL SALNILBGFALTSLVSREGALHWAFTLKTALALARGGDEVTOL SALNILBGFALTSLVSREGALHWAFTLKTALALARGGDEVTOL SALNILBGFALTSLVSREGALHWAFTLKTALALARGGDEVTOL SALNILBGFALTSLVSREGALHWAFTLKTALALARGGDEVTOL SALNILBGFALTSLVSREGALHWAFTLKTALALARGGDEVTOL SALNILBGFALTSLVSREGALHWAFTLKTALALARGGDEVTOL SALNILBGFALTSLVSREGALHWAFTLKTALALARGGDEVTOL SALNILBGFALTSLVSREGALHWAFTLKTALALARGGDEVTLA LGANGARGLGGGGGGGRGARGSSSSSGSGTEPVCFPARDOLGGRG KFLITISSTVSIYLGLGVVERVERVERVERVERVERVERVERVERVERVERVERVER	ļ			QFCVNTEGSYECRDCAKACLGCMGAGPGPCKKCSPGVOOVGEVC
6617 118 673 VWRAMQVSLLELEDRLQCFICLEVFKESIMLQCGISTYCKGCIVS LSYHLDYKNCPMCMQANDGSSIPNTLAWITAMINGTHERSENVLOPTIC SYHLDYKNCPMCMQANDGSSIPNTLAWITAMINGTERINLPGDPEP KVCVHRRNPLSLPCEKOQELICGLCGLGLGSHQHHPVTPISTVCS RMKEELAALFSELKGEQKKVDELIAKUVKNRTRIDGSAPSLCPC LGPATFTPL GENTER 6618 548 136 DEKVARRAPNSPAFQNDIYPLVSAFRATTASSPWKVLQNTQCR NVFKMTSERSRIPCLSSAAARCTCKKQGEGRAMATLDRKVPSPE APLIGKEWSSWIDAARLHCEDRVDLEEAGKEGGKSREWMRINKEA KKYGT 6619 246 842 PASSEVLTAAWMILLINCIVAVSONMGIGKNGDLERPFILRNEFR FORMTTISSVEKONLVIMGRKTWEF JEHKNRPLKURINULIS RELKEPPQGAHFLARSLDDALKLTERPELANKVUMITWINGGSV VKEAMMIGHLKLFVPTROOPPESDTFFSELDLEKKKLLPEYDG ILSDVQEGKHIKVKFFEVCEKDD 3 1879 NSRVDDFVARARMAENERGGESALGAVSPVDWHSTTSFPRLPE DEPAPAPLRGRRDEDBAFLGDPDTDDSFLKSARLORLPSSSSE MSSQGSSPLRETIKDFSAAARCSCRODGLTVIVTACLTFRTG VTVALVMGITVERDPGTOGGOAVVTDAACHEAHOLVSGSSV DAAVAAALCLGIVAPHSGGLAGGGVMLVHDIRRNESHLIDBRES APGALREETLQRSWETKEGLLVSVFGWLARHOLVSHEAHOLVSGRLPWS OVLAFAAAVAQDCFNYTEDLARALASCLPNMSERRETPLDSG RPPLEGSLLHERPLAEVLDLUGGTGGAAFYAGGNLTLEMVAEAQ HAGGVITEBDFSNYSALVEKPVCGVVRGHLVLBPPPRTGPALI SALNILBEFNLTSUVSREQALHVVAETLKALALASRIGDPVVT STITESMODMLSKVEAAVLKGHNDGAAPLPLEVYELDGAPT AAQVLINGPDFIVAMVSSLNQPFGSGLITPSGILINSQMLDRS WNNTANABAPSLENSVYDCKKRPSPLDEVYELDGAPT AAQVLINGPDDFIVAMVSSLNQPFGSGLITPSGILINSQMLDRS WNNTANABAPSLENSVYDCKKRPSPLDEVYENDGAPT AAQVLINGPDRIVAMVSSLNQPFGSGLITPSGILINSQMLDRS WNNTANABAPSLENSVYDCKKRPSPLDVVPRAGGCGTYLA LGANGARGLGSLTOVRFTWLAFFSREDSCGLDCCLSYLWLV SIPHAAMMG SKYLISETVSITLGLGVEITGSSVYDVVNPGGHVERAEQLGMK LFPGRGLLSSGGTABGGASSSSSSSSTPVVCPPAGEGGTYLA LGANGARGLGSLTVKRYCKRYEVSKYLATGIGDYGVTKVHORGEIKVN IFDMAGHPFFYEVKRPF GRAGGAGETEGAGGFREAKRMEANNPKREFGRSCRKVISMGN IFDMAGHPFFYEVKRPF AVVIGNGTRANGTSKYRLTRIGIDYGVTKVHVNRGEIKVN IFDMAGHPFFYEVKRPF AFMLHINDQYDPLYSKRFAVFISSVESHKLKQLKNINGENTPEKK LFSKNSVSKYRLDHUNGSLKHVINGSUKHTBKLINGLKSLKYT LFSKNSVSKYRDAUGLKSLELIKKVEMT LFSKLKSVSKYRPAULSSUKSKILKGLKSLIKKVEMTD LSKNSVSKYROAULOMTGSKNELSLIKMINNEWTPEKL LSKNSVSKYROAULOMTGSKNELSLIKMINNEWTPEKL LSKNSVSKYROAULOMTGSKNELMINGENTELSLIKKVEMT LESTKNSVSKYROAULOMTGSKNELDLISHLIMINNIKKENTIN]			DDVDECETEVCPGENKQCENTEGGYRCICAEGYKOMEGICYKEO
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RMKEBLAHFSELKOECKKUDELIAKUKRRTRIDGSAPSLCPC LGPATFIFL BGKVARRANSPAFONDIYPLVSAPRATTAESPWSKVLQNTQCR NVPKMTSERSRIPCLSAAAAECTGKKQQEGRAMATLDRKVPGPE APLGKRWSSWIDAKALHCSDNYDLEBAGKEGGKRVMELINKEA WKWGT 6619 246 842 PASSEVLTAAVMFLLLINCLVAVSONMGIGNGDLPRPPLRNEFR YFORMTITSSVEGKONLVIMGRKTFSI PEKNRPLKDRINLVLS RELKEPPQGAHFLARSLDDALKLTERPELANKVDMIWIVGGSV YKEAMHAGHLKLPVTINODPESDTFFSEDLEKYKLLPEYPG ILSDVQEKHKYKFEVCSKDD 1879 NSRVDDFVARARMAENEASGESALGAYSFVDYMSITSFPRLPE DEPAPAAPLGRKRDEDAFIGPPTDTDSFLKSARLORLPSSSSE MGSQDSSPLRETRRDPFSAAAACCRGODGLTVTVTACLTFATG VTVALVMQIYFGDPG1PGQGAVVTAGHTVTACLTFATG VTVALVMQIYFGDPG1PGQGAVVTAGHTVTACLTFATG VTVALVMQIYFGDPG1PG0GAVTAGARCTSIGIEVLSKQGSSV DAAVAAALCLGIVAPHSSGLGGGGVMLVHDIRRNSSHLIDFRES APGALREETLQRSWETKPGLUVGPGWVKGLHEARQLYGRLPWS QVIAFAAAVAQDCFRVTHHLARALAGACTSIGIEVLSKQGSSV DAAVAAALCLGIVAPHSSGLGGGGVMLVHDIRRNSSHLIDFRES APGALREETLQRSWETKPGLUVGTGGPAPFYAGGNTLEMVAEAQ HAGGVITEDFSNYSALUVEKVCGVYKGHLVLSPPPPFTGPALI SALNILBEFRLITSLVSREQALHWVAETLKIALALSRLGPPVTD STITESMDMLSKVEAAYLGHINDSQAAFPALPVYELDGAPT AAQVLIMGPDDFIVANVSSLNOPFGSGLITFSGILLNSQMLDFS WENRTANHSAPSLENSVQPGKRPLSFLLPTVYTDAEGLCGTVILA LGANGAARGLGSGLTVORTFTPHLAFFSREPSCGLDCRCLSYLMLV SIPHAANMG 6621 1 662 VGGITSYGORLQALREKSRDAASSRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWLRRGEGPPNT SVKVIGAQRRRSBSALAIEVVEAHLGSHLUSDLDGVFALNGEG KFLYLISSTVSITLGLSQVEITGSSVPYPGDEVCPPPABDQFLL LVSKVGTTVSIVGLOGGTETGSSVPROFFFFFELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWLRRGEGPENT SVKVIGAQRRRSBSALAIEVVEAHLGSHLUSHLDGVYFALNGEG KFLYTISTVSITLGLSQVEITGSSVPLOGTGFDDIYKNHVRGEIKVN 1PDMGHPPFIVVRRPF 6622 2 319 GRASGAGGREFGAGGERAMAENMRKEFFFFEGESLRIKVISMGN AEVGKSCLIKRVCEKRFVSKYLATIGIDYGVTKVHVDREIKVN 1PDMGHPPFIVVRRPF VSIYGLICTYTYVHLYRSGRSYSTEVPUCPPBADQFLL VSIYGLICTYTYVHLYRSGRSSANSSCSETEPVUCPPBADQFLL VSIYGLICTYTYVHLYRSGRSSANSFTGREFFFYELGKLEIKVN 1PATIAQLDNIQBISJURJSKPLOVEGTGFDDIPDVKNDF AFMIHMIDQYDDLYSKRFAVFLSEVSENKLKQUNINNEWTFDKL ROKLOTNANNRLEEPPLIMGGSGUSHIGHGTNYTLESURDDKWMM 1PATIAQLDNIQBISJURGSSKIDDSNVTLESURVEKTBORDTKUMMINKMTN 1PATIAQLDNIQBISJURSHILORDTKUMMINKMTN	1			LSYHLDTKVRCPMCWQAVDGSSSLPNVSLAWVIEALDI.DCDDED
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ASSEVITARAWMFLLINCIVAVSONMGIGKNGDLFRPFLRNEFR PASSEVITARAWMFLLINCIVAVSONMGIGKNGDLFRPFLRNEFR YFORMTTISSVEGKONLVIMGRKTWFSIPEKNRPLKURINLVLS RELKEPPQGAHTLARSLDDALKLTERPBLANKVDMINIVUGGSSV YKEAMMHLGHLK.FYTRIMOPESTIFFSEIDLEKYKLLPEYPG ILSDVQEGKHIKYKFEVCEKDD		1		NVPKMTSERSRIPCLSAAAAEGTGKKQQEGRAMATLDRKVPSPE
PASSEVITAAVMFLLINCIVAVSONMGIGKNGDLFRFPLRNEFR YFQRMTTISVECKONLVIMGRKTWFSTPEKNRPLKURINLVLS RELKEPPQGAHFLARSLDDALIKERPBLANKUDMINIVGSSV YKRAMHLIGHLKIFVTRIMODFESDTFFSEIDLEKYKLLEFYPG ILSDVOEGKHIKYKFEVCEKDD 3 1879 NSRVDDFVARARMAAENERSGESALGAYSPYDYMSITSFPRLPE DEFAPAAPLRGRKDEDAFLGPDTDPDSFLKSARLQRLPSSSSE MGSOGSPLRETRKDPFSAAAAECSCRODGLTVIVTALTFATG VTVALVMQIYFGDPQIFQGGAVVTDAARCTSLGIEVLSKQSSSV DAAVAAALCLGIVAPHSSGLGGGGVMLVDIRRNESHLIDFRES APGALRESTLQRSWETKFDLLUGVPGWVKGHLHEAQLYGRLPWS OVLAPAAAVAQDCFNVTHDLARALAEQLPPNMSERPREFFLFSG RPPLPGSLLHRPDLAEVLDVLGTGSPAAFTAGGNLTLEMVAEAQ HAGGVITEDPSNYSALVEKEVCGVYRGHLVLBPPPHTGPALI SALNILEGFNITSLVSREQALHWVAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSAPPALPVYELDGAFT AAQVLIMGPDDFIVAMYSLNQPFGSGLIFPSGILINSGMLDFS WFNRTANHSAPSLENSVQFGKRPLSFLLPTVVRPABGLGGTVLA LGANGARGLGSLTOVRFTPWLAFFSREDSGLDCRCLSYLMLV SIPHAANNG 6621 1 662 VQGITSVQGLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSGLDKASIIRLTISVLKRRDFANQGPPPMLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHILOSLDGYVFALNCEG KFLYISETVSIYIGLSQVEITGSSVPDVVPFOPBADDFLL SVKVIGAQRRSPSALAIEVFEAHLGSHILOSLDGYVFALNCEG KFLYISETVSIYIGLSGVEITGSSVPDVVPFOPBADDFLL LPSKGCILKRYCEKRFVSKYLATIGIDTGVTKVHVRDREIKVN IFDMAGHPFFYEVRKFF 6622 2 319 GRASGAGETTAGGPERARMEANMPKREPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDTGVTKVHVRDREIKVN IFDMAGHPFFYEVRKFF 6623 1886 189 KALPEKYKRPLHVESGILINGVKHVKNRREIKVN IFDMAGHPFFYEVRKFF AEVEKKYRILVERSGUTLVAMYVEOTVLKVIKFLIITAYNSA LVSKVGPTVDCNUDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLRETSFFYVRQETGFDDIDDVKNDF AFMLHMIDGYDPLYSKRFAVFLSEVSENKLKQLMINNEWTDKLK QKLGTNANNELELPLIMLSGIPDTYFEITELQSLKLEI IKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFILKENLKVLISVKFDD MRELPPWMGLRNLEELYLVGSISBILISRAVTLESLARDLKKLET LSIKSWSSIPQAVDVDVSHLOKMCHHNDGTKLWMANT				WKYGT
RELKEPPQGAHFLARSLDDALKLTERPELANKUMINIVUSGSSV YKRAMNHLGHLKLFVTRIMODFESDTFFSEIDLEXYKLTHEYPO ILSDVQBKHIKYKFPUCBKDI ILSDVQBKHIKYKFPUCBKDI ILSDVQBKHIKYKFPUCBKDI ILSDVQBKHIKYKFPUCBKDI ILSDVQBKHIKYKFPUCBKDI ILSDVQBKHIKYKFPUCBKDI ILSDVQBKHIKYKFPUCBKDI ILSDVQBKHIKYKFPUCBKDI ILSDVQBKHIKYKFPUCBKDI ILSDVQBKHIKYKFPUCBKDI ILSDVQBKHIKYKFPUCBKDI ILSDVQBKHIKYKFPUCBKDI ILSDVQBKHIKYKFPUCBKDI ILSDVQBKHIKYKFPUCBKDI ILSDVQBKHIKYKFPUCBKDI ILSDVQBKHIKYKFPUCBKDI ILSDVQBKHIKYKFPUCBKDI ILSDVQBKHIKYKFUCBKDI INSRVDFYARARNAABCSCROQDLIVITACLITFATO VTVALVMQIYFGDPGIFQGAVVTDARCTSIGIFVISKQGSSV DAAVAAAALCLGIVAPHSSGLGGGGVWLVHDIRRNESHLTDFRSS ADGALREFILQRSWETKFGLVAVPGMVKGHLYALDLIFATO OVLAPRAAVAQDCFNVTHDLARALAEQLPPMNSEHFRETFLBSG RPPLPGSLLHRPDLAEVLDVLGTSGGAPYNAGGNLTLEWVAERQ HAGGVITEDFSNYSALVEKPVCGYVRGHLVLSPPPPHTGPALI SALNILBGFNITSLUSREQALHWVASTIKIALALASRLGDPVVD STITESMDDMLSKVEAAYLRGHINDSQAPAPLLEVYSLDGAPT AAQVLIMGPDDFIVAMVSSLNOPFGSGLITPSGILINSGMLDFS WPNRTANHSADSLENSVQPGKRPLSFLLPTVVRPAEGLCGTVLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLMLV SIPHAANNG OVGITSYQORLQALRKEKSRDAARSRGKENFEFYELAKLLDLP AAITSQLDKASIIRLTISYLKNRDPANGGDPPWNIRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHLQSLDGYVFALNQEG KFLYISETVSIYILGLGQUELTGSSVPTVHRGDRIVEMAEQLGMK LPPGGGLISQGTAEDGASSASSGSETPPPVCFPPARDGFLL LPSGKGCIIKRYCEKRFVSKYLATIGLYGJTKVHVADREIKVN IFPMGGIPFYEVKRP G622 2 319 GRASGAGETENGGFERRAMEANMPKRKEPGRSLRIKVISMGN AEVCKSCIIKRYCEKRFVSKYLATIGLYGYTKVHVADREIKVN IFPMGGIPFYEVKRP KALFFEKVKKFRLHVEEGDILVAMYVROTVLKVIKFLIIAYNSA LVSKVQFTVORNVDIQDMTGYKNFSCNHTWAHLFSKLSFCYLCF VSIYGLTCLYTLWLBFYRSLRSYSFEVVRGETGFDDIPDVKNDF AFHLHMIDQYDPLYSKRFAVFLSEVSENKLKQINLINNEWTPDKL RQKICOTNANNELELPILMIGSLEPDTVFEITELQSLKLEI IKNVM IPATIAQLDNLQELSLHQCSVKHSAALSFUKMIKKLINIKWTPDKL LSKNVSKIPQAVVDVSGLIKMCKHNIDMTTLESLRDLKSLKI LSKNVSKIPQAVVDVSGLIKMCKHNIDMTTLESLRDLKSLKI LSKNVSKIPQAVVDVSGLIKMCKHNIDMTTLESLRDLKSLKI LSKNVSKIPQAVVDVSGLIKMCKHNIDMTLIBSRDLKSLKI LSKNVSKIPQAVVDVSGLIKMCKHNIDMTTLESLRDLKSLKIK	6619	246	842	
RELKEPQGAHFLARSLDDALKLTERPELANKUDMIWIVGGSSV YKRAMMILGHIKLPVIRIMODPESDTFFSEIDLEKYKLIPEYPG ILSDVORGKHIKYKFEVCEKDD 3 1879 NSRVDDFVARARMAEMEASGESALGAYSPVDYMSITSFPRLPE DSPAPAAPLAGRKNEDAHGIDPDTDDGFLKSARLORLPSSSSE MGSQDGSPLRETRKDPFSAAAAECSCRQDGLTVITVACLTFATG VTVALVMQIYFGDPQIFQGAVVTIDARCTSLGIEVLSKQGSSV DAAVAAALCLGIVAPHSSGLGGGGWMLVHDIRRNESHLIDFRES APGALREETLORSWETKPGLLVGVPGMVKGLHEAHQLYGRLPWS QVLAFAAAVAQDGFNVTHDLARALAEQLPPMMSERFRETFILSG RPPLPGSLLHREPDLABVLDVLGTSGPAAFVAGGKLTLEMVARAQ HAGGVITEBDFSNYSALVEREVCGVYRGHLVLSPPPPHTGPALI SALNILEGFRITSLVSREQALHWVAETLKIALALASRLGDBVYD HAGGVITESDFSNYSALVEREVCGVYRGHLVLSPPPPHTGPALI SALNILEGFRITSLVSREQALHWVAETLKIALALASRLGDBVYD HAGGVITESDFSNYSALVEREVCGVYRGHLVLSPPPPHTGPALI GANGAARGLSGLTQVRFTTWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG LGANGAARGLSGLTQVRFTTWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG UGGTSYQORLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGPPPNNLRNEGGPPPNT SVKVIGAQRRRSPSALAIEVFRAHLGSHLQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVPDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDQASSASSSSQSETPEPVVCFPPASDQFLL GRASGAGETENGGFRRAMEANMEKREPGRSLRIKVISMGN AEVCKSCIIKRYCEKRFVSKYLATHGIDYGVTKVHVDRGRIKVN IFPMAGHPFFYEVRKPF 6623 1886 189 KALFEKVKKFRLHVEEGDILYAMYVROTVLKVIKKFLIITAYNSA LVSKQFFVDCNVIOLQDMTGYKNFSCHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLREYSFEYVRQETGFDDIPDVKNDP AFFILHMIDQVDPLYSKRFAVFLSEVSENKIKQLININNEWTPDKL USSKQFTVDCNVIOLQDMTGYKNFSCHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLREYSFEYVRQETGFDDIPDVKNDP AFFILHMIDQVDPLYSKRFAVFLSEVSENKIKQLININNEWTPDKL RQNICOTNAHNRIEDFLIUGLSCHDUFSTLIVGLIKLEILRUKN IPATIAQLDNLQBLSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLLVGSLESHEDISRNVYLESLRUKKUL	ſ			VEOPMITTES VEOVOU VIVON
1879 ILSDVQBEKHIKYKPEKDD 1879 NSRVDDFVARARMAAENEASQESALGAYSPVDYMSITSFPRLPE DBFAPAAPLRGRKDEDAFLGPDTDTDDFSLKSARLQRLPSSSSB MGSQDGSPLRETRKDPFAAPAACSCRODGLIVUTACLTFATG VTVALVMQIYFGDPQIFQQGAVVTDARCTSIGIEVLSKQGSSV DAAVAAALCLGIVAPHSSGLGGGGVMLVHDIRRNESHLIDFRES APGALREETLQSWETELGLUGVPGMVKGLHEAHQLYGRLPWS QVLAFAAAVAQDGFNVTHDLARALAEQLPFNMSEFRETFLPSG RPPLPGSLLHRPDLAEVLDVLGTSGPAAFVAGGNLTLEMVABAQ HAGGVITEBDFSNYSALVERVCGVYRGHLVSLSPPPHTGPALI SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDEVYD STITESMDDMLSKVBAAYLRGHINDSQAAPAPLLPVYELDGAPT AAQVLINGPDDFIVANVESULOVLGFSGGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQFGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVFFTFWLAFFSREDSCGLDCRCLSYLWLV SIPHAANNG SVKVIGAQRRSPSALAIEVFEAHLGSHLQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVPTYVHPGDHVEMAEQLGMK LPPGRGLLSQCTAEDGASSASSSGSETPFVVVFPDASDQFLL GRASGAQEETENGGPERRARMAANMFKREFGESLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFYEVRRPF 6622 2 319 GRASGAQEETENGGPERRARMAANMFKREFGESLRIKVISMGN LPPGRGLLSQCTAEDGASSASSSSGSETPFVVVFPDASDQFLL CSKCYIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFYEVRRPF 6623 1886 189 KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIITAYNSA LVSKCYFTVDCNUDIQDMTGYKNFSCHHMAHLFSKLSFCYLCF VSIYGLTCLYTLYNLFYRSLREYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLINLNNEWTPDKL GRALGTAHNREEDFLINGSLPDTVFFTELGGSKLEIKKVLSWM IPATIAQLDNLQELSLHQCSVKHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRAUEELYLLUSGLEDIGRNVTLESLRDLKSLKIL LSIKSNVSKIPQAVYDGSHLOKMCHHOGTKLVMLINKKWMIN	ļ			RELKEPPOGAHELARGIDDAL VITERDEL ANVENTALVIS
11879 NSRVDDFVARRAMABENEASQËSALGAYSPVDYMSITISFPRLPE DEPAPAAPLRGRKDEDAFLGDPDTDDSFLKSARLQRLPSSSSE MGSQDGSPLRETRKDFFSAAAECSCRODGLTVIVTACLTFATG VTVALVMQIYFGDPGJFQQGAVVTDAARCTSLGIEVLSKQGSSV DAAVAAALCLGIVAPHSSGLGGGGVMLVHDIRRNESHLDTRES APGALRETILQRSWETKFGLLGVPFGMVKGLHEAHQLYGRLPWS QVLAFAAAVAQDGFMVTHDLARALASGLSPDNMSERPRETFLPSG RPPLPGSLHRPPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKEVCGYVRGHLVLSPPPPHTGPALI SALNILEGFNITSLVSREQALHWVASTLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLFVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPGGSGLITPSGILLINSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLPTVVRPABGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRNEGGPPNT SVKVIGAQRRRSPSALAIEVFEBHLGSHLOSLDGVFFALNOEG KFLYISETVSIYLGLSQVELTGSSVPDVVHFGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL GRASGAQEETENGGPERARAMPKRKEFGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFEURKPF 6623 1886 189 KALFEKVKRFPSKYLATIGIDYGVTKVHVRDREIKVN LVSKVQFFVDCNVDLQDMTSYKMFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLREYSFCYRQETGFDDIPDVKNDF AFMLHMLDQYDDCNVDLYDDMTSYKMFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLREYSFEYVRQETGFDDIPDVKNDF AFMLHMLDQYDDFLYSKRFFAVESENSKLKQLNLINNEWTPDKL RQXLQTTAAHNRLEEFLIMLSGLEDTVEFTITLOGLKLEII KNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRANGELETLINGSLSHDLSRNVTLESLRDLKSKMTN LEIKSNSKYRPQAVVDVSSHLOKMCHNDGTKLWNINKKMTN	1			YKEAMNHLGHI,KI,FVTPIMODEFCDTPECETDI TITILI
1879 NSRVDDFVARARMAAENEASGESALGAYSPVDYMSITSFPRLPE DEPAPAPLRGRKDEDAFLGDPDTDPDSFIKSARLQRIPSSSSE MGSQDGSPLRETRIDPFSAAAAECSCRQDGLTVITVACLTFATG VTVALVMQIYFGDPQIFQQGAVVTDAARCTSLGIEVLSKQGSSV DAAVAAALCLGIVAPHSSGLGGGGVMLVHDIRRNESHLIDFRES APGALREETLQRSWETKPGLLVGVPGWVKGLHEHAPLDLYGRLPWS QVLAFAAAVAQDGFNVTHDLARALAEQLPPNMSERFRETFLPSG RPPLPGSLLHRPDLAEVLDVLGTSGFAAFYAGGNLTLEMVAEAQ HAGGVITEBFSNYSALVERVYCGVYGGHLVABPPPHTGPALI SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAFAPLLPYYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGGSLTPPSGILTNSQMLDPS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTFWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG OVGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRNEGPPPNT SVKVIGAGRRSPSALAIEVFEAHLGSHILQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDVVHPDDHVEMAEQLGMK LPPCRGLLSQGTAEDCASSASSSSSTPEPVVCPPPASDQFLL CFRASGAQRETEAGGPERARAMEANMPKRKEPGRSLTKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVNDREIKVN IFDMAGHEPFFYEURKPF KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVKVKTRLTIAYNSA LVSKVQFTVDCNVDIQDMTGYKMFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLPYRSLRBYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLINNEWTPDKL RQXLQTMAHNRLEEFLIMLSGLSHDISRNVTLESLRDLKSLKI IRVINM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLNDLESLHNLGSLSHDISRNVTLESLRDLKSLKI				ILSDVQEGKHIKYKFEVCEKDD
MGSQOGSPLRETRIGPDTDPDSFLKSARLQRLPSSSSE MGSQOGSPLRETRIGPTDTDPDSFLKSARLQRLPSSSSE VTVALVMQIYFGDPQIFQQGAVYTDARCTSIGIEVISKQGSSV DAAVAAALCLGIVAPHSSGLGGGGWMLWHDIRRNESHLIDFRES APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHQLYGRLPWS QVLAFAAAVAQDGFNVTHDLARALABQLPPNMSERFRETPLDSG RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEBDFSNYSALVEKPVCGVYRGHVLSPPPPHTGFALI SALNILEGFRLTSLVSREQALHWVAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLEVYELDGAPT AAQVLIMGPDDFIVAMVSSLNOPFGSGLITPSGILINSQMLDFS WPNRTANSAPSLENSVQPGKRPLSFILLPTVVRPAEGLCGTYLLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG 6621 1 662 VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKNRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHIQSLDGVYFALNQGG KFLYISETVSIYJGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLUSGGTAEDGASSASSSSQSETPEPVVCFPPASDQFFLL LPPGRGLUSGGTAEDGASSASSSSQSETPEPVVCFPPASDQFFLL LPPGRGLUSGGTAEDGASSASSSSQSETPEPVVCFPPASDQFFLL FDMAGHPFFYEURKPF AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVRKPF VSIYGLTCLYTLYWLFYRSLERYSFFYNQETGFDDIPDVKNDF AFMLHMIDQYDLYSKRFAVFLSEVSENKLKQLNINNEWTPDKL RQKLQTNAHNLEELPIMLSGLPDTVFETTELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELLYGSLEHDISRNVTLESLRDLKSLKII LSIKSNVSKIPQAVVDVSSHLOKMCIHNDGTKLVMINNILKMTN	6620	3	1879	NSRVDDFVARARMAAENEASOESALGAYSDVDVMSTTSEDBLDE
MOSQUESPLETRKDPFSARARECSCRODGLTVIVTACLTFATG VTVALVMQIYEDPQIFQQGAVVTDARCTSIGIEVLSKQGSSV DAAVAAALCLGIVAPHSSGLGGGVMLVHDIRRNESHLIDFRES APGALREETLQRSWETKPGILVGVPGMVKGLHEAHQLYGRLPWS QVLAFAAVAQDGFNVTHDLARALABQLPPNMSERFRETFLPSG RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEBDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI SALNILEGFNLTSLVSRGALHWVAETLKIALLALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAPPAPLLPVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPABGLCGTYLA LGANGAARGLSGITQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG 6621 1 662 VQGITSYQQRLQALRKEKSRDARRSRGKENFEFYELAKLLPLP AALTSQLDKASIIRLTISYLKMRDFANQGDPPWNLEMGPPPNT SVKVIGAQRRRSFSALAIEVFEAHLGSHLQSLDGYVFALNQEG KFLYISETYSIYIGLSQVELTGSSVEDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCPPPASDQFLL FFMAGHPFFYEVRKPF 6622 2 319 GRASGAQETEAGGPERARAMEANMPKRKEFGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVRKPF 6623 1886 189 KAPFEKVKFFLHVEGGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVIGQMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLRSYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQINLNHEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFETTELQSLKELI IKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELLYLGSLEHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLOKWCHNDGTKLWMLNNLKKMTN	1			DEPAPAAPLRGRKDEDAFLGDPDTDPDSFLKSARLOPLDESSER
DAAVAAALCLGIVAPHSSGLGGGVMLVHDIRRNESHLIDFRES APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHGLYGRLPWS QVLAFAAAVAQDGFNTTHDLARALAEQLPPMMSERFRETFLPSG RPPLPGSLLHRPDLAEVLDVLGTSGPAFYAGGRITLEMVAEAQ HAGGVITEBDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI SALNILEGFNLTSLVSREQALHWVAETLKIALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT AAQVVLMGPDDFIVAMVSSINQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLGTYLA LGANGAARGLGGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG 6621 1 662 VQGITSYQORLQALRKEKSRDAARSRRGKENFFEYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNIRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHLQSLDGYVFALNQEG KFFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSOSETPEDVVCFPPASDQFLL 6622 2 319 GRASGAQEETEAGGPERARMEANMPKRKEPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFMMAGHPFYEVKRFF 6623 1886 189 KALFEKVKKFRLHVEEGDILYAMYVROTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYKSLRFXSFEVVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IFATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRCHKSUKMTN	1 1		İ	MGSQDGSPLRETRKDPFSAAAAECSCRODGLTVTVTACLTEATC
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APGALRET-QRSWETKPGLLVGVPGMVKGLHEAHQLYGRLPWS QVLAFAAAVAQDGFNVTHDLARALABQLPPNMSERFRETPLPSG RPPLFGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI SALINILEGFNITSLVSREQALHWVAETLKIALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT AAQVLIMGPDDFIVAMVSSLNOPFGSGLITPSGILINSQMLDPS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAAITSGLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVPEAHLGSHILQSLDGYVFALNOEG KFLYISETVSIYIGLSQVELTGSSVPDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSGSETPEPVVCFPPASDQFLL AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN 1FPMAGHPFFYEVRKPF 6623 1886 189 KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIITAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYULPYRSLRBYSFEYVRGETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNINNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQGLKLEIIKNVM 1PATIAQLDNLQELSLHQCSVKIBSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESSLRDLKSIKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMINNLKKMINN	1 1	,		DAAVAAALCLGIVAPHSSGLGGGGVMLVHDIRRNESHIJDERE
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6622 2 319 GRASGAÇETEAGGASASSSSQSETPEPVVCFPPASDQFLL ARAGGAÇETEAGGPERARAMEANMPKRKEPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN 1FPMAGHPFFYEVRKPF KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLRBYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM 1FPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLOKMCIHNDGTKLYMLNNLKKMTN	1 1			KFLYISETVSIYLGLSOVELTGSSVFDYVHPGDHVENA POLGMY
GRAGGAGETEAGGPERARAMEANMPKRKEFGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFPMAGHPFFYEVRKPF KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLRBYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLELPLINLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLOKMCIHNDGTKLYMLNNLKKMTN	1-2222-1			LPPGRGLLSQGTAEDGASSASSSSOSETPEPVVCFPPASDOFLT
AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPPFYEVRKPF KALPEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLRBYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLELPLINLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLOKMCIHNDGTKLYMLNNLKKMTN	6622	2	319	GRASGAQEETEAGGPERARAMEANMPKRKEPGRSLRTKVTGMCN
1886 189 KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLRBYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNINNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLOKMCIHNDGTKLYMLNNLKKMTN	i i		1	AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKUN
AALPEKVKKFRLHVBEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLRBYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLOKMCTHNDGTKLYMLNNLKKWTN	6622			1FDMAGHPFFYEVRKPF
LYSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLRBYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNINNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLOKMCIHNDGTKLYMLNNIKKMTN	0023	T882	189	KALFEKVKKFRLHVEEGDILYAMYVROTVIKVIKFITITAVNGA
VSIYGLTCLYTLYWLFYRSLRBYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNINNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLOKMCIHNDGTKLYMLNNIKKMTN	1			LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHI,FSKI,SFCVI.CR
AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLOKMCIHNDGTKLVMLNNIKKMTN	1	İ	1	VSIYGLTCLYTLYWLFYRSLRBYSFEYVROETGFDDIPDVKNDF
RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLVGSLSHDLSRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLOKMCIHNDGTKLVMLNNIKKMTN		į	[·	AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKOLNI NNEWTDDKI.
1PATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLVGSLSHDLSRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN	ŀ	ļ	1 -	RQKLQTNAHNRLELPLIMLSGLPDTVFEITELOSI.KLEITKNUM
MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLOKMCIHNDGTKLVMLNNIKKMTN	1		I	1PATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD
LSIASNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMIN LTELELVHCDLERIPHAVFSLLSLQELDLKENNLKSIEEIVSFQ			13	MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKI
HIELELVHCDLERIPHAVFSLLSLQELDLKENNLKSIEEIVSFQ	1		1 :	LSIKSNVSKIPQAVVDVSSHLOKMCIHNDGTKLVMLNNI,KKMTN
				LIELBLUNCOLERIPHAVFSLLSLQELDLKENNLKSIEEIVSFQ

SEC	Predicted	-1	
ID	-	Predicted end	
NO:	beginning	nucleotide	
1	nucleotide location	location	Giucamic Acid, F=Phenvialanine G_Clicaia_
		corresponding	n-nistiding, leisolencing V-trains
ı	corresponding	to first	L=Leucine, M=Methionine N=Asparacine
l l	to first	amino acid	P=Proline, O=Glutamine P=Arginine
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine V=IInk==== + 0:
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
j			HLRKLTVLKLWHNSITYIPEHIKKLTSLERLSFSHNKIEVLPSH
l.			LFLCNKIRYLDLSYNDIRFIPPEIGVLQSLQYFSITCNKVESLP
ł	J	1	DELYFCKKLKTLKIGKNSLSVLSPKIGNLLFLSYLDGKGNHFEI
			LPPELGDCRALKRAGLVVEDALFETLPSDVREQMKTE
6624	218	1786	GSRRGGGSRIPAVSTHVAPGRSVLRPFASGALRLRSLVKALGGC
- 1	1		RGRPSGLAHLGOFTSUMPAVEGGRAGALRLRSLVKALGGC
1	ļ		RGRPSGLAHLSQETSHWRAKRSGRACLGDFPGEILRSFIMKCTA
1			REWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEDGEWWIA
í			KQRGKRAITDNDMQSILDLHNKLRSQVYPTASNMEYMTWDVELE
i	1	1	RSAESWAESCLWEHGPASLLPSIGQNLGAHWGRYRPPTFHVQSW
1	ł	Ĭ	YDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGC
1			AINLCHNMNIWGQIWPKAVYLVCNYSPKGNWWGHAPYKHGRPCS
1	1		ACPPSFGGGCRENLCYKEGSDRYYPPREEETNEIERQQSQVHDT
1			AVKIKSDDSSRNEVISAOOMSOIVSCEVRIRDOCKGTTChrypo [
İ	1	· '	PAGCEDSKAKVIGSVHYEMOSSICRAATHYGITDNDGGGGGGGTTTTD
- 1	1		QGRAHIFIKSNRNGIOTIGKYOSANSETVSKUTVOAUTORITISTET
6625	1124		QLCPFRKPASHCPRVYCPRKLYASKSTI.CSCNWNSSI D
1		543	PGPRGGGGSLLSTKALGRSRGLGMHDGDSSGGTDGGVDTDAY DDS
1	i i		GPLVPSTSDDNLLKNIELFDKLALRFHGRIJFLKDULGDETGGT
ſ	1		SFIGGGRKINEVCCTSIVYNTEKKOTKUREDPAD IPPERIORAL
	j		IETPRGPDPALLEATGGAAGAGGAGRGEDEENDEUDURD TURBE
6626			I HI THUCKPHGOOIVFKD
1 0020	3	1498	SAVEFVYTDRFHLILGISVEFLCSLRSDATMESITACLHALQAL
	ŀ		I DOVEMPROKIGSDODSGIELLNVI, HRVII, TOPEDCIOTA CORDO
1			KQ11CAAQEHVKEKRRSAEVDDGAAFFFTI.DPPCBGFTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
	i I		GRELVEATLELCVCILVROLPELNDKI.TCCDCVVDTVDATT TO
1	1		GSRLVSAALVILSELPAVCSPEGSISILPTILYLTIGVLRETAV
	1 1		KLPGGQLSSTVAASLQALKGILSSPMARABKSRTAWTDLLRSAL
J	1		TTILDCWDPVDETHQELDEVSLLTAITVFILSTSPEVTTIPCLQ
1	1		KRCIDKFKATLEIKDPVVQIKTYQLLHSIFQYPNPAVSYPYIYS
	1		LASCIMEKLQEIDKRKPENTAELEIFQEGIKVLETLVTVAEEHH
1	1		RAQLVACLLPILISFLLDENSLGSATSIMRNLHDFALQNLMQIG
	1		PQYSSVFKSLVASSPALKARLEAAIKGNQESVKVKIPTSKYTKS
			PGKNSSIQLKTSFL
6627	1	697	GIPHLSSRDMTGTPGAVATRDGEAPERSPPCSPSYDLTGKVMLL
			GDTGVGKTCFLIQFKDGAFLSGTFIATVGIDFRNKVVTVDGVRV
1	1		KLQIWDTAGQERFRSVTHAYYRDAQALLLLYDITNKSSFDNIRA
			WLTEIHEYAQRDVVIMLLGNKADMSSERVIRSEDGETLAREYGV
1	1		PFLETSAKTGMNVELAFLAIAKELKYRAGHQADEPSFQIRDYVE
	<u> </u>		SQKKRSSCCSFM
6628	1	1861	QCAE FGGGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
]	1	1	KEFGDSLSLEILQIIKESQQQHGLRHGDFQRYRGYCSRRQRRLR
į	1		KTLNFKMGNRHKFTGKKVTEELLTDNRYLLLVIMDAERAWSYAM
i	1	i	QLKQEANTEPRKRFHILLSRLRKAVKHAEELERLCESNRVDAKTK
	i		LEAQAYTAYLSGMLRFEHQEWKAAIEAFNKCKTIYEKLASAFTE
	[EQAVLYNQRVEEISPNIRYCAYNIGDQSAINELMQMRLRSGGTE
!	J		GLLAFKLEAL TROUBAYOR AMAGUNET TO THE STATE OF THE STATE O
ľ		1	GLIAEKLEALITOTRAKQAATMSEVEWRGRTVPVKIDKVRIFLL
			GLADNEAAIVQAESEETKERLFESMLSECRDAIQVVREELKPDQ
		1	KQRDYILEGEPGKVSNLQYLHSYLTYIKLSTAIKRNENMAKGLQ
		İ	RALLQQQPEDDSKRSPRPQDLIRLYDIILQNLVELLQLPGLEED
	}	1.	KAFQKEIGLKTLVFKAYRCFFIAQSYVLVKKWSEALVLYDRVLK
	İ	1.	YANEVNSDAGAFKNSLKDLPDVQELITQVRSEKCSLQAAAILDA
ı J	1	į -	NDAMQTETSSSQVKDNKPLVERFETFCLDPSLVTKOANT VILEDD
1	1	f '	GFQPIPCKPLFFDLALNHVAFPPLEDKLEQKTKSGLTGYIKGIF
6629	5653		3FRS
1			JATPLGSVGGRTGKMDAATLTYDTLRFAEFEDFPETSEPVWILG
			RKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGC

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	acdacuca	Codon, /=possible nucleotide deletion,
		 	\=possible nucleotide insertion)
1			MLRCGQMIFAQALVCRHLGRDWRWTQRKRQPDSYFSVLNAFIDR
Į.	i		KDSYYSIHQIAQMGVGEGKSIGQWYGPNTVAQVLKKLAVFDTWS
j.		1	SLAVHIAMDNTVVMEEIRRLCRTSVPCAGATAFPADSDRHCNGF
			PAGAEVINRPSPWRPLVLLIPLRLGLTDINEAYVETLKHCFMMP
		İ	QSLGVIGGKPNSAHYFIGYVGEELIYLDPHTTQPAVEPTDGCFI
1			PDESFHCQHPPCRMSIAELDPSIAVVRGGHLSTQAFGAECCLGM
6630	2	423	TRKTFGFLRFFFSMLG
	-	423	LVQCGGTRRRSAWGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS
ļ	1		LGDQYVKDEFRRHKTVGSDEAQRFLQEWEVYATALLQQANENRQ
1	Í		NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFSI
6631	2	403	SESMKPKF
		423	LVQCGGIRRRSAWGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS
			LGDQYVKDEFRRHKTVGSDEAQRFLQEWEVYATALLQQANENRQ
			NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFSI
6632	1273	568	SESMKPKF
1 0000	12/3	288	WNSRGRTQRGAAPLAPAAAMKAVVQRVTRASVTVGGEQISAIGR
1 .			GICVLLGISLEDTQKELEHMVRKILNLRVFEDESGKHWSKSVMD
1 1			KQYEILCVSQFTLQCVLKGNKPDFHLAMPTEQAEGFYNSFLEQL
	,		RKTYRPELIKDGKFGAYMQVHIQNDGPVTIELESPAPGTATSDP
			KQLSKLEKQQQRKEKTRAKGPSESSKERNTPRKEDRSASSGAEG
6633	1145	617	DVSSEREP
	1	617	ATGRHEGVPTLEGIIQQLVNGIITPATIPSLGPWGVLHSNPMDY
	1		AWGANGLDAIITQLLNQFENTGPPPADKEKIQALPTVPVTEEHV
1 !	i		GSGLECPVCKDDYALGERVRQLPCNHLFHDGCIVPWLEQHDSCP
6634	1	1134	VCRKSLTGONTATNPPGLTGVSFSSSSSSSSSSSSSSSSNENATSNS
1	_	7732	CGGIPRKGSGPRRLPMARLRDCLPRLMLTLRSLLFWSLVYCYC
1 1	ł		GLCASIHLLKLLWSLGKGPAQTFRRPAREHPPACLSDPSLGTHC YVRIKDSGLRFHYVAAGERGKPLMLLLHGFPEFWYSWRYQLREF
1 1	1		KSEYRVVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLGY
!!	ļ		SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINFPHPNVFTEYI
}			LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHSTG
1 1	,		IGRXGCQLTTEDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH
			HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEASH
			WLQQDQPDIVNKLIWTFLKEETRKKD
6635	1420	470	EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAFSSSG
, ,			GRGGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK
			ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG
1 1	1	ļ	LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS
!!	J	j	HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL
j 1	İ		LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL
1			LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI
!		}	AAIRGFLV
6636	1514	1801	SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE
1			QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD
		1	DGGDGVF
6637	2	1501	CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI
1			KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT
ŀ		,	VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD
Ī	!	İ	LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG
1	Ī		DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS
1			CIPICGETENTTAREFOCIONDES ATTENTOCIONA
i	i		CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW
ſ	1		FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS
ı			TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL
1	ľ	i	RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC
- 1	1		TAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid. E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
6638	1391	224	TKVLPFKDWIERNMK
""	1391	224	GGIPQAGGKMAAPWWRAALCECRRWRGFSTSAVLGRRTPPLGPM
			PNSDIDLSNLERLEKYRSFDRYRRAEQEAQAPHWWRTYREYFG
	1		ektdpkekidiglpppkvsrtqqllerkqaiqelranveeeraa
	ł		RLRTASVPLDAVRAEWERTCGPYHKQRLAEYYGLYRDLFHGATF
	1		VPRVPLHVAYAVGEDDLMPVYCGNEVTPTEAAQAPEVTYEAEEG
1	i		SLWTLLLTSLDGHLLEPDAEYLHWLLTNIPGNRVAEGQVTCPYL
1	i .		PPFPARGSGIHRLAFLLFKQDQPIDFSEDARPSPCYQLAQRTFR
			TFDFYKKHQETMTPAGLSFFQCRWDDSVTYIFHQLLDMREPVFE
6639			FVRPPPYHPKQKRFPHRQPLRYLDRYRDSHEPTYGIY
0039	2046	1268	IGCFIMDGGDDGNLIIKKRFVSEAELDERRKRRQEEWEKVRKPE
1			DPEECPEEVYDPRSLYERLQEQKDRKQQEYEEQFKFKNMVRGLD
1			EDETNFLDEVSRQQELIEKQRREEELKELKEYRNNLKKVGISQE
	ļ		NKKEVEKKLTVKPIETKNKFSQAKLLAGAVKHKSSESGNSVKRL
ŀ	i .		KPDPEPDDKNQEPSSCKSLGNTSLSGPSIHCPSAAVCIGILPGL
6640	117	2042	GAYSGSSDSESSSDSEGTINATGKIVSSIFRTNTFLEAP
0040	**/	1043	VLEPPDVSMAESEDRSLRIVLVGKTGSGKSATANTILGEEIFDS
ľ	l i		RIAAQAVTKNCQKASREWQGRDLLVVDTPGLFDTKESLDTTCKE
ļ			ISRCIISSCPGPHAIVLVLLLGRYTEEEQKTVALIKAVFGKSAM
			KHMVILFTRKEELEGQSFHDFIADADVGLKSIVKECGNRCCAFS
			NSKKTSKAEKESQVQELVELIEKMVQCNEGAYFSDDIYKDTEER
			LKQREEVLRKIYTDQLNEEIKLVEEDKHKSEEKKEKEIKLLKLK
6641	1	894	YDEKIKNIREEAERNIFKDVFNRIWKMLSEIWHRFLSKCKFYSS
0041	±	894	SAAVGRRSEVRGCAPRPRLRRSARRMDPVPGTDSAPLAGLAWSS
i .			ASAPPPRGFSAISCTVEGAPASFGKSFAQKSGYFLCLSSLGSLE
1			NPQENVVADIQIVVDKSPLPLGFSPVCDPMDSKASVSKKKRMCV
ļ į			KLLPLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK APRPVPKPRGLSRDMQGLSLDAASQPSKGGLLERTASRLGSRAS
1			TLRRNDSIYEASSLYGISAMDGVPFTLHPRFEGKSCSPLAFSAF
1 1			GDLTIKSLADIEEEYNYGFVVEKTAAARLPPSVS
6642	22	1296	PLEERMMTKMDPNDQAQRDIIFELRRIAFDAESDPSNAPGSGTE
		2250	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV
i i			HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP
			NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN
			KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER
			MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG
			NRRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPV
			ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF
	ļ		IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMBMKLRL
	Ì		LDLENIQIPEAPPPIPKEPSSYDFVYHYG
6643	3049	2265	SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI
	j		DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHOSHPLOYIG
	1		HDRTMQDIVYXLVPGLQEAEMRKQREFYHKLGMEVPGDIKGETC
	1		SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI
İ	!		CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL
	į.		DILCNEEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL
6644	1489	290	FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDOR
	[LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR
	j		TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL
	ŀ		LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFO
			LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT
j	}		EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL
[KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF
ļ		ļ	LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY
ł		i	EVINIOATODOORSEELARIMGEFEITEOPRLSTSKGDDLLAMM
	j		DEL

SEQ Predicted beginning nucleotide nucleotide nucleotide location corresponding to first amino acid residue of residue of residue of segment containing signal (A=Alanine, C=Cysteine, D=Asparatic ACID, F=Phenylalanine, G=GID (A=Alanine, C=Cysteine, D=Asparatic ACID, F=Phenylalanine, G=GID (A=Alanine, C=Cysteine, D=Asparatic ACID, F=Phenylalanine, G=GID (A=Alanine, C=Cysteine, D=Asparatic ACID (A=Alanine,	Acid, E= .ycine,
NO: nucleotide location corresponding to first amino acid residue of S=Serine, T=Threonine, V=Aspartic A Glutamic Acid, F=Phenylalanine, G=GI H=Histidine, I=Isoleucine, K=Lysine, M=Methionine, N=Asparagir P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine.	ycine,
location corresponding to first amino acid residue of S=Serine, T=Threonine, V=Valine, G=G] location corresponding to first amino acid residue of S=Serine, T=Threonine, V=Valine,	
corresponding to first L-Leucine, M-Methionine, N-Asparagir to first amino acid residue of S-Serine, T-Threonine, V-Valine,	
to first amino acid P=Proline, Q=Glutamine, R=Arginine, amino acid residue of S=Serine, T=Threonine, V=Valine.	
amino acid residue of S=Serine, T=Threonine, V=Valine,	ıe,
3=3etime, finiteonine, v=valine.	
Willyprophan, interprophan, interpretation	*=Stop
	n,
(-possible nucleotide insertion)	
FVEGLAGIVYKAASEGKVLTLAALLLINRSESDIRYI	LGYVSQQG
GQRSTPLIIAARNGHAKVVRLLLEHYRVQTQQTGTV	RFDGYVID
GATALWCAAGAGHFEVVKLLVSHGANVNHTTVTNST	PLRAACFD
GRLDIVKYLVENNANISIANKYDNTCLMIAAYKGHT	DVVRYLLE
QRADPNAKAHCGATALHFAAEAGHIDIVKELIKWRA	AIVVNGHG
MTPLKVAAESCKADVVELLLSHADCDRRSRIEALEL	LGASFAND
RENYDIIKTYHYLYLAMLERFQDGDNILEKEVLPPI	HAYGNRTE
CRNPQELESIRQDRDALHMEGLIVRERILGADNIDV	SHPIIYRG
AVYADNMEFEQCIKLWLHALHLRQKGNRNTHKDLLR	FAQVFSQM
IHLNETVKAPDIECVLRCSVLEIEQSMNRVKNISDA	NOMAKIHVO
YECNLYTFLYLVCISTKTQCSEEDQCKINKQIYNLI	HLDPRTRE
GFTLLHLAVNSNTPVDDFHTNDVCSFPNALVTKLLL	DCGAEVNA
VDNEGNSALHIIVQYNRPISDFLTLHSIIISLVEAG	AHTDMTNK
QNKTPLDKSTTGVSEILLKTQMKMSLKCLAARAVRA IPRTLEEFYGFH	MDIMAODÓ
FBSRINGIDFEDWENALIGSOSSHASLRNIHSINPTO	LMARIESY
EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVI	NGGIENTL
EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLI TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILA	RHWWATAL
FKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQF	MIELMELD
GSEEAEEKODSEKPI.I.ET.	SPPESEA
6647 176 890 PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQ	MADADA
EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVI	JUAR LES Y
EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLE	ARMIN' LYL
TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAV	TETWELD
FKVLPQEABEENRLLIVQDASERAALIPGGLSDGQF7	SPPESED
GSEEAEEKQDSEKPLLEL	
6648 413 897 RNCWNCFTKYFNSPPEDIDHKDSYLITRSIMAEPDY	EDDNPET.
IRPQKLINPVKTSRNHQDLHRELLMNOKRGLAPONKI	RLOKIME
KRKRDQVIKQKEEEAQKKKSDLEIELLKROOKLEOLE	LEKOKLO
EEQENAPEFVKVKGNLRRTGOEVAOAQES	
6649 1357 832 WIPRAAGIRHEVKWDVKEIMSQHNIYVDALLKEFEQF	NRRLNEV
SKRVRIPLPVSNILWEHCIRLANRTIVEGYANVKKCS	NEGRAIM
QLDFQQFLMKLEKLTDIRPIPDKEFVETYIKAYYLTE	NDMERWY
KEHREYSTKOLTNLVNVCLGSHINKKAROKLLAAIDD	IDRPKR
765 LVPLVFSLLVQSCKQVYRSIAMKFVPCLLLVTLSCLG	TLGOAPR
QKQGSTGEEFHFQTGGRDSCTMRPSSLGOGAGEVWLR	VDCRNTD
QTYWCEYRGQPSMCQAFAADPKSYWNQALQELRRLHH	ACQGAPV
LRPSVCREAGPQAHMQQVTSSLKGSPEPNQQPEAGTP	SLRPKAT
VKLTEATQLGKDSMEELGKAKPTTRPTAKPTQPGPRP	GGNEEAK
KKAWEHCWKPFQALCAFLISFFRG 6651 3425 1353 AKELLKYGDESLCAGDYOWTA DOWNER CHERT A GIFTLE	
AREBUKVGDFSLCAGPYONTADTMENLSKEPLASFVS	ESFDISA
CGIATEHVKIDNSGEGLTAEAGSETLSRDGEVGVNSD	MHYELSG
DSDLDLLGDCRNPRLDLEDSYTLRGSYTRKKDVPTDG	YESSLNF
HNNNQEDWGCSSWVPGMETSLPPGHWTAAVKKEEKCV	PPYVQIR
DLHGILRTYANFSITKBLKDTMRTSHGLRRHPSFSAN	GLPSSW
TSTWQVADDLTQNTLDLEYLRFAHKLKQTIKNGDSQH:	SASSANV
FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLV	VVESDP
RPQGQPRRGYTASSLDSSSSWRERCSHNRDLRNSQRNE	HTVSFHL
NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNOFII	ODKELN
DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLH	RSVVKEA
CKSTFLFYLVETEDKSFFVRTKNLLRKGGHTEIEPOH	COAFHR
ENDTLIIIIRNEDISSHLHQIPSLLKLKHFPSVIFAG\	DSPGDV
LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILE	KLNGNG
RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFQSAN YHQCDSRSSTKAEILKCLLNLQIQHIDARFAVLLTDKE	LIELLH
gebendel nærtandutgighidarfavllitöke	TIPREV

SEQ	Predicted	Predicted end	Amino poid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
-	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
6652			FENNGILVTDVNNFIENIEKIAAPFRSSYW
6652	2	1343	IPGSTISCSCHSRRLRGGSPAPRLSLGAASPRPRPPSLPLPLPL
1			PFPLFLPTRPAERAWIRSRRASEWVGKMEVPRLDHALNSPTSPC
1			EBVIKNLSLEAIQLCDRDGNKSQDSGIAEMEELPVPHNIKISNI
1	1		TCDSFKISWEMDSKSKDRITHYFIDLNKKENKNSNKFKHKDVPT
	l i		KLVAKAVPLPMTVRGHWFLSPRTEYTVAVQTASKQVDGDYVVSE
i	j l		WSEIIEFCTADYSKVHLTQLLEKAEVIAGRMLKFSVFYRNQHKE
			YFDYVREHHGNAMQPSVKDNSGSHGSPISGKLEGIFFSCSTEFN TGKPPQDSPYGRYRFEIAAEKLFNPNTNLYFGDFYCMYTAYHYV
			ILVIAPVGSPGDEFCKQRLPQLNSKDNKFLTCTEEDGVLVYHHA
İ			QDVILEVIYTDPVDLSIGTVAEITGHQLMSLSTANAKKDPSCKT
1	[CNISVGR
6653	170	1910	FFLEPRLRPFPASRARFVPARTRPSPLHPCCFCFEGGGSMLSPQ
ľ			RVAAAASRGADDAMESSKPGPVQVVLVQKDQHSFELDEKALASI
!			LLQDHIRDLDVVVVSVAGAFRKGKSFILDFMLRYLYSQKESGHS
ļ			NWLGDPEEPLTGFSWRGGSDPETTGIQIWSEVFTVEKPGGKKVA
}			VVLMDTQGAFDSQSTVKDCATIFALSTMTSSVQIYNLSQNIQED
į			DLQQLQLFTEYGRLAMDEIFQKPFQTLMPLVRDWSFPYEYSYGL
			QGGMAFLDKRLQVKEHQHEEIQNVRNHIHSCFSDVTCFLLPHPG
			LQVATSPDFDGKLKDIAGEFKEQLQALIPYVLNPSKLMEKEING
	}		SKVTCRGLLEYFKAYIKIYQGEDLPHPKSMLOATAEAYNLAAAA
	İ		SAKDIYYNNMEEVCGGEKPYLSPDILEEKHCEFKQLALDHFKKT
1 1			KKMGGKDFSFRYQQBLEEEIKELYENFCKHNGSKNVFSTFRTPA
			VLFTGIVALYIASGLTGFIGLEVVAQLFNCMVGLLLIALLTWGY
			IRYSGQYRELGGAIDFGAAYVLEQASSHIGNSTQATVRDAVVGR
6654	1	705	PSMDKKAQ
1100	- 1	703	RTSLSPSQCSSFNLAMASAGMQILGVVLTLLGWVNGLVSCALPM
			WKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQMQCKVYDSLLAL PQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARL
			VLTSGIVFVISGVLTLIPVCWTAHAVIRDFYNPLVAEAQKRELG
			ASLYLGWAASGLLLLGGGLLCCTCPSGGSQGPSHYMARYSTSAP
			AISRGPSEYPTKNYV
6655	341	16	KDAYMFKKGLLALALVFSLPVFAAEHWIDVRVPEQYQQEHVQGA
[INIPLKEVKERIATAVPDKNDTVKVYCNAGRQSGQAKEILSEMG
			YTHVENAGGLKDIAMPKVKG
6656	2	1212	TELPPRPANLAIQPPLSPLRALAPLPEKPGAVPPPQKRMAKVAK
			DLNPGVKKMSLGQLQSARGVACLGCKGTCSGFEPHSWRKICKSC
}		j	KCSQEDHCLTSDLEDDRKIGRLLMDSKYSTLTARVKGGDGIRIY
			KRNRMIMTNPIATGKDPTFDTITYEWAPPGVTQKLGLQYMELIP
ſ		İ	KEKQPVTGTEGAFYRRRQLMHQLPIYDQDPSRCRGLLENELKLM
1	. 1	ł	EEFVKQYKSEALGVGEVALPGQGGLPKEEGKQQEKPEGAETTAA
ŀ	İ		TTNGSLSDPSKEVEYVCBLCKGAAPPDSPVVYSDRAGYNKQWHP
]		TCFVCAKCSEPLVDLIYFWKDGAPWCGRHYCESLRPRCSGCDEI
l	1		IFAEDYQRVEDLAWHRKHFVCEGCEQLLSGRAYIVTKGQLLCPT CSKSKRS
6657	830	2120	LLTCQERAGDCLLSASTMKEVVYWSPKKVADWLLENAMPBYCEP
1			LEHFTGQDLINLTQEDFKKPPLCRVSSDNGQRLLDMIETLKMEH
1			HLEAHKNGHANGHLNIGVDIPTPDGSFSIKIKPNGMPNGYRKEM
ŀ	ļ		IKIPMPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER
J		j	VPPKEVQPPLPDTFFDHFNRVQWAFSICEINGMILVGLWLIQWL
j		ĺ	LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHFNCSPK
	Ī	ŀ	LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL
	ļ		TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLAHDHYTVDVVV
	1		AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYFEK
			NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT
6658	35	855	HCCALGAPGSPYRGLYFSSAAPCTAPRKAKHOSTLEGLTKRMLM

SEO	Predicted	Predicted end	Dmino poid company
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			FDPVPVKQEAMDPVSVSYPSNYMESMKPNKYGVIYSTPLPEKFF
1	1	j	QTPEGLSHGIQMEPVDLTVNKRSSPPSAGNSPSSLKFPSSHRRA
			SPGLSMPSSSPPIKKYSPPSPGVQPFGVPLSMPPVMAAALSRHG
f		1	IRSPGILPVIQPVVVQPVPFMYTSHLOOPLMVSLSERMENSSSS
			MQVPVIESYEKPISQKKIKIEPGIEPQRTDYYPEEMSPPLMNSV
-55			SPPQALLQE
6659	18	523	EPQRGDCETWFQNCSLPKFVCFFCWGFWLWRAHSMSNLHSLPGL
1			RGLTSISRNQLQCTNAMRVINNYQRRWKNQNTFLLATFANVVNV
			CGNPTITCPHNRTLNNCHHSGVQVPLMYCNLTTPSPONISNCRY
			AQTPANMFYIVACDNRDQRRDPPQYPVVPVHLHTII
6660	514	1707	CAASLDCRHHLCEPDMKLVWPSAKLLQAAAGASARACDSVTSNV
			LPLLLEQFHKHSQSSQRRTILEMLLGFLKLQQKWSYEDKDORPL
			NGFKDQLCSLVFMALTDPSTQLQLVGIRTLTVLGAQPDLLSYED
			LELAVGHLYRLSFLKEDSQSCRVAALEASGTLAALYPVAFSSHL
			VPKLAEELRVGESNLTNGDEPTQCSRHLCCLQALSAVSTHPSIV
			KETLPLLLQHLWQVNRGNMVAQSSDVIAVCQSLRQMAEKCQQDP
i			ESCWYFHQTAIPCLLALAVQASMPEKEPSVLRKVLLEDEVLAAM
			VSVIGTATTHLSPELAAQSVTHIVPLFLDGNVSFLPENSFPSRF QPFQDGSSGQRRLIALLMAFVCSLPRNVSEHIWEVLLFNLDKVT
1			PG
6661	179	430	GVHAASGTLSATWLAEAKMFDSLAKAGKYLGQAAKLMIGMPDYD
			NYVEHMRVNHPDQTPMTYEBFFRERQDARYGGKGGARCC
6662	185	423	RSLPKPAPAQPASIHCARFSGVTPPTAKTAMSDGNTAFNALMYC
			GPKADDGNIFSACAPASSAVKASVSVAQPGQAVIP
6663	3	1005	RPVLSSRVDDFVPPLPETSGRRKKLERMYSVDRVSDDIPIRTWF
1			PKENLFSFQTASTTMQAISNFRKHLRMVGSRRVKAQTFAERRER
			SFSRSWSDPTPMKADTSHDSRDSSDLQSSHCTLDEAFEDLDWDT
]			EKGLEAVACDTEGFVPPKVMLISSKVPKAEYIPTIIRRDDPSII
	i		PILYDHEHATFEDILEEIERKLNVYHKGAKIWKMLIFCQGGPGH
			LYLLKNKVATFAKVEKEEDMIHFWKRLSRLMSKVNPEPNVIHIM
1			GCYILGNPNGEKLFQNLRTLMTPYRVTFESPLELSAQGKQMIET YFDFRLYRLWKSRQHSKLLDFDDVL
6564	58	968	PRLLRLPRSVVVMDSPWDELALAFSRTSMPPFFDIAHYLVSVMA
1		200	VKRQPGAAALAWKNPISSWFTAMLHCFGGGILSCLLLAEPPLKF
1	ŀ		LANHTNILLASSIWYITFFCPHDLVSQGYSYLPVQLLASGMKEV
			TRIWKIVGGVTHANSYYKNGWIVMIAIGWARGAGGTIITNFERL
[ļ		VKGDWKPEGDEWLKMSYPAKVTLLGSVIFTFQHTQHLAISKHNL
į l	i		MPLYTIFIVATKITMMTTQTSTMTFAPFEDTLSWMLFGWQQPFS
			SCEKKSEAKSPSNGVGSLASKPVDVASDNVKKKHTKKNE
6665	171	1278	DERRLACROVVTQQRSELYPGFOKRORFLFKAGEEAAAOGGRHL
		!	PGRWLGPGCTQNPCSVHTATGPEPRKLPLLPPDSPNSGYPKEPA
ľ		ļ	ALCPGIPSPCRMTHQDLSITAKLINGGVAGLVGVTCVFPIDLAK
		1	TRLQNQHGKAMYKGMIDCLMKTARAEGFFGMYRGAAVNLTLVTP
			EKAIKLAANDFFRRLLMEDGMQRNLKMEMLAGCGAGMCOVVVTC
i i			PMEMLKIQLQDAGRLAVHHQGSASAPSTSRSYTTGSASTHRRPS
1	}		ATLIAWELLRTQGLAGLYRGLGATLLRDIPFSIIYFPLFANLNN
1	1		LGFNELAGKASFAHSFVSGCVAGSIAAVAVTPLDVLKTRIQTLK
6666	400		KGLGEDMYSGITDCAR
0000	498	2868	MTTFLPVPQMMAGFSFGTFGNPPMESPSAWQTIHQPFIVSCLTL
			WSPGCWPQPIQKEGVGLWDIRKPQSSLLRYGGNLSLQSAMSVRF
i			NSNGTQLLALRRRLPPVLYDIHSRLPVFQFDNQVYFNSCTMKSC
1	1	!	CFAGDRDQYILSGSDDFNLYMWRIPADPEAGGIGRVVNGAFMVL
		ĺ	KGHRSIVNQVRFNPHTYMICSSGVEKIIKIWSPYKQPGCTGDLD
- 1		j	GRIEDDSRCLYTHEEYISLVLNSGSGLSHDYANQSVQEDPRMMA FFDSLVRREIEGWSSDSDSDLSESTILQLHAGVSERSGYTDSES
	į	į	SASLPRSPPPTVDESADNAFHLGPLRVTTINTVASTPPTPTCED
			TO THE TANGED THE PROPERTY OF THE TANGE OF T

SEQ	Predicted	Predicted end	Draine and A
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	[M=MlStidine, I=Isoleucine, K-typine
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
Į	to first amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
1	residue of	residue of	S=Serine, T=Threonine, V=Valine
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Chan
1	sequence	sequence	Codon, /=possible nucleotide delation
			\=possible nucleotide insertion)
1	1		AASRQQRLSALRRYQDKRLLALSNESDSEENVCEVELDTDLFPR
ŀ	[PRSPSPEDESSSSSSSSSSEDEELNERRASTWORNAMRRRQKT
	ĺ		TREDKPSAPIKPTNTYIGEDNYDYPOIKVDDLSSSPTSSPERST STLEIQPSRASPTSDIESVERKIYKAYKWLRYSYISYSNNKDGE
		!	TSLVTGFADEGRAGTSHKDNPAPSSSKEACLNIAMAQRNQDLPP
			EGCSKDTFKEETPRTPSNGPGHEHSSHAWAEVPEGTSQDTGNSG
1		1	SVEHPFETKKLNGKALSSRAEEPPSPPVPKASGSTLNSGSGNCP
			RTQSDDSEERSLETICANHNNGRLHPRPPHPHNNGONLGELEDAY
}			AYSSPENSDTDRDNSSLTGTLLHKDCCGSRMACTTDNACTDNACTDNACTDNACTDNACTDNACTDNACTD
6667	121		TDTPATDSSRAVHGHSGLKRORIELEDTDSENSSSEKKI.VT
550,	171	1310	ASEVERLAAMRSDSLVPGTHTPPIRRRSKFANLGPTPVDWVWDV
1 !			KKSEKFKHTSAALERKISMROSREELIKRGVIKETVDVDGBLGT
]			SNEEDSLENGQSLSSSQLSLPALSEMEPVPMPRDPCSYEVLQPS
			DIMOGPOPGAPVKLPCLPVKLSPPLPPKKVMICMPVGGPDLSLV
1 1			SYTAQKSGQQGVAQHHHTVLPSQIQHQLQYGSHGQHLPSTTGSL
1 1			PMHPSGCRMIDELNKTLAMTMORLESSEQRVPCSTSYHSSGLHS GDGVTKAGPMGLPEIRQVPTVVIECDDNKENVPHESDYEDSSCL
]			YTREEEEERDEDDDSSLYTSSLAMKVCRKDSLAIKPSNRPSKR
			ELEEKNILPROTDEERLELROOIGTKL
6668	714	358	TLAVATGPALTLRCHVCTSSSNCKHSVVCPASSRFCKTTNTVEP
! !			LRGNLVKKDCAESCTPSYTLOGOVSSGTSSTOCCOEDLCNEVLU
6669	450		NAAPTRTALAHSALSLGLALSLLAVILAPSI
1 2003	459	1207	KDEETRKDYDYMLDHPEEYYSHYYHYYSRRI A PKYDYPYYTT VS
1	1		VCAISVFQFFSWWNSYNKAISYLATVPKYRIOATEIAKOOGILK
1 1	i		KAKEKGKNKKSKEEIRDEEENIIKNIIKSKIDIKGGYOKPOTCO
1 1			LLLFQIILAPFHLCSYIVWYCRWIYNFNIKGKEYGEEERLYIIR
			KSMKMSKSQFDSLEDHQKETFLKRELWIKENYEVYKQEQEEELK KKLANDPRWKRYRRWMKNEGPGRLTFVDD
6670	184	594	VARI*GEAAKMSSEPPPPYPGGPTAPLLEEKSGAPPTPGRSSPA
			VMQPPPGMPLPPADIGPPPYEPPGHPMPQPGFIPPHMSADGTYM
[PPGFYPPPGPHPPMGYYPPGPYTPGPYPGPGGHTATVLVPSGAA
			TTVTV
6671	1	763	LPAEKPRSAPNMAGGRCGPQLTALLAAWIAAVAATAGPEEAALP
	ſ	1	PEQSKVQPMTASNWTLVMEGEWMLKFYAPWCDSCOOTDGEWEAR
]		AKNGELLQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIFPB
	Ì		YRGPGIFEDLQNYILEKKWOSVEPLTGWKSPAST.TMSGMAGTEC
			ISGKIWHLHNYFTVTLGIPAWCSYVFFVIATLVFGLSMDLVL*V
6672	304	1089	ISQCNWDPPYRHVS*/RPSTNLGVHTAHTSEHLRL
			APGSKPVQFMDFEGKTSFGMSVFNLSNAIMGSGILGLAYAMAHT
l			GVIFFLALLLCIALLSSYSIHLLLTCAGIAGIRAYEOLGORAFG PAGKVVVATVICLHNVGAMSSYLFIIKSELPLVIGTFLYMDPEG
ĺ	į	İ	DWFLKGNLLIIVSVLIILPLALMKHLGYLGYTSGLSLTCMLFF
1			LVSVIYKKFQLGLCYRATMKQQWESEALVGTPQPRDSTAAVKAQ
-6673			MFHS*LTGVLTQWPIMAFAFVCHPGGAGPSITELCRAFOAOD
6673	. 1116	1963	LQIQTHHTHHGARVTHLGSHOLLANAGTMLCROOSSEMADAREO
1	1	• 1	SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEGG*G*CTNV
I			WLCPCVAFHRGARPQAEEGGARWNSLVSSDWTDDND*HCCTCAE
ı		1	NAVPRP*QG*KVNPSGOEROS\WVLPLPVPGEPI.KT.PGI.PG*NV
	. 1		CECDII (COOMONIA DE CALLES
	•		SFSRV/SGSKGKWILPRQLM*AS*R\TPRFVPGTQWVPITW/PL
			SFSRV/SGSKGKWILPRQLM*AS*R\TPRFVPGTQWVPITW/PL ITWH*SAPTPPLKACPAPRESDPCSSCLSCPCVTQHPRFSDTGW
6674	1		TTWH*SAPTPPLKACPAPRESDPCSSCLSCPCVTQHPRFSDTGW FGAGHCHSSCDFTRKGAAGGPG
6674	i	440	TWH*SAPTPPLKACPAPRESDPCSSCLSCPCVTQHPRFSDTGW FGAGHCHSSCDFTRKGAAGGPG LEFDYMCQYDYVEVRDGDNRDGOIIKRVCGNRPDADIOSIGSST
6674	1	440	1TWH*SAPTPPLKACPAPRESDPCSSCLSCPCVTQHPRFSDTGW FGAGHCHSSCDFTRKGAAGGPG LEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSL HVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVJDKAGSY
6674	1	440	TWH*SAPTPPLKACPAPRESDPCSSCLSCPCVTQHPRFSDTGW FGAGHCHSSCDFTRKGAAGGPG LEFDYMCQYDYVEVRDGDNRDGOIIKRVCGNRPDADIOSIGSST

SEQ	Predicted	Predicted end	Amino and d
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
6675	277	1678	GNWPTERMAFLDNPTILLAHIRQSHVTSDDTGMCEMVLIDHDVD
			LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR
1	1	i	RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE
1	ł		KKSLYFYDDISCYOCII CUDI DOCUL OLARANSKQSAQBLKSLFE
i	i		KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV
Į			GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF
[•	GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM
]	1		KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH
1			HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS
1			ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ
}	1 .		KASTKFWIKQKPISIDSDLLCAC\DLAEE
6676	277	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD
1			LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR
	i		RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE
İ			KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV
	!		GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWO
1	1		YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF
			GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM
İ			KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH
			HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS
1			ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ
			KASTKPWIKQKPISIDSDLLCAC\DLAEE
6677	277	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD
			LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR
1			RRSNTAQRLERLRKERQNQIKCKNIOWKERNSKOSAOELKSLEE
I i			KKSLKEKPPISGKQSILSVRLEQCPLOLNNPFNEYSKFDGKGHV
1 !	i		GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVODLIGLICWO
1 1			YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPTHKF
			GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIOVDNTKVTM
1 1	' i		KEILLKAVKRRKGSQKVSGSRADGVFEEDSOIDIATVODMISSH
			HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS
	•		ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNO
6678	221		KASTKFWIKQKPISIDSDLLCAC\DLAEE
30,0	221	865	GPSNQSSGSLSLIVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR
			PFPCSQLPMSQGCLWHLDCCCPWVPYIPGOOWRKGRORMRN*OS
Į į			LLGSDQESVGLEDLCVFVNFLLHVLLGLFP*PHELFLLPVVDLG
[i		FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN
6679	2	706	HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP
	•	786	LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSFVSDL
	1		SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAE*QNQNS\DFH
]			QEKWIYVHKGSTKERHGYCTLGBAFNRLDFSTAILDSRRFNYVV
	ĺ		RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR
1	ł	J	ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN
6680	1498	2051	NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF
	~ 250	2951	PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVGSISEE
]			P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGABIQTSA*ALP
			/NQVSPPQPM*GAEENGDQRGGKEEAGEELHRSSSGLTAAPGF?
!		į	EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS
		İ	MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS
1	1	ļ	SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD
İ	1	ļ	PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS
1	İ	1	TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV
1			*LPAPLSQPPGATEPOVRACGMAPPSPGTSGRLVANGRHPGPQV
[i		AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH*
}			WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR
	~— 		FQGGGGG

SEQ	Predicted	Predicted end	l'mino poid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6681	1169	511	INYIYYNQQQRAFHELK\EKLMSAPALGLPDLTKLFTLHVSERE
	į		KMTVGVLTQTVGPWSRPGAYLSKOLDGVSKGWPPCPPAI.AATAI.
	1		LAQEADELTLRONLNRKSPHA\VVTLINTKGHH*I.TNADI.TDVO
1	ı		TLLCENPHKTIEVSNT/LNPATLLLVTRSpvkHNCLEVLDSvvc
1	1		SRPNLRDHP*TSVDWELYVDGSGFANPCKVTLKKETSPAPVTPR
6682			S
0002	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD
		1	VRRRIELIQDFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT
			YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIEFHSQSG
ŀ			FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN
J	1		PLOTDAAENNVCDINSVHGLFATGTIEGRVECWDPRTRNRVGLL
Į	1		D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGQVLLY
1	.		DLRSDKPLLVKDHQYGLPIKSVHFQDSLDLILSADSRIVKMWNK
J	(NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL GPAPRWCSFLDNLTEELEENPESNE
6683	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD
	1		VRRRIELIODFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT
			YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIBFHSQSG
1	1 1		PYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN
	į j		PLQTDAAENNVCDINSVHGLFATGTIEGRVECWDPRTPNPVGL.
1			D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGOVT.v
			DLRSDKPLLVKDHQYGLPIKSVHFODSLDLILSADSRIVKMWNK
1	1		NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL
6684	111	F07	GPAPRWCSFLDNLTEELEENPESNE
""	1 1	527	GLRGGTSRGRAGREPEFAAGVLCVVAGFCQSPCPPGGRGREAPA
1	1		PP\SGRRHA*RPA*WLGGPGGDSGREEGGS/GELQRAMESKMG
	l i		ELPLDINIQEPRWDQSTFLGRARHFFTVTDPRNLLLSGAQLEAS RNIVONYR
6685	258	1473	KLLGDNFEGFCNKFELSDSENGSNS*QSPL\FDRLFDPDPQKVL
	1		QGVIDMKNAVIGNNKQKANLIVIGAVPRLLYLLQQETSSTELKT
1	1 1	Í	ECAVVLGSLAMGTENNVKSLLDCHIIPALLQGLLSPDLKFIEAC
1	1 1		LRCLRTIFTSPVTPEELLYTDATVIPHLMALLSRSRYTQEYICQ
			IFSHCCKGPDHQTILFNHGAVONIAHLLTSLSYKVRMOALKCES
İ	1		VLAFENPQVSMTLVNVLVDGELLPOIFVKMLORDKPTEMOLTSA
1	1		KCLTYMCRAGAIRTDDNCIVLKTLPCLVRMCSKERIJEERVEGA
[1		ETLAYLIEPDVELQRIASITDHLIAMLADYFKYPSSVSAITDIK
	1		RLDHDLKHAHELRQAAFKLYASLGANDEDIRKKVSLGEGRPPVI.
6686	310	927	TASRQGVTST
1			DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY
1	1	İ	QLFKPSLISWLEQEESRTVQRGDFQASEWKVQLKTKELALQQDV LGEPTSSGIOMIGSINGGEVERVYCGGRVGGRVGA
		[LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDV
			VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT
6687	181	915	EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST
	1		IGETSNRSRDRDRYRRRNSRSRSPGRQCRHRSRSWDRRHGSESR
			SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR
]	j	IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGTAVVEFCETOSV
ĺ	1		PLAIGLTGQRLLGVPIIVQASQAEKNRLAAMANNLQKGNGGPMR
6600			LYVGSLHFNITEDMLRGIFEPFGKV
6688	1025	1	AEVPNYPRVFHKCPDSCWRFKFQPIOLOPYILLSFSSEKPPISF
] 1		SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD
		√ .	LPSDGGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS
]	1 :	STSVGSVVAAFTSSSSSSTNRDVAGLDFSTVITSVSGSLVPSRR
		1	VAVICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSSFSTC
		1	TMSELEELFSLFSPAPLLSKLFTSSGSIAICCODSGPSDTGRIS
ئـــــــــــــــــــــــــــــــــــــ			VCQLWLADSDTGKLSDCQEVVTVGDSGGLTCPELSLGRM*MSLL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
]	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	ì	\=possible nucleotide insertion)
			SSAVIPGYSSSSDSRLNTVPTVDLLCPFOTKSST
6689	640	1299	SSSASYATSATSISDTAFSGSLKLKHGLLSALDSSSRTS*STSS
1			AEDSTFRICSPSVSDTSSDSSGSKDNVLILFSKVST*scretes
			FFSDSISFCFSSSSFCKR*FVSSKVSONALLSSRLSNGPGGSSK
1			QRNSLTARQLAMSL*ATKF*RNACNPNCLSSKKSAT.*I.SI.NOPE
6690			GGSASRKPGNISFNSQKCSALSYCCNFVIKPREVSVSSENYPAF
8630	1	442	GTRGKMAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGOGP
		}	QQVGAGQTFEYLKREHSLSKPYOGVGTGSSSI,WNI,MGNAMUMTO
			YIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKIHGOGKKNL\H
6691	287		GDGLAIWYTKDRMQP
3051	287	1401	LKTETSEEKARRYKDRPSQLNAVFQEQKKMIQAQESITLEDVAV
1			DFTWEEWQLLGAAQKDLYRDVMLENYSNLVAVGYOASKPDALEK
1	ĺ		LEQGEQLWTIEDGIHSGACSDIWKVDHVLERLOSESIANDREDC
Į.			HEHDAFENIVHCSKSQFLLGQNHDIFDLRGKSLKSNLTLVNQSK
1			GYEIKNSVEFTGNGDSFLHANHERLHTAIKFPASQKLISTKSQF
1			ISPKHQKTRKLEKHHVCSECGKAFIKKSWLTDHQVMHTGEKPHR
			CSLCEKAFSRKFMLTEHQRTHTGEKPYECPECGKAFLKKSRLNI
			HQKTHTGEKPYICSECGKGFIQKGNLIVHQRIHTGEKPYICNEC /GKGFIQKTCLIAHQRFHTER
6692	178	939	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCQVE
			RQEGHSQGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV
			DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL
	,		IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL
			DPSDISESLIDKCLYTNRSPHPDILIRTSGEVPLSDELLWOTTEN
6693			SCLVFQPVLWPEYTFWNLFEAILOFOMNHSVLOK
6693	178	939	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCOVE
1			RQEGHSQGFNKLAETLRWCLNLGILEVTVYAFSTENERDSKSBV
1		1	DGLMDLARQKFSRLMEEKEKLOKHGVCIRVLGDLHLLDLDLOFL
1 1			IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL
1	ł		DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH
6694	292	813	SCLVFQPVLWPEYTFWNLFEAILQFQMNHSVLQK
1 1		813	SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAAESRQHELPVR
		1	EVHSLGQILPQDGLTAEAGPPEAQDPWGSPGISLPAAHIGFAAA
]		1	LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
6695	292	813	SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAAESRQHELPVR
1 1			EVHSLGQILPQDGLTAEAGPPEAQDPWGSPGISLPAAHIGFAAA
1			LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV
			NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
6696	1	782	PRVRGRVGERWAPLSVPAAMSSEMEPLLLAWSYFRRRKFQLCAD
!		1	LCTQMLEKSPYDQAAWILKARALTEMVYIDEIDVDQEGIAEMML
]		1	DENAIAQVPRPGTSLKLPGTNQTGGPSOAVRPITOAGRPTTGFL
	İ		RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGREVPLGTAGMI
1			TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALD
6697			LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYREAEKOTKSS
1 600/	3	782	PPLFLRRLNSRALRPGSRKVMAVVPASLSGODVGSFAVITTKDP
	1	1	IPQILTKVIDTLHRHKSEFFEKHGEEGVEAEKKAISLLSKI.PMF
!		1	LQTDKPFIPLVEKFVDTDIWNOYLEYOOSLLNESDGKSPWFYSD
			WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQES
			IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL
6698	668	754	SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK
6699	325	754	VGSCACAGSCKCKECKCTSCKKSECRAFP
	1	492	EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV
1	ļ	;	LLGKRKGSVGAGSFQLPGGHLEFGETWEECAQRETWEEAALHLK
			NVHFASVVNSFIEKENYHYVTILMKGEVDVTHDSEPKNVEPEKN

S	EQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	ID	beginning	nucleotide	(A-Alanine, C=Cysteine, D=Aspartic Acid, E=
N	0:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ĺ		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		to first	amino acid	P-Proline O-Cluberine, N=Asparagine,
1		amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
		residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ı		amino acid	1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į		sequence	sequence	Codon, /=possible nucleotide deletion,
		seduence		\=possible nucleotide insertion)
	100	1000		ESKRIIYNHAFFFQESKWSGGILQ
"	700	1098	1392	TQCWRSSTPGMRTHFRTQP/RLECGQGFSQQENGHCMDTNECIQ
				FPFVCPRDKPVCVNTYGSYRCRTNKKCSRGYEPNEDGTACVERT
<u></u>				LLLGLCNLLGK
67	01	2	1485	AAAGPRTRVRRAAAFEGQPSPSPGLGPTSDKAAAPRTPKRRRLW
1			İ	RQRQ/HPAMLCYVTRPDAVLMEVEVEAKANGEDCLNOVCRRLGT
ļ				IEVDYFGLQFTGSKGESLWLNLRNRISQQMDGLAPYRLKLRVKF
ŀ				FVEPHLILQEQTRHIFFLHIKEALLAGHLLCSPEQAVELSALLA
ł	į			QTKFGDYNONTAKYNYEELCAKELSSATLNSIVAKHKELEGTSQ
-	- 1			ASAEYQVLQIVSAMENYGIEWHSVRDSEGQKLLIGVGPEGISIC
1	l			KDDFSPINRIAYPVVQMATQSGKNVYLTVTKESGNSIVLLFKMI
1	1			STRAASGLYRAITETHAFYRCDTVTSAVMMQYSRDLKGHLASLF
1	ı	Î		LNENINLGKKYVFDIKRTSKEVYDHARRALYNAGVVDLVSRNNQ
1	ł			SPSHSPLKSSESSMNCSSCEGLSCQQTRVLQEKLRKLKEAMLCM
	ı	ļ		VCCEBEINSTFCPCGHTVCCESCAAQLQVGESAAHFCLQPHLSL
	- 1			LLTGSRSQVLAR
67	02	397	1971	PLAKFLKLDLVNVLCLPMEDVFLFYRTCFCSMGLGSSCHLSLPK
	- 1		· · · · ·	RAEALLCSRKATVVRDLVAVRMAEEQEFTQLCKLPAQPSHPHCV
	- 1			NNTYRSAQHSQALLRGLLALRDSGILFDVVLVVEGRHIEAHRIL
	ı			LAASCDYFKGMFAGGLKEMEQEEVLIHGVSYNAMCQILHFIYTS
-	F		•	ELELSLSNVQETLVAACQLQIPEIIHFCCDFLMSWVDEENILDV
1				YRLAELFDLSRLTEQLDTYILKNFVAFSRTDKYRQLPLEKVYSL
i	- 1			LSSNRLEVSCETEVYEGALLYHYSLEQVQADQISLHEPPKLLET
1	- 1			VPPDI MENEUT ORI UPVI DECAY DECAY COLLARIZATION OF THE
1				VRFPLMEAEVLQRLHDKLDPSPLRDTVASALMYHRNESLQPSLQ
				SPOTELRSDFOCVVGFGGIHSTPS\MSSATRPKYLNPLLGEWKH
	ľ			FTASLAPRMSNQGIAVLNNFVYLIGGDNNVQGFRAESRCWRYDP
1	- 1	i		RHNRWFQIQSLQQEHADLSVCVVGRYIYAVAGRDYHNDLNAVER
670	03	45	1244	YDPATNSWAYVAPLKREVYAHAGATLEGKMYITCGRKGRIT
,	1		1244	GVGPRAAMPLELELCPGRWVGGQHPCFIIAEIGQNHQGDLDVA
ł	ĺ	l	•	KRMIRMAKECGADCAKFQKSELEFKFNRKALERPYTSKHSWGKT
1	1	ł		YGEHKRHLEFSHDQYRELQRYAEEVGIFFTASGMDEMAVEFLHE
i	- 1			LNVPFFKVGSGDTNNFPYLEKTAK/TRGWHSVLRDVCGVQLNDE
1	- 1			TSSWDVLGRVRTSKEKVLMVLVLDYSGRPMVISSGMQSMDTMKQ
				VYQIVKPLNPNFCFLQCTSAYPLQPEDVNLRVISEYQKLFPDIP
				IGYSGHETGIAISVAAVALGAKVLERHITLDKTWKGSDHSASLE
1			ĺ	PGELAELVRSVRLVERALGSPTKQLLPCEMACNEKLGKSVVAKV
1	J			KIPEGTILTMDMLTVKVGEPKGYPPEDIFNLVGKKVLVTVEEDD
670		82	1000	TIMEE
""	· *	02	1007	TMNTRNRVVNSGLGASPASRPTRDPQDPSGRQGBLSPVEDQREG
	- 1	1		LEAAPKGPSRESVVHAGQRRTSAYTLIAPNINRRNEIQRIAEQE
		ļ	. [LANLEKWKEQNRAKPVHLVPRRLGGSQSETEVRQKQQLQLMQSK
	ı	ļ.	ĺ	YKQKLKREESVRIKKEAEEAELQKMKAIQREKSNKLEEKKRLQE
				NLRREAFREHQQYKTAEFL/RQTEHRIARQKCLSKCCLWPTILN
İ	ŀ			MGQKLGLQ\DSLKAEENRKLQKMKDEQHQKSELLELKRQQQEQE
ı	- 1	1	ì	RAKIHQTEHRRVNNAFLDRLQGKSQPGGLEQSGGCWNMNSGNSW
635	-			GI
670	3	2	786	RLCRNSARVPCGWSASRSLGEGAGFIGPLRGPHPRAGGTGTSFT
1	ŀ		1	SYKRKGGIMSTIAAFYGGKSILITVATGFLGKELMEKLFRTSPD
1	1		i	LKVIYILVRPKAGQTLQHRVFQILDSKLFEKVIEVRPNVHEKIR
	- 1		ļ	AIYADLNQNDFAISKEDMQELLSCTNIIFHCAATVRFDDTLRHA
		r ·		TOTAL TOTAL
		(J	VQLNVTATROLLLMASOMPKLEAFIHISTAYSNCNTKHIDEVITY (
			1	VQLNVTATRQLLLMASQMPKLEAFIHISTAYSNCNLKHIDEVIY PCPVEPKKIIDSLEW\LDDAIIDEITPKIIRDWPNIYTYTY
670	6	130	53)	PCPVEPKKIIDSLEW\LDDAIIDEITPKLIRDWPNIYTYTK
670	6	130	531	PCPVEPKKIIDSLEW\LDDAIIDEITPKLIRDWPNIYTYTK FTHSSSSHSQEMLGKLNMLRNDGHFCDITIRVQDKIFRAHKVVL
670	6	130		PCPVEPKKIIDSLEW\LDDAIIDEITPKLIRDWPNIYTYK FTHSSSSHSQEMLGKLNMLRNDGHFCDITIRVQDKIFRAHKVVL AACSDFFRTKLVGQAEDENKNVLDLHHVTVTGFIPLLEYAYTAT
670	6	130		PCPVEPKKIIDSLEW\LDDAIIDEITPKLIRDWPNIYTYTK FTHSSSSHSQEMLGKLNMLRNDGHFCDITIRVQDKIFRAHKVVL

SEQ	Predicted	Predicted end	Amino acid coment
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ì	residue of	amino acid	W-Trimbanhan V Course
İ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- [sequence	Dequence	Codon, /=possible nucleotide deletion,
6707	2233	1343	\=possible nucleotide insertion)
ı		1747	YWSGIGYELQHFHWRKFHFEKKGPPSTCQBRLYESRSRWPCIS*
	i		GMVVVGWTAVNGSW*GGQLRCVCVCTSHSSDSTRSSQRASKCHS
- i	l		FFILSQ*KT*SSWENWVFAKYSRIYSYGHSCSKGRGD*DFK*NV
	İ		SQAR*SRFCGLCNPCGHCGLDINLRGGSSPWTDKHSCVHNNLLC
	-	1	NRRVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEH
)			TD*LPK*GPGYIOHFHCDSNILCILYNISFNLFSYSF*GVARYA
6708	115		C*RCHWYFEWLLYNHCGDILVACL*RRQL*SSQ
0,00	113.	1729	TVGSWSRSGRSPPVGRQLLLTGRGAQAAGSPQGGMALQVELVPT
1	1	1	GEIIRVVHPHRPCKLALGSDGVRVTMESALTARDRVGVODFVLL
1	1	į	ENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVNPVRDLOTVSD
1	1		QHMERYRGVSFYEEPPHLLAVADTVYRALRTERRDOAVMTSVFS
1	1		GAGKTDATKRLLQLYAETCPAPORGGAVRDRLLOSNEVI.FARGN
j	}		AKTLRNDNSSRFGKYMDVQFDFKGAPVGGHILSYLLEKSPVVHO
İ	1		NHGERNFHIFYQLLEGGEEETLRRLGLERNPOSYLVIJVKGOCAK
İ			VSSINDKSDWKVVRKALTVIDFTEDEVEDLLSIAASVIHLGNIH
]			FAANEESNAQVTTENQLKYLTRLLSVEGSTLREALTHRKITAKC
-}			EELLSPINLEQAAYARDALAKAVYSRTFTWLVGKTNRSLASKDV
	1	1	ESPSWRSTTVLGLLDIYGFEVFOHNSFEOFCINYCNEKLOOLET
ł	1		ELTLKSEQEEYEAEGIAWEPVQYFNNKIICDLVEEKFKGII\SI
6709			LDE\ECLRPGE .
1 8,09	3	894	PPHEHLFPSGERGPFSFLVSRRGLGPGKMGKKGKKEKKGRGAEK
1	1 1		TAAKMEKKVSKRSRKEEEDLEALIAHFOTLDAKRTOTVELPCPD
1	1 1		PSPRINASISVHPEKDELILFGGEYFNGOKTFLYNFI,VVVNTEK
1			DTWTKVDIPSPPPRRCAHQAVVVPOGGGOLWVFGGEFASPNGFO
1	<u> </u>		FYHYKDLWVLHLATKTWEQVKSTGGPSGRSGHRMVAWKROLLLE
j	ł i		GGFHESTRDYIYYNDVYAFNLDTFTWSKLSPSGTGPTPRSGCO\
6710	158		IPSLPRAASSVYGGYSKQRVKKDVDKGTRHSDMF
1 0720	136	980	RHKMTNYRVESSSGRAARKMRLALMGPAFIAAIGYIDPGNFATN
	l i		IQAGASFGYQLLWVVVWANLMAMLIQILSAKLGIATGKNLAEQI
	1		RDHYPRPVVWFYWVQABIIAMATDLAEFIGAAIGFKLILGVSLL
1 .]		QGAVLTGIATFLILMLQRRGQKPLEKVIGGLLLFVAAAYTVET.T
	!		FSQPNLAQLGKGMVIPSLPTSEAVFLAAGVL\GATIMPHVI/YI
1 :			WHSSLTQHLHGGSRQQRYSATKWDVAIAMTIAGFVNLAIMATAA
6711	3	246	SELNFYGHTGVA
	,	347	VTECKTMTCKMSQLERNI*TMINTLHHYSVKLGHPDTLIHGEFK
1		i	ELVRTDLHNILMKENKNDQAI*HIMEDLDTNAHMQIIFKELIML
6712	118	578	MAMLTW3YHDNMHDADYGPGQQHRPG
[[3,0	PHGQKRTRYPQVRAPGQQPQAQLAMALCLKQVFAKDKTFRPRKR
1 1	1	•	FEPGTQRFELYKKAQASLKSGLDLRSVVRLPPGENIDDWIAVHV
!!	1		VDFFNRINLIYGTMAERCS*TSCPVMAGGPRYEYRWQDERQYRR
6713	2485	3	PAKLSAPRYMALLMDWIESLI
l i		-	QARGSDSEDGEFEIQAEDDARARKLGPGRPLPTFPTSECTSDVE
1	i		PDTREMVRAQNKKKKKSGGFQSMGLSYPVFKGIMKKGYKVPTPI
1			QRKTIPVILDGKDVVAMARTGSGKTACFLLPMFERLKTHSAQTG
) J			ARALILSPTRELALQTLKFTKELGKFTGLKTALILGGDRMEDQF
	[1	AALHENPDIIIATPGRLVHVAVEMSLKLQSVEYVVFDEADRLFE
		}	MGFAEQLQEILARI.PGGHQTVLFSATLPKLLVEFARAGLTEPVL
]	IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV
			VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL
]			GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA
1	j	1	RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA
		į	GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ
- 1	1	İ	YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRFEEEELQRLRL
1	1	ł	VDS1KNYRSRAT1FEINASSRDLCSQVMRAKRQKDRKA1ARFQQ
į			GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEERAGESVEDIFS
			EVVGRKRQRSGPNRGAKRRREEARQRDQEFYIPYRPKDFDSERG

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
i	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
i			LSISGEGGAFEQQAAGAVLDLMGDEAQNLTRGRQQLKWDRKKKR
1]		FVGQSGQEDKKKIKTESGRYISSSYKRDLYQKWKQKQKID*S*L
1	1		GRRRGILTRRPRTEEVGEARPLAQAGCIPGPHAPRHPLQAESA
		<u></u>	LELKTKQQILKQRRRAOKAALSLORWWPOAAT.CDO
6714	169	1416	NNCQELLPPPPAPMAHIPSGGAPAAGAAPMGPOYCUCKUFT.GUS
i			GQNLLDRDVTSKSDPFCVLFTENNGRWIEVDRTETAINNINDAR
1			SKKFVLDYHFEEVQKLKFALFDODKSSMRIDEHDELGOPSCSIC
1			TIVSSKKITRPLLLLNDKPAGKGLITIAAORI,SDNDVITLGIAG
I			RRLDKKDLFGKSDPFLEFYKPGDDGKWMIAHPTEVIKYTI.DDVM
1			KPFTVPLVSLCDGDMEKPIOVMCYDYDNDGGHDFTGFFOTSVSO
1			MCEARDSVPLEFECINPKKORKKNYKNSGITTLRSCKINDDVG
ĺ			FLDYLLGGCQLMFTVGIDFTASNGNPLDPSSLHYTNPMGTNEVI.
J]		SAIWAVGQIIQDYDSDKMFPALGFGAQLPPDWKVSHEFAINFNP
6715	32	493	TNPFCSGVDGIAQAYSACLP
	"2	493	GPAGAESGSLHCLPATVQALAGAAHSPHGGQPPRRGPLIGSGMP
Ī	. 1		GKPXHLGVPNGRMVLAVSDGELSSTTGPQGQGEGRGSSLSIHSL
1]		PSGPSSPFPTEEQPVASWALSFERLLQDPLGLAYFTEFLKKEPS
6716	1	176	AENVTFWKACERFQQIPASDT
	_	1/6	GAGGPAPRSFGSEEPRAALERDKMSARAAAKSTAMEETAIWEQ
6717	115	896	HTVTLHRVSLCCSK
1		050	LFAMSGFENLNTDFYQTSYSIDDQSQQSYDYGGSGGPYSKQYAG
1	i		YDYSQQGRFVPPDMMQPQQPYTGQIYQPTQAYTPASPQPFYGNN
1 :			FEDEPPLLEELGINFDHIWQKTLTVLHPLKVADGSIMNETDLAG
			PMVFCLAFGATLLLAGKIQFGYVYGISAIGCLGMFCLLNIMSMT GVSFGCVASVLGYCLLPMILLSSFAVIFSLQGMVGIILTAGIIG
<u> </u>			WCSFSASKIFISALAMEGQQLLVAYPCALLYGVFALISVF
6718	290	599	KQSSTVPGTILPSLKWHNSGLCKFPETGGKMTTFKEGLTFKDVA
]		VIFTEEELGLLDPVQRNLYQDVMLENFRNLLSVGHHPFKHDVFL
			LEKEKKLDIMKTATQ
6719	1	691	PTRPEEQDREDGKCHKMEMNPISGNLNCDPIAMSQCSSDHGCET
	1		DLDSDDDKIEKPNNFMKDSASQDNGLSRKISRKRVCSSDSDSSL
	1		QVVKKSSKARTGLLRITRRCAATAANKIKI,MSDVEDVSI,RNVUT
ľ			RSKNGRKKPLHLACTTAKKKI.SDCEGSVHCEVDSPAVACEGVDD
			DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK
6720	3		RKSSSVTSSG
0.20	3	822	HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA
1			VPITEKSNPLTQDLDKADAENIVRLLGOCDAEIFOFEGOALSTV
1			QRLYSESILTTMVQVAGKVOEVLKEPDGGLVVI.SGGGTGGDMAR
- 1	1	i	LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG
ı	•		IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP
j			VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE
6721	3	822	
- 1	1		HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA
J			VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY
		ļ	QRLYSESILITMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF
			LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP
1	ſ		VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM
			SVVTLISE SVVTLISE
6722	1		RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE
	1	ľ	LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK
		j	PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGOHHNYQNW
6723	173	659	VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT
1	1	! .	GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL
		1	AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL

Deginning nouleotide location corresponding corresponding to first amino acid residue of acid residue of acid residue of acid residue of acid residue of acid residue of acid residue of acid re	SEQ	Predicted	Predicted end	1 Amilion 12
No:	ID			GOLD SEGMENT CONTAINING SIGNAL SOCIETY
Location Corresponding Lofirst	NO:	nucleotide		Glutamic Acid Fanhancial Acid, E=
amino acid amino acid	1	location		H=Histidine T-Tooleysia M. V.
amino acid residue of amino acid sequence sequence 6724 173 659 VVYVCIARRADRISHAGUPVAVIDIES, VLUKINOWN, *=stop control of control ocid sequence 6724 173 659 VVYVCIARRADRISHAGUPVAVWARKSSPVALKGUVKKOAL ADVENTIARRADRISHAGUPVAVWARKSSPVALKGUVKKOAL ADVENTIARRADRISHAGUPVAVWARKSSPVALKGUVKKOAL ADVENTIARRADRISHAGUPVAVWARKSSPVALKGUVKKOAL ADVENTIARRADRISHAGUPVAVWARKSSPVALKGUVKKOAL ADVENTIARRADRISHAGUPVAVWARKSSPVALKGUVKKOAL ADVENTIARRADRISHAGUPVAVWARKSSPVALKGUVKKOAL ADVENTIARRADRISHAGUPVAVWARKSSPVALKGUVKKOAL ADVENTIARRADRISHAGUPVAVWARKSSPVALKGUVKKOAL ADVENTIARRADRISHAGUPVAVWARKSSPVALKGUVKKOAL ADVENTIARRADRISHAGUPVAVWARKSSPVALKGUVKKOAL ADVENTIARRADRISHAGUPVAVWARKSSPVALKGUVKKOAL ADVENTIARRADRISHAGUPVARVADRISHAGUPVARVATARRADRISHAGUPV		corresponding		LaLeucine Manual
residue of amino acid sequence some properties of amino acid sequence seque			amino acid	Paproline O-Glutomine, Nasparagine,
amino acid sequence codon, /=possible muclectide deletion, /=possible deletion, /=possible muclectide				
Codon, /=possible nuclectide dissertion -possible nuclectide dissertion -possible nuclectide dissertion -possible nuclectide dissertion -possible nuclectide dissertion	1	residue of	amino acid	W=Tryptophan V=Tryptophan V-Try
VPOKELGREIPLE ENGSVERHEIGHEIDEN		amino acid	sequence	Codon. /=possible nucleotide deleti-
6724 173 659 VEVKELGREFLTPREVOSVREHIGHESDNI. VEVKELGREFLTPREVOSVREHIGHESDNI. AERARILARDEGLIFLKEPVGAVVENKSSPYERLKGLUDKIGAN- GNEGRVSVENIKGLLQSAHKESSPPILILSGLVPGSTTLISGRI AERARILARDEGLIFLKEPVGAVVENKSSPYERLKGEALTLSGI VEVKELGREFLTPERVGSVREHLGRESDNI. 6725 356 722 RETPPVLATMODOPTRIGGESDNI. ASRELVDPTDLQALFVOFNDOPTRIGGLRAVEVKSVSVRTLGGE LCSYEKGGROSTILSS DILKLAR PRODLUEVFFV ASRELVDPTDLQALFVOFNDOPTRIGGLRAVEVKSVSVRTLGGE LCSYEKGGROSTILSS DILKLAR PRODLUEVFFV 6726 98 714 HLGWERKIBREKEKETEGRINSLEDTDGKNCKSTILMTINV GULYTYGKGTLKTYDTTLEGIVSKKILCPPADGIFYTDROG LPHVLAFIRNGELLIPEGFRINGLLAGEREFFCLKGLAEVKK REKEQLIPRETTELEITDNHDRSGGIRTFCNAPDTISKIKSRI VAVSKSKLOPFEBFSISSNIJGKYFIK 6727 1 831 FRÖMEDERPTYGRIGFFQKKOPFTFKGFTVINGLSEVK REKEQLIPRETTELEITDNHDRSGGIRTFCNAPDTISKIKSRI VAVSKSKLOPFEBFSISSNIJGKYFIK LAIVSVAVGLIAMTHODPTSKULTYDNSSGFCQGKGTMENENK ROLLAWSVAVGLIAMTHODPTSKULTYDNASSKSROFTVSNEWGLISKERI VALVSVAVGLIAMTHODPTSKULTYDNASSKSROFTVSNEWGLISKERI VALVSVAVGLIAMTHODPTSKULTYDNASSKSROFTVSNEWGLISKERI ROLLAMTIFEDTVSWWMDISLGIAMASSKITUKVGOLGGK ROLLAMTIFEDTVSWWMDISLGIAMASSKITUKVGOLGGK ROLLAMTIFEDTVSWWMDISLGIAMASSKITUKVGOLGGK ROLLAMTHERDTVSWWMDISLGIAMASSKYLDERPTSPRICKTYDDOLGG LLFRODDRIGGLANATHOPISKEMMETFKVLLERPTSPROK ROLLAMATIFEDTVSWWMDISLGIAMASSKYLDERPTSPROKOG VALDAVWARHVAQOGAVAGRAVAGRAVARVELLARTVOFDLAGSV VALDAVAKRDVPCGGROGGCCYPERGGRGQOPOPVGQGVNGDP GLGOFFOLGGRAVAGRAVAGRAVARVELLARTVOFDLAGSV LLAGVKKFDVPCGGROGGGCCYPERGGRGGOPOPVGQGVNGDP GLGOFFOLGGRAVAGRAVAGRAVARVELLARTVOFDLAGSV LLAGVKKFDVPCGGROGGGCGCCYPERGGRGGOPOPVGQGVNGDP GLGOFFOLGGRAVAGRAVARVELARTVORGERGRGGGFORGHVORGGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		sequence	-	\=possible nucleotide insertion\
VCQYCTARMADFGISAGGFVAVWINSSPYBALKGIUDKIGAL GRORGWSUS HIS KQLIQSANHESSPYLIAGSTYLLISAGI ABIARILAPGGLIFLKEPVSTAVDINSKVKTASKLCSALTLSGI VEVKELGREPLITEBVGJUSVEHLGHESGMI ABIARILAPGGLIFLKEPVSTAVDINSKVKTASKLCSALTLSGI VEVKELGREPLITEBVGJUSVEHLGHESGMI GRAVELVIPT DELOALFVQFNOQFFROGRAVEVKSVSTATLCAG ICSYSGKOGMCSIRLSSPILKERPKGLEAREDHAQESLSLVI ASSELVIPT DELOALFVQFNOQFFROGRAVEVKSVSTATLCAG ICSYSGKOGMCSIRLSSPILKERPKGLEAREDHAQESLSLVI ASSELVIPT DELOALFVQFNOQFROGRAVEVKSVSTATLCAG ICSYSGKOGMCSIRLSSPILKERPKGLEDVKGKLGEDVKSTATLCAG ICSYSGKOGMCSIRLSSPILKERPKGLEDVKGKGLGENTLINVG GTLITTCKGTLTKYPPTTLEGUTVMKTLCPTGCKNCKSTIMTLINVG GTLITTCKGTLTKYPPTTLEGUTVMKTLCPTGCKNCKSTIMTLINVG GTLITTCKGTLTKYPPTTLEGUTVMKTLCPTGCKNCKSTIMTLINVG LIFRKINDELBJEGGFFTGLGUTANGTYFIKTSCT LAIVAYVAVGILAMFHOROGUTFYFTGLTGUTVKCKSTIMENTKY VLYFKNIVKASPIVLLEFGCYPTGVTGVKGCFTGNTGVKNENTKY VLYFKNIVKASPIVLLEFGCYPTGVTGVKGCFTGNTGVKNENTKY VLYFYNIVKASPIVLLEFGCTPTGVTGVKGCFTGDTVTLTVLNARSS RAFEYKKGFCVFGFKNKGVAREVLRDGDCFAVLIPSKPLARCT PALIAYKGVLAVGSPTVALRFUTVGTTGTAGGCGTGTVTLPSKPLARCT RAFLAKKGVLAVGSPTVALRFUTVGTTGTAGGCGTGTVTLPSKPLARCT RAFLAKGVLAVGSPTVALRFUTVGTTGTAGGCGTGTGVTCAGAKANGVLER ROLAMFIFEDYTVSWYMDI ISLGIAMAMSLLFILLERPLAGTMA ROLAMFIFEDYTVSWYMDI ISLGIAMAMSLLFILLERPLAGTMA ROLAMFIFEDYTVSWYMDI ISLGIAMAMSLLFILLERPLAGTMA ROLAMFIFEDYTVSWYMDI ISLGIAMAMSLLFILLERPLAGTMANLOGGCGCCCTPKGGGGGGPGPVGDGGGC ROLAMFIFEDYTSWYMDI ISLGIAMAMSLLFILLERPLAGTMANLOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG			<u> </u>	VEVKELOREPLTPREVOSUPERI CHECONI
ARTARILARGEGELFLEREVETAVONNSKYLSKICSALTUSGE ARTARILARGEGELFLEGENALOGASKICSALTUSGE FOR STARILARGEMENGESDIL RETEPPILARGEGELFLEGENALOGASKICSALTUSGE ASSELVDPTDLQALFVQFNDQFPRGQLEAVEVKSVAMTLCAC ICSYBCKGGKCSILIS.RPLKLRDGENALOGASKICHAVEVKSVAMTLCAC ICSYBCKGGKCSILIS.RPLKLRDGENALOGASKICHTINNO GYLYITQKQTITKYPDTLQALFVQFNDQFPRGQLEAVEVKSVAMTLCAC ICSYBCKGGKCSILIS.RPLKLRDGENALOGASKICHTINNO GYLYITQKQTITKYPDTFLEGIVRGKILCPFADGHYPTDRDGI LERHVLAFFLKRGELLFBEGFRENOLLAGASEFFCLKGLAEVEK REKEQLTPRETTFLEITDNHDRSGGLRIFCNAADDFISKIKSRI VUVSKSKBLDGFPERFISISNITJGKYFIK AND VUVSKSKBLDGFPERFISISNITJGKYFIK FRÜMDERPHYYGKHGFPEKVINFTKGFTYTARGETDITGCVFLL LAIVVAVAVGITAMHODPTRAGTITGKFTKATATURKS REFEYKRGFCVGFRKNIKGVARVITYDDSGEFCQXGGTKNENKY VLFFYRIVKCASPLVLLEFOCTFTGITCVEKCPDPVLLTYLINARSS REFEYKRGFCVGFRKNIKGVARVITYDTGGISGFCQXGGTKNENKY LAIVVAVAVGTPTVSWYMDIISLGIAMAMSLLFILLERKLAGING RGMIIMGILVLLGY FCSSMLESLJABSELGINKRHLVQLTGGIASGKSSVIVOFQQLGGA KRIMGHILVLGY FCSSMLESLJABSELGINKRHLVQLTGGIASGKSSVIVOFQQLGGA LIFMOPDROLLANATHIPFIRKEMMEFFKKFLRERFTSPRGKK LAIVVAVAVGTPVSWYMDIISLGIAMAMSLLFILLERFLAGING FCSSMLESLJABSELGINKRHLVQLTGGIASGKSSVIVOFQQLGGA LIFMOPDROLLANATHIPFIRKEMMEFFKKFLRERFTSPRGKK LAGVKKFDVGGGRGCGGCCYPEKGGRGGPPVGGYNGNGF GROGGGRGRGFPADFGRGGGGGCCYPEKGGRGGPPVGGYNGNG GROGGGRGFPADFGRGGNGGRGGAVGEFTVGGFTVGGMG GROGGGRGFPADFGRGGNGGRGGAVGEFTVGGDFTAGGG GROGGGRFPADFGRGNGGNRGGFTVGGDFTAGGSGFTDPDPGG GROGGGRFPADFGRGNGGNRGGFTVGGDFTAGGSGFTDPDPGG GROGGGRFPADFDFTAGGGSGRGCCYPEKGGRGGPVGGPNGGNGG GROGGRGFPADFTHAGTTAGASSCCPSSNLCHERFTSPLKNDBGG GROGGGRFTADFFTAGGSGFTAGTPGGGAG GROGGAAPGFFTAGGGRGGAGGFTAGGGRGGFTAGGAGG GROGGAAPGFTAGGGGGGGGGGGGGTGGFTAGGAGG GROGGAAPGFTAGGGGGGGGGGGGGGGGGGTGGGFTAGGGGGGGGGG	6724	173	659	VCOYCTARMADECT SACOPUARMINACOPURATION
ASIANILRPGGCLFILRSPVSTAVDNISKVRTASKICSALTLIGG FOR THE VEWIELGREPULTEBYGGVSPELIGHESDUN ASSELVDPT PID QALFVORDOFFWGCLASEVRTAGESLSLVI ASSELVDPT PID QALFVORDOFFWGCLASEVRTAGESLSLVI ASSELVDPT PID QALFVORDOFFWGCLASEVRTAGESTANICAE ICSYBERGGRCSIRLS.PLLKURPRKDLVEVFVV ILLEKKERSIRLSEVREKSEEDTDGGRNCKSTLWTLING GYLYITOKOCHKYPDFTLEGIVNGKILCFPDADGIYFILNOG GYLYITOKOCHKYPDFTLEGIVNGKILCFPDADGIYFILNOG GYLYITOKOCHKYPDFTLEGIVNGKILCFPDADGIYFILNOG GYLYITOKOCHKYPDFTLEGIVNGKILCFPDADGIYFILNOG GYLYITOKOCHKYPDFTLEGIVNGKILCFPDADGIYFILNOG RESEDLIAGSESISSNIIGKYFIK FREMEDELFYVGRGFTGFGKYPDFTKGTTURGAEFVS. RESEDLIAGSESISSNIIGKYFIK FREMEDELFYVGRGFTGFGKYPDFTKGTTURGAEFVS. FREMEDELFYVGRGFTGFGKYPDFTKGTTURGAEFVS. RESEDLIAGSELVSHPTKGTTURGAEFTGLGGTAGESKINGVLRG LAIVSYVAVGILAMTHODPRKUIPTUSKGFFCQKOTKINENKE YLFYFNIVKASPLVLLBETGCTPTQTCVEVKFCPDFYLITILNARSS REFEYYKQFCVFGFKNKKVAREVLRDGCFRAVLIFSKLARGCF FRIMAYKGVHAVGSFTYARHUNGGTTYAUGGCFAVLIFSKLARGCF ROLIMARIFEDYTVSWYMDIISIGIAAMSLLFIILLRFLAGIMG ROLIMARIFEDYTVSWYMDIISIGIAAMSLLFIILLRFLAGIMG FRIMAYKGVHAVQGFYDARRINIVENGTGTAGGTASKKSSVIQVFQCGGCA ROLIMARIFEDYTVSWYMDIISIGGTAAGSSIVAVGAAGSKKANGVLRB ROLIMARIFEDYTVSWYMDIISIGIAAMSLLFIILLRFLAGIMG FOSSMLASIASSILSSKMPLUGITGGIAAGSLFRILLLGTVVYCHAGGIRKVLAD LIFROPDRRQLIANITHPEIRKEMKEFFKYFLREPRTSPRGKK HYBSALKEADBAMRDT VOLYGAGGGGRTASKGRQCAYAGSPALKRRILLGTVVVCHAGGIRKVLAD LIFROPDRRQCIAMASSAAGAAGSPALRRRLLLGTVVVCHAGGIRKOLD LIFROPGGGGGRGRPYDCOCKOCYPENGGROOP PVGCGTURGP GLOOFFGLGGKKGDKGRGAGAGVTGDKKGVKGSGFPGADGI GOGGKGEPVALDKREEBDYRGEPGGPGGPGSEGFTGDGGRGAG GUGAFFGLGGKKGDKGRGAGAGVTGDKKGVKGSGFPGADGI GOGGKGAFPVALDKREEBDYRGEPGGPGPGGPGFGGPGGGGGGGGGGGGGGGGGGGGGGG	1			GNEGRVSVENTKOLLOGAUVEGGEDITI GGLUDGGEDI
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6732 102 1205 GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRIHIRQEN LGSIKPSSRSTKATSTTMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRMLEQL LLAEKCHRRTVYFLENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELOEKNKSLELVSFERVAVHFFWEEWODLDD	1	}	j	NDLOVEYGKCOLOMKELMKKEKETOTOMEGA TATENOOT TOTAL
GRWQRRPPPPSPPLWCLQFGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTTMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQOHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVMFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELOEKNKSLELVSFERVAVHFFWERWOLDD	!			LIKTARVEINRKDEET
AQKQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYDDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVMFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSENQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELOEKNKSLELVSFERVAVHFFWEEWODLDD	6732	102	1205	GRWORRPPPPSPPIWCLOPGGGSDDOOT TOT BUGT STORES
GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQFR PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQFR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVMPSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW 6733 613 1311 ESCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELOEKNKSLELVSFERVAVHFFWEEWODLDD	ļ		1	AQRQVCYTAATTOAAAPATRNCI,DDUCCUDDEDDDCITTUTT
GRGRLAFQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PLVAKERSPVGKTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVMPSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHNLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELOEKNKSLELVSFERVAVHFFWEEWODLDD	1	į.	i	LGSIKPSSRSTKATSTIMAGDGRDARAVDRGMCVVVMDDARA
PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLAEKCHRRTVYFLENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELOEKNKSLELVSFERVAVHFFWEEWODLDD	İ		[GRGRLAPQNGGSSDAPAYRTPPSPCCPPFUPFCPPPPPUPCPPPP
POETEEMKTRITIRLOQOHSEQPPLOPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRS IQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLAEKCHRRTVYFLENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELOEKNKSLELVSFERVAVHFFWEEWODLDD	ŀ		ŀ	PLVAKERSPYGKRTRLEEFRSDSAKEFUDPGAVYT DODGEDOS
6734 189 551 SAAMFPVFSGCFQELOEKNKSLELVSFERVAVHFFWEEWODLDD	j			PUBLICEMKTRRTTRLOOOHSEOPPLOPSPVMTRRGLPDSUGGER
6733 613 1311 ESCRQVGMFSEGETEEDDQDSSHSSVTTVKARSRDSDESG KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELOEKNKSLELVSFERVAVHFFWERWODLDD	1	1	ĺ	DEASSQTDLSQTISKKTVRSIOFAPAVSEDIATELDEBET BYDE
6733 613 1311 RSCRQVGMRSRNQGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELOEKNKSLELVSFERVAVHFFWEEWODLDD		ļ		YEATSVQQKVNFSEEGETEEDDODSSHSSVTTVKARSEDECTE
613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELOEKNKSLELVSFERVAVHFFWEEWODLDD				DKTTRSSSQYIESFW
KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELOEKNKSLELVSFERVAVHFFWEEWODLDD	6133	613	1311	RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSISEDAV
QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 551 SAAMFPVFSGCFQELOEKNKSLELVSFERVAVHFFWEEWODLDD	i	ĺ	1	KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLT
VLHRDA LAÇEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 551 SAAMFPVFSGCFQELOEKNKSLELVSFERVAVHFFWERWODLOD		j	1	QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEDEKVID
6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWERWOOD DD	- 1		1	VLHRDA1LAQEKSIGEDVYEKPISELDRLEEKOKETVRPMI.FOI.
6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWREWOOLDD	1	İ	ſ	LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEGERERLKK
SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWERWOOLDD	6734			LLEQEKAYQARKE
AQRTLYRDVMLETYSSLVSLGHCITKPEMIFKI.FOCA PDM TUPE	0/34	189	551	SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWEEWODLOD
				AQRTLYRDVMLETYSSLVSLGHCITKPEMIFKLEQGAEPWIVEE

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	
No:	nucleotide	location	In-mailie, Cecvereine D-Agnageia x-is -
1	location	corresponding	Glucamic Acid, F=Phenvialanine C=Cluster
]	corresponding	to first	n=nistidine, l=Isoleucine K-lycine
[to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- {	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence		Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
6735	280	558	TLNLRLSGGSKKQVFSGICHRSLVELQEVHLV
		320	KSRRAGVTKMSNPFLKQVFNKDKTFRPKRKFEPGTQRFELHKKA
1	1		QASLNAGLDLRLAVQLPPGEDLNDWVAVHVVDFFNRVNLIYGTI XDGCT
6736	195	808	
1			MNYELNFKREMPNIKSLGLTNLNFLLKRLSSVLPLITDYVYFEN
i	1	1	SSSNPYLIRRIEELNKTASGNVEAKVVCFYRRRDISNTLIMLAD
ĺ			KHAKEIEBESETTVEADLTDKQKHQLKHRELFLSRQYESLPATH
			IRGKCSVALLNETESVLSYLDKEDTFFYSLVYDPSLKTLLADKG BIRVGPRYQADIPEMLLEGTFFCVFAVL
6737	150	1209	PVIMPLUEGROTUPEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
		-	PVIMPLHFSPGDIVRPSCCVSSSPKLRRNAHSRLESYRPDTDLS
1	İ		REDTGCNLQHISDRENIDDLNMEFNESDHPRASTIFLSKSQTDV REKRKSLFINHHPPGQIARKYSSCSTIFLDDSTVSQPNLKYTIK
1			CVALAIYYHIKNRDPDGRMLLDIFDENLHPLSKSEVPPDYDKHN
i			PEQKQIYRFVRTLFSAAQLTAECAIVTLVYLERLLTYAEIDICP
ļ			ANWKRIVLGAILLASKVWDDQAVWNVDYCQILKDITVEDMNELE
	i		ROFLELLOFNINVPSSVYAKYYFDLRSLAEANNLSFPLEPLSRE
			RAHKLEAISRLCEDKYKDLRRSARKRSASADNLTLPRWSPAIIS
6738	148	653	CACAEQPARAEVGAATALPVRWASGEMAPSGSLAVPLAVLVLLL
1			WGAPWTHGRRSNVRVITDENWRBLLEGDWMIEFYAPWCPACQNL
1			QPEWESFAEWGEDLEVNIAKVDVTEODGI.copgr.tmpr.pmr.tm
6739			KDGEFRRYQGPRTKKDFINFISDKEWKSIEPVSSWF
0/39	3	631	SWPDMAEEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ
1 1	1		ANAESSSESFISRLLAIVADLYEOFOVGDIVIVOCODUL CANNO
f l			VLAAKSDSWSLANLSSTKELDLSDANPEVTMTMI.DUTVEDER DE
			REDDVFLIELMKLANRFOLOLLRERCEKCUMSLUMUDNGTDEVO
6740			TABELNASTLMNYCAEIIASHWVSEVEGVNKAI.
0,10	3	631	SWPDMAEEEVAKLEKHLMLLROEYVKI.OKKI.ARTEKRCALI. B.B.C.
!			ANKESSESFISRLLAIVADLYEOFOVSDIKTRUGDDUTCALIZE
{			VLAAKSDSWSLANLSSTKELDLSDANDEUTMTMI.BUTVTDELED
l i			REDUVILIELMKLANRFOLOLIRERCEKGIMGLINDENGTERVO
6741	141		TACELNASTLMNYCAEIIASHWVSEVEGUNKAI.
	141	960	PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGVDPTVDFWGA
			ASGICTRIVOHODSOVNALEVTPDRSMIAANOBUSE CYCUTEN
1			IDLNSNNPNPIISYDGVNKNIASVGFHEDGDWMVTGGEDGWADT
- 1	,		WDLKSKNLQCQRIFQVNAPINCVCLHPNOAELTVGDOGGATHTW
- 1		į	DUATUHNEQLIPEPEVSITSAHIDPDASYMAAMICTLUBECGT
			PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP
6742	141	960	
		1	PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA
1	1		HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNDNDITSYDSYNDYYI ARABAVQPVSLGYQHIRM
1	ł	Í	YDLNSNNPNFIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW
- 1			DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
ŀ			PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ
			LIPKTKIP
6743	1	412	MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK
1		İ	ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN
			FAEGQETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL
6744			LQNIR .
6744	95	1343	RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD
1	İ	1:	RQKVSTVGYGMDEVEQDQHBARLKELFDSFDTTGTGSLGQEELT
1	İ		DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILSRT
l	į	 	LSNEEHFQEPDCSLEAQPKYVRGGKRYGRRSLPEFQESVEEFPE
1		3 '	VIVIEPLDEEARPSHIPAGDCSEHWKTORSEEVEARGOLDERNID
			DDLNASQSGSSPPQDWIEEKLQEVCEDLGITRDGHLNRKKLVSI
	-		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
- }	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
ļ	sequence		\=possible nucleotide insertion)
		l	CEQYGLQNVDGEMLEEVFHNLDPDGTMSVEDFFYGLFKNGKSLT
		i	PSASTPYRQLKRHLSMQSFDESGRRTTTSSAMTSTIGFRVFSCL
		ľ	DDGMGHASVERILDTWQEEGIENSQEILKALDFGLDGNINLTEL
6745	1	588	TLALENELLVTKNSIHQACI
	_	300	TFRDQGWAQRRRWLLGCASWESWEAAIAAGPGLPSSTARQQNNP
1			AAGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERRRDP
1	!		ELPVTSFDCAVCLEVLHQPVRTRCGHVFCRSCIATSLKNNKWTC
			PYCRAYLPSEGVPATDVAKRMKSEYKNCAECDTLVCLSEMRAHI
6746	110	492	RTCQKYIDKYGPLQELEETA
1		176	GATGAMAESAPARHRRKRRSTPLTSSTLPSQATEKSSYFQTTEI
1			SLWTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCEKMA VEFGNQLEGKWAVLGTLLQEYGLLQRRLENVENLLRNRN
5747	247	484	EAVTFKDVAVVFTEEELGLLDLAQRKLYRDVMLENFRNLLSVGH
1			QPFHRDTFHFLREEKFWMMDIATQREGNSVYAGVC
6748	201	665	MTTFKEAVTFKDVAVVFTEEELGLLDPAQRKLYRDVMLENFRNL
1			LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGGKIQIEMET
1 1			VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGDVPC
			QIEARLSISXVQQXPYRCNECKQ
6749	95	719	RREVKGGDGVCPRARGSPQSQQFPSCAGGGEGLQQSGEALDGAM
			SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFDKAF
1 1	1		VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAOLCHKAOSVSO
			INHKLEAQLVDLKSELTETQAEKVVLEKEVHDOLLOLHSIOLOL
6750		· · · · · · · · · · · · · · · · · · ·	HAKTGQSADSGTIKAKLSGPSVEELERELKAN
0750	3	428	SCESRRPGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRATMGT
1 1	}		TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQEEAERMFTR
1 1			EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSRRKS
6751	152	1417	RSSQLSSRR
1	702	141/	PTKATEMAGASVKVAVRVRPFNSREMSRDSKCTIQMSGSTTTIV NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGEEML
1 1	1		QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLCEDL
1			FSRINDTINDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE
1 (HPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETS
	1		SRSHAVFNIIFTQKRHDAETNITTEKVSKISLVDLAGSERADST
j j			GAKGTRLKEGANINKSLTTLGKVISALAEMDSGPNKNKKKKKTD
]]		ſ	FIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLR
1			YADRAKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLYAQGLGD
<u> </u>			ITDMTNALVGMSPSSSLSALSSRNV
6752	24	1834	RNCVPPLGCYRSRVKFHSDIKMQYSHHCEHLLERLNKQREAGFL
1 1	1		CDCTIVIGEFQFKAHRNVLASFSEYFGAIYRSTSENNVFLDOSO
1			VKADGFQKLLEFIYTGTLNLDSWNVKEIHOAADYLKVERVVTKC
	}		KIKMEDFAFIANPSSTEISSITGNIELNOOTCLLTLRDYNNREK
1	1	1	SEVSTDLIQANPKOGALAKKSSOTKKKKKAFNSPKTGONKTTOV
1	1	Į	PSDILENASVELFLDANKLPTPVVEQVAQINDNSELELTSVVEN
1	į	į	TFPAQDIVHTVTVKRKRGKSQPNCALKEHSMSNIASVKSPYEAF
			NSGEELDQRYSKAKPMCNTCGKVFSEASSLRRHMRIHKGVKPYV
Į į	i	1	CHLCGKAFTQCNQLKTHVRTHTGEKPYKCELCDKGFAQKCQLVF
1	Ì	j	HSRMHHGEEKPYKCDVCNLQFATSSNLKIHARKHSGEKPYVCDR
[]	ļ	i	CGORFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR
1		ļ	KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED
			HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV
6753	2	1305	TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY
j (-505	VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEBKAS PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG
			SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV
ı		1	AHPGPPPASSQTPAPEHDKAANKMPLAQKPALAPKPTSQTPPAS
	1	Į.	ARPGPPPASSOTPAPEHDKAANKMDI.hovbat.abvbrcompass

SEQ	1 22-32		
ID	Predicted	Predicted end	
NO:	beginning	nucleotide	\A=AIdnine, C=CVSteine
1	nucleotide location	location	Glucamic Acid, Faphenvialaning C.Cl
Į		corresponding	n=nistidine, I=Isoleucine K-Lycine
1	corresponding to first	to first	Laboucine, Mamethionine Naganawagine
1	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
1	residue of	residue of	S=Serine, T=Threonine, V=V=line
1		amino acid	W=Tryptophan, Y=Tyrosine, Y=Unknown + Charles
1	amino acid	sequence	Codon, /=possible nucleotide deletion
 	sequence		\=possible nucleotide insertion)
1			PLSKLSRPYLVELLSRRAGRPDPEPSEPSKEDQESSDRRPPSPF
1	İ		GPEERKGQKRDEEEEATERKPASPPLPATQQEKPSQTPEAGRKE
1	· ·		KPMLQSRHSLDGSKLTEKVETAQPLWITLALQKQKGFREQQATR
1			EERKQAREAKQAEKLSKENVSVSVQPGSSSVSRAGSLHKSTALP
	1		BEARPETAVSRLERREOLKKANTI, DTGVTVPT CVCCD3 3 DT 1777
<u> </u>		<u></u> .	VSKRFSSPDDAPVSSEPAWLALAKRKAKAWSDCPLIIK
6754	2	413	FVRRRRRLGGPEVNTMSSLHKSRIADFQDVLKEPSIALEKLRE
Ì	1		LSFSGIPCEGGLRCLCWKILLNYLPLERASWTSILAKQRELYAQ
	1	i	PLREMIIQPGIAKANMGVSREDVTFEDHPLNPNPDSRWNTYFKD
			NEVLL
6755	298	1343	PGLQLQVALEADWFLDMPGGRRGPSRQQLSRSALPSLQTLVGGG
			CGNGTGLRNRNGSAIGLPVPPITALITPGPVRHCQIPDLPVDGS
	1		LLFEFLFFIYLLVALFIQYINIYKTVWWYPYNHPASCTSLNFHL
			IDYHLAAFITVMLARRLVWALISEATKAGAASMIHYMVLISARL
ĺ	[VLTTLCGWVLCWTLVNLFRSHSVLNLLFLGYPFGVYVPLCCFHQ
	i I		DSRAHLLLTDYNYVVQHEAVEESASTVGGLAKSKDFLSLLLESL
	1		KEQFNNATPIPTHSCPLSPDLIRNEVECLKADFNHRIKEVLFNS
			LFSAYYVAFLPLCFVKVSGYLTFMCFLDLCVNYINWVFLV
6756	180	754	IERALGSLPLSIPVSWGSLRTLKYQQQPLRPKVLLCQTRVQCHD
]		LRSLQPQPPGLKQSFCLRVLGLQTGATTPGLRDLTCKELIILTE
	1		REAQKRKKRKEKESGMALTQGPLTFRDVAIEFSQEEWKSLDPVQ
			KALYWDVMLENYRNLVFLGKDNFALEVKICPRVFLYFLCCLSWE
			PFHYLTETEALLTHK
6757	2	459	NSRVEAPEAHSRESQGSDAMRKHLSWWWLATVCMLLFSHLSAVQ
	!		TRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRKLDID
	· ·		FGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQ
			AANQGEFQKPDNKLHQQVLW
6758	1	1008	ASGPELPGRRFRDRAPWLPARLLRGVLAVWVSLSALGPGSFCRR
ı			RVPSLAQLGHSEAAPSPDDVRWSRVPDRCPEERDRAWPPPPPPPS
			LPPSFRRNMANNSPALTGNSQPQHQAAAAAAQQQQQCGGGGATK
1	1	}	PAVSGKQGNVLPLWGNEKTMNLNPMILTNILSSPYFKVQLYELK
1	1		TYHEVVDEIYFKVTHVEPWEKGSRKTAGQTGMCGGVRGVGTGGI
	[VSTAFCLLYKLFTLKLTRKQVMGLITHTDSPYIRALGFMYIRYT
J	1	İ	QPPTDLWDWFESFLDDEEDLDVKAGGGCVMTIGBMLRSFLTKLE
		1	WFSTLFPRIPVPVQKNIDQQIKTRPRKI
6759	1	513	RKHNFHSLDGTSTRAFHPQTGLPLLSSPVPQRKTQSGCFDLDSS
ŀ		i	LLHLKSFSSRSPRPCLNIEDDPDIHEKPFLSSSAPPITSLSLLG
1		İ	NFEESVLNYRFDPLGIVDGFTAEVGASGAFCPTHLTLPVEVSFY
		ļ	SVSDDNAPSPYMGVITLESLGKRGYRVPPSGTIQVVCVL
6760	239	606	VLSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGIT
1	1		AMSVKEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLE
		İ	VLESQLSEGSQKHASLQKSIEKAKIGRCETEERT
6761	29	1733	ERTLRGLREVAAPSDVADAAVSRGRCCCCLHCTQTQVAQDCPS
- 1	į.	İ	SSSSVQRCELSLFQSLHTMTSKKLVNSVAGCADDALAGLVACNP
	1		NLOLLOGUPUAL BEDI DEL VODULLA GEGENDALAGLVACNP
1	1] '	NLQLLQGHRVALRSDLDSLKGRVALLSGGGSGHEPAHAGFIGKG
1	1	1.	MLTGVIAGAVFTSPAVGSILAAIRAVAQAGTVGTLLIVKNYTGD
	İ] :	RLNFGLAREQARAEGIPVEMVVIGDDSAFTVLKKAGRRGLCGTV
		[]	LIHKVAGALAEAGVGLEEIAKQVNVVTKAMGTLGVSLSSCSVPG
J	. 1] ;	SKPTFELSADEVELGLGIHGEAGVRRIKMATADEIVKLMLDHMT
- 1		1;	NTTNASHVPVQPGSSVVMMVNNLGGLSFLELGIIADATVRSLEG
[}	',	RGVKIARALVGTFMSALEMPGISLTLLLVDEPLLKLIDAETTAA
1	1	1.	AWPNVAAVSITGRKRSRVAPAEPQEAPDSTAAGGSASKRMALVL
		f 1	SKVCSTLLGLEEHLNALDRAAGDGDCGTTHSRAARA TOEWLYEG
i	J	! •	DDA CDAOLT COM COM COM COM COM COM COM COM COM COM
		1 4	PPPASPAQLLSKLSVLLLEKMGGSSGALYGLFLTAAAQPLKAKT SLPAWSAAMDAGLEAMQKYGKAAPGDRTMLDSLWAAGQRL

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- }	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
6762	3	613	ASTISWRLCVAGAEARRPVPVAGERAGGGAMWFMYLLSWLSLFI
	_	1	QVAFITLAVAAGLYYLAELIEEYTVATSRIIKYMIWFSTAVLIG
ł			LYVFERFPTSMIGVGLFTNLVYFGLLQTFPFIMLTSPNFILSCG
Į.			LIGHTLY A ECCENTRICATED STATES
1	}		LVVVNHYLAFQFFABEYYPFSEVLAYFTFCLWIIPFAFFVSLSA
6763	2	760	GENVLPSTMQPGDDVVSNYFTKGKRGK
'	_	, 00	SGPDFPGRRFRGCCCVRPPAGAGMELGGHWDMNSAPRLVSETAE
	ļ.		RKQEQKTGTEAEAADSGAVGARRFLLCLYLGGFLDLFGVSMVVP
			LLSLHVKSLGASPTVAGIVGSSYGILQLFSSTLVGCWSDVVGRR
			SSLLACILLSALGYLLLGAATNVFLFVLARVPAGIFKHTLSISR
1	1		ALLSDVVPEKERPLVIGHFNTASGVGFILGPVVGGYITELEDGF
6764	80	420	YLTAFICFLVFILNAGLVWFFPRREAKPGSTE
""	60	438	LKKMDTMMLSVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFR
1			KKWQRTDHBLGKYKDLLMKAETERSALDVKLKHARNQVDVEIKR
6765	3		RQRAEADCEKLERQIQLIREMLMCDTSGSIQ
0,05] 3	550	ARYSRVDHFCRRCRAVARAPRFLLQFPSGPSRHFLAACVARWL
1	ſ		RGSVLVSEALSGSAMDGIVTEVAVGVKRGSDELLSGSVLSSPNS
1			NMSSMVVTANGNDSKKFKGEDKMDGAPSRVLHIRKLPGEVTETE
· I			VIALGLPFGKVTNILMLKGKNQAFLELATERAAITNGNYYSAVT
6766	1		PHLRNQ
0,00	,	1287	EGGSFKASLTWLWPLGEMKLHCEVEVISRHLPALGLRNRGKGVR
			AVLSLCQQTSRSQPPVRAFLLISTLKDKRGTRYELRENIEQFFT
i i			KFVDEGKATVRLKEPPVDICLSKANSSSLKGFLSAMRLAHRGCN
1			VDTPVSTLTPVKTSEFENFKTKMVITSKKDYPLSKNFPYSLEHL
			QTSYCGLVRVDMRMLCLKSLRKLDLSHNHIKKLPATIGDLIHLQ
		•	ELNLNDNHLESFSVALCHSTLQKSLWSLDLSKNKIKALPVQFCQ
1			LQELKNLKLDDNELIQFPCKIGQLINLRFLSAARNKLPFLPSEF
]			RNLSLEYLDLFGNTFEQPKVLPVIKLQAPLTLLESSARTILHNR
1 1			IPYGSHIIPFHLCQDLDTAKICVCGRFCLNSFIQGTTTMNLHSV
6767	336	919	AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI
"""	330	313	APMICLCSSDLQFRYKEAFLRDRGLQIGYCSVDDDPRMKHFLMV
1 1			GRLQSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY
	J		RQPLPQPTCDPEQLGLRHAQXAHQLQSDVKYKSDLNLTRGVGWT
1 1	i		PPGSYKVEMARRAAELANARGLGLQGAYRGAEAVEAGDHQSGEV
6768	2	363	NPDATEILHVKKKKALLL
1 0,00	2 1	363	PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE
1 1	1		LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV
6769	284	396	ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL
6770			MSTPDFSTAENNQELANEVSCLKAMLTLMLQAMGQAD
""	1	397	QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK
] [j	į	ITLNMGVGEAIADKKLLDNAAADLAAISGQKPLITKARKSVAGF
6771			KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS
["'']	3	378	APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR
			WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM
			QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG
6772	1	1400	AAAFLQGMTVNGFINTVITSL\ERRYDLHSYOSGLIASSYDIAA
] []		CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG
	1		P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL
1	1	ł	HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY
1 1	1	ļ	LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT
1	ļ	1	AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT
1 1		1	IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES
[[QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK
		ŀ	FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL
	1	ĺ	TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG
L		ļ	QKVYRDCSCIPQNLSSGFGHATAGKCTST

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
No:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ı	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- }	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
i	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	-oquonoc	Codon, /=possible nucleotide deletion,
6773	1	630	\=possible nucleotide insertion)
1	1		PWEAPKEHKYKAEEHTVVLTVTGEPCHFPFQYHRQLYHKCTHKG
1	•		RPGPQPWCATTPNFDQDQRWGYCLEPKKVKDHCSKHSPCQKGGT
			CVNMPSGPHCLCPQHLTGNHCQKEKCFEPQLLRFFHKNEIWYRT
L	1		EQAAVARCQCKGPDAHCQRLASQACRTNPCLHGGRCLEVEGHRL CHCPVGYTGPFCDVGE*GSGASRRPAPRWDGLAR
6774	146	389	LTELSDQQYFLFFILSS/WVPTFLSMDVDGRVIKADSFSKIISS
	1		GLRIGFLTGPKPLIERVILHIQVSTLHPSTFNQLMISQ
6775	104	614	TCPSQLRVLTARGGRAPSPQLWTLVLALIEEKWRSHRILRMNS
ł	ì		GRPETMENLPALYTIFQGEVAMVTDYGAFIKIPGCRKQGLVHRT
Ī	ì		HMSSCRVDKPSEIVDVGDKVWVKLIGREMKNDRIKVSLSMKVVN
			QGTGKDLDPNNV\SLSKKRGGGDPSRITLGRRSPLRLS
6776	3	1108	HERHERHEGALSQDALLRISIPLDSNMRPEKCRRFVHPQWQLLH
1			LNGTFPNTSDADMEPCVDGWVYDRISFSSTIVTEWDLVCDSQSL
			TSVAKFVFMAGMMVGGILGGHLSDRFGRRFVLRWCYLQVAIVGT
	}		CAALAPTFLIYCSLRFLSGIAAMSLITNTIMLIAEWATHRFQAM
1			GITLGMCPSGIAFMTLAGLAFAIRDWHILOLWASVDVEVIELTE
ı			SWILLESARWLIINNKPEEGLKELRKAAHRSGMKNADDTITLETT
			KSTMKKELEAAOKKKPFLGERLHMPNTCKPTGT.DDTKDANTA
1			YFGLNLHG/LKHLGNNVFLLOTLFGAV/TPPGOLVT.HIGHWGGG
6777			RVSSRGRVNCLGLFVLOVW
. """	779	63	CFFHGPAWRDCEVRATFAKKQGQSGIISCIAFSPAQPLYACGSY
			GRSLGLYAWDDGSPLALLGGHOGGITHLCPHDDGNDFFSGARVO
1	i		ABLLCWDLRQSGYPLWSLGREVTTNORIVEDI.DDWGOFI.VCCom
		_	SGAVSVWDTDGPGNDGKPEPVLSFLPOKDCTMCVGLUDGLDIIG
1	!	•	HCLPVSVCFLSPTESGGRRRGAGPSLGSPRRHVHLECPLOLIMIC
6778	311		GGGARLQHP**SPRARKGR
'''	311	805	IQSITDESRGSIRRKNPANTRLRLNVP\EETAGDSE/ERSPEEE
	1		VQADPKIRSASPKCPTSSPFPKGRSPFGRGRT\ DDRKTHEUDOD
}			KDKSVAEKN\KGP\SPVSSEGIKDFFSMKDFWFNT.NOCNTDDMT
6779	2	535	T\AVRLNEVIVKKSRDAKLVLLNMPGPPRNRNGDENY
1 -	-	535	RALRRQPRLLAANGIEPESMAISEPIKGSRKPCVNKEELALKKP
1	1		MAKCAWKGPREPPODARAEAESPGGASESDODGGUEGDDVVVAI
1 1	1		AWVSAKNPAPMRKKKKVSLGPVSYVLVDSEDGRKKPVMPKKGPG
1			SRREASDQKAPRGQQPAEATASTSRGPKAKPEGSPRRATNESRK
6780	3	403	
! I	-	403	HEVNDNKPEININLMSPGKEEISYIFEGDPIDTFVALVRVQDKD
, ,	į.	.	SGLNGEIVCKLHGHGHFKLQKTYENNYLILTNATLDREKRSEYS
I		. [LTVIAEDRGTPSLSTVKHFTVQINDINDNPPHFQRSRYEFVISE
6781	1	1269	APTRPVFPTLQDLSSSKEPSNSLNLPHSNELCSSLVHPELSEVS
ļ !		-]	SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT
į l	ļ	l	SAALPTHLQSALMSTVVTMPNAGSKVMVSEGQSAAQSNARPQFI
]]			TPVFINSSSIIQVMKGSQPSTIPAAPLTINSGLMPPSVAVVGPL
[i	HIPQNIKESSAPVPPNALSSSPAPNIOTGPDIJI.ccpampyor p
1		ļ	SPECISSPVVPSHPPVOOVKELNPDEASPOVNTSADONTIDESO
1			STTMVSPLLTNSPGSSGNRRSPVSSSKGKGKVDKIGQILLTKAC
	1		KKVIGSLEKGEEQYGADGETEGOGLDTTAPGI.MGTEOI.GTEI DG
			KTPTPPAPTLLKMTSSPVGPGTASAGPSI.PCGAI.PTSVPSTVPP
6300			DVPSELISAVPTTKSNHGGIASESLAG
6782	3	1327	RKPTVIRIPAKPGKCLHEDPQSPPPLPAEKPIGNTFSTVSGKLS
j		1:	NVERTRNLESNHPGQTGGFVRVPPRLPPRPVNGKTIPTQQPPTK
ŀ	j		VPPERPPPPKLSATRRSNKKLPFNRSSSDMDLQKKQSNLATGLS
	l	1:	KAKSQVFKNQDPVLPPRPKPGHPLYSKYMLSVPHGIANEDIVSQ
i		1.	NPGELSCKRGDVLVMLKOTENNYLRCOKGEDTGDVHLCOMVLTT
			PLDEHLRSRPNPFSPPKAPSHAQKPVDSGAPHAVVLHDFPAEQV

SEQ	Predicted	Predicted end	Amino soid
Œ	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
-	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ļ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	1	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion
	bequence	<u> </u>	\=possible nucleotide insertion\
			DDLNLTSGEIVYLLEKIDTDWYRGNCRNOIGIEDANYUVUTIDI
j			PEGGNGKRECVSSHCVKGSRCVARPEVICEOKDRICECECETTT
1	1		LARI VNEEWARGEVRGRTGIFPLNFVEPVEDVPTSCAMUI CTVI
- 1			PLKTKKEDSGSNSQVNSLPAEWCEALHSFTAETSDDLSFKRGDR
			I
6783	3	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
1	İ	İ	TMPASVVGQRPTIAMVTAINSQKAVLSTDVQNTPVNLQTSSKVT
Í		i	GPGAEAVOTUAKNITUTT OVOATIADORATITATION OF THE OFFICE OFFICE OFFICE OFFICE OFFICE OFFIC
1	1	<u> </u>	GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF
	1		LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL
- 1			PTSQNSIHPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
1			QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN
1			POKLAFMVSLGLVTHDHLEEIQSKRQERKRRTTANPVYSGAVFE
1	1		PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
			SAPUSPENEKTETTFTFPAPVOPVSLPSPTSTDCDTHEDECSIC
			RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPPCODOMI V
1	1		KEEAI PWPGTLAIVHSYIAYKAAKEEEKOKLI KWSSDLKOEPPO
	1 1		LEQKVKQLSNSISKCMEMKNTILAROKEMHSSI.FKVVOT.TDI TIX
İ	i l		GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSOSCT
6784	3		ANCNOGEETK
0.01	1 3 1	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
ł	l		TMPASVVGQRPTIAMVTAINSOKAVLSTDVONTDVMI.OTSSEVUT
			GPGAEAVQIVAKNTVTLOVOATPPOPIKVPOFTDDDDI.TDDDDIE
1	1		DPQVKPKPVAQNNIPIAPAPPPMLAAPOLTORPVMLTKETDTDT
	ļ		PTSQNSIHPVRVVNGQTATIAKTFPMAOLTSIVIATDGTPLACD
	[QIVQLSKPSLEKQTVKSHTETDEKOTESRTITDDAADVDVDCDN
1	• [POKLAFMVSLGLVTHDHLBEIOSKROERKRRTTANDUVCCAUDE
1	l j		PERKASAVTYLNSTMHPGTRKRGRPPKYNAVIGECALTPTEDAG
1	1		SHPDSPENEKTETTFTFPAPVOPVSLPSPTSTDGDTHEDECGUG
1			RASGULMCDTCSRVYHLDCLDPPLKTIPKGMWICPPCODOMI V
	i		ABBAL PWPGTLAIVHSYIAYKAAKEREKOKI J.KWSSDI KOPPPO
1 1			LEUKVKULSNSISKCMEMKNTILAROKEMHSSIEKVKOLTDITTI
1 1	1		GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSQSCT
		_	ANCNOGEETK
6785	1	528	LGNTVLHYCSMYSKPECLKLLLRSKPTVDIVNQAGETALDIAKR
l i	İ		LKATQCEDLLSQAKSGKFNPHVHVEYEWNLRQEEIDESDDDLDD
l i			KPSPVKKERSPRPQSFCHSSSISPQDKLALPGFSTPRDKQRLSY
			GAFTNQIFVSTSTDSPTSPTTEAPPLPPRNAGKGPTGPPITPHR
6786	1820	1397	RSPKVLVLAPTRELANHVSRDFKDI\TRKLTVARFYGGTSYQSQ
1 !		1	INHIRNGIDILVGTPGRIKDHLQSGRLDLSKLRHVVLDEVDQML
1			DIGEAFOVEDITHECKERDADOSGREDESKLRHVVLDEVDQML
1 1	1	1	DLGFAEQVEDIIHESYKTDSEDNPQTLLFSATCPQWVYTVA\KK
1 1	1	1	YMKSRYEQVDLDGKMTQKAATTVEHLAIQCHWSQRPAVIGDVLQ
!	i		VYSGSBGRAIIFCETKKNVTEMAMNPHIKQNAQCLHGDIAQSQR
	į.		EITLKGFREGSPKVLVATNVAARGLDIPEVDLVIQSSPPQDVES
	1		YIHRSGRTGRAGRTGICICFYQPRERGQLRYVEQKAGITFKRVG
1	i		VPSTMDLVKSKSMDAIRSLASVSYAAVDFFRPSAQRLIEEKGAV
1	ļ		DALAAALAHISGASSFEPRSLITSDKGFVTMTLESLEFTODVCC
1		1	AWKELNRKLSSNAVSQITRMCLLKGNMGVCFDVDTTEGEDIONE
		1	WHOSDWILSVPAKLPEIEEYYDGNTSSNSRORSGWSSGPSGPSG
[ļ		RSGGRSGGRSGRQSRQGSRSGSRODGRRRSGNRNESPSGGHVD0
		ŀ	FD*VFYHLVDFLSDFLVDSVYLTGRQIDHLTGLTGLIDHLTSHS
6787	2646		SVWN
0,01	2646	2270	PSSFPKNVPLEELEEPPK*KRSGLGSLTPKSQIQNGP*PQTFFF
J		!	FELGSPSGVISAHCNLRLLGSSDSPAPASRVAGIIGTCHHAWLI
			LVFLVEMGFHHVGQAGLKLLTL\VIHPPWPPKVLGLQT
6788	16	936	GGTVDLR\DMLAVSVLAAVRGGR/ATVRRVRESNVLHEKSKGKT
			REGAEDKMTSGDVLSNRKMFYLLKTAFPSVQINTEEHVD\ELDQ
			TOWNER TOWNEY TOWNEY TO THE PROPERTY OF THE PR

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, TaThreonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		/ \=possible nucleotide insertion\
	İ		EVILWGS*DS*GYPKGK*LLPKEVPSR/RVLLSGLTDIDATION
			FIEDLSK\YVTTMVCVAVNGKPMLGVIHKDESEVTAWAMIDCCS
1			NVKARSSYNEKTPRIVVSRSHSGMVKOVALOTEGNOTTI IDAGG
			AGYKVLALLDVPDKSQEKADLYIHVTYIKKWDICAGNATI.VALG
1			GHMTTLSGEEISYTGSDGIEGGLLASIRMNHOALVRKLPDLEKT
6789	2	678	GHK
1	_	1 0/8	GNGINVLKIAPESAIKFMAYEQIKRLVW**PGDS*GF/YERLVA
			GSLAGAIAQSSIYPMEVLKTRMALRKTGQYSGMLDCARRILARE
			GVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSAD
1			PGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVT MSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLKI
			TLGVOSR
6790	2	4068	APPAGRRRMQAAPRAGCGAALLLWIVSSCLCRAWTAPSTSQKCD
Į.			EPLVSGLPHVAFSSSSSISGSYSPGYAKINKRGGAGGWSPSDSD
			HYQWLQVDFGNRKQISAIATQGRYSSSDWVTQYRMLYSDTGRNW
			APIHQUGNIWAFPGNINSDGVVRHELOHDITADVVDIVDI DUMO
1			EGRIGLRIEVYGCSYWADVINFDGHVVI.PVRFDNKKMVTT VDVIT
			ALMERTSESEGVILHGEGOOGDYITLELKKAKI, VI.SINI GENOL
1			GPLIGHTSVMTGSLLDDHHWHSVVIEROGRSINITIDEGMOUPE [
1			TNGEFDYLDLDYEITFGGIPFSGKPSSSSRKNFKGCMESTNYNG (
1 1			VNITDLARRKKLEPSNVGNLSFSCVEPYTVPVFFNATSYLEVPG
]		RLNQDLFSVSFQFRTWNPNGLLVFSHFADNLGNVEIDLTESKVG
			VHINITQTKMSQIDISSGSGLNDGQWHEVRFLAKENFAILTIDG
1			DEASAVRTNSPLQVKTGEKYFFGGFLNQMNNSSHSVLQPSFQGC MQLIQVDDQLVNLYEVAQRKPGSFANVSIDMCAIIDRCVPNHCE
1 1			HGGKCSQTWDSFKCTCDETGYSGATCHNSIYEPSCEAYKHLGQT
1 1			SNYYWIDPDGSGPLGPLKVYCNMTEDKVWTIVSHDLQMQTPVVG
1 1			YNPEKYSVTQLVYSASMDQISAITDSAEYCEQYVSYFCKMSRLL
			NTPDGSPYTWWVGKANEKHYYWGGSGPGIQKCACGIERNCTDPK
1 1			YYCNCDADYKQWRKDAGFLSYKDHLPVSOVVVGDTDROGGFAYI
!!			SVGPLRCQGDRNYWNAASFPNPSSYLHFSTFOGETSADICEUSE
1 1			TLTPWGVFLENMGKEDFIKLELKSATEVSFSFDVGNGDVFTVAR
1			SPIPLINDDQWHRVTAERNVKOASLOVDRIPOOTRKAPTECUTET
1 1			BLYSQLFVGGAGGQQGFLGCIRSLRMNGVTLDI,EERAKVTECET
l İ			SGCSGRCTSYGTNCENGGKCLERYHGYSCDCSNTAVDGTECNVD
			VGAFFEEGMWLRYNFQAPATNARDSSSRVDNAPDQQNSHPDLAQ
1 . 1	i	}	EEIRFSFSTTKAPCILLYISSFTTDFLAVLVKPTGSLQIRYNLG GTREPYNIDVDHRNMANGQPHSVNITRHEKTIFLKLDHYPSVSY
	1		HLPSSSDTLFNSPKSLFLGKVIETGKIDQBIHKYNTPGFTGCLS
i i			RVQFNQIAPLKAALRQTNASAHVHIQGELVESNCGASPLTLSPM
' <u>]</u>			SSATDPWHLDHLDSASADFPYNPGQGQAIRNGVNRNSAIIGGVI
		•	A\VVIFTPSLCTP\VI.P*SR*HVSPUVGTI.DIDVERVGRGGGGGGG
6791	1000		KPGRRPSMNNDPPTSQRPIDESKKEWPHLRGGYLAMG
~.,,,	1801	1193	TGHEGAKGEKGDKGDLGPRGERGOHGPKGEKGYPGTPPET/PGW
1	ŀ	l	SAVV*SWLTAASTKVQAILLPOPLE*LGLOIAFMASLATUESNO
}	J	J	NSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMVUEDV
ł	Ì	ļ	EEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVI,KI,AKGDEUM
6792	33	1073	LRMGNGALHGDHQRFSTFAGFLLFETK
		1073	VRHTNWGVDMYLFSLGSESPKGAIGHIVSTEKTILAVERNKVLL
ĺ			PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRCLCAV
1	j	1	CPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAV
1			TCLAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGISA
- 1	1	1	ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC
	j		CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDVCSWTASRRG APGSASKPKRPQVGEEPGLESRAGR+HCFDREAQQNQP\PVTAL
		[]	AVSRNHTKLLVGDERGRIFCWSADG*EERGSRGSGTTVPG
		····	DALLASTIC CHOMPA DEVONGRALIANS

SEO	Predicted	Predicted end	
ID	beginning		Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ı	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
6793	2340	805	\=possible nucleotide insertion)
1 -750	2010	805	GRKEANY\YGSLTQAGTVSLGLDAEGQEVFVPFSAVLPMVAPND
			LVFDGWDISSLNLAEAMRRAKVLDWGLQEQLWPHMEALRPRPSV
ľ	į.		YIPEFIAANQSARADNLIPGSRAQQLEQIRRDIRDFRSSAGLDK
İ	1		VIVLWTANTERFCEVIPGLNDTAENLLRTIELGLEVSPSTLFAV
1			ASILEGCAFLNGSPQNTLVPGALELAWQHRVFVGGDDFKSGQTK
i			VKSVLVDFLIGSGLKTMSIVSYNHLGNNDGENLSAPLQFRSKEV
1	!	•	SKSNVVDDMVQSNPVLYTPGEEPDHCVVIKYVPYVGDSKRALDE
	!		YTSELMLGGTNTLVLHNTCEDSLLAAPIMLDLALLTELCQRVSF
ì	1 1		CTDMDPEPQTFHPVLSLLSFLFKAPLVPPGSPVVNALFRQRSCI
1			ENILRACVGLPPQNHMLLEHKMERPGPSLKRVGPVAATYPMLNK
			KGPVPAATNGCTGDANGHLQEEPPMPTT*GPGHTVSRLFLPAAP
6794	169		HDPTLKAPTNKGRCHFSPPSTWGSWGL
6734	169	1349	DDVKRKPEASAH*EKPGPPSRPGVRGGRERAGGRGSHGARSCR\
-	i i		EPAPPAPAPPEDHPDEEMGFTIDIKSFLKPGEKTYTQRCRLFVG
			NLPTDITEEDFKRLFERYGEPSEVFINRDRGFGFIRLESRTLAB
1			IAKAELDGTILKSRPLRIRFATHGAALTVKNLSPVVSNELLEQA
			FSQFGPVEKAVVVVDDRGRATGKGFVEFAAKPPARKALERCGDG
			AFLLTTTPRPVIVEPMEQFDDEDGLPEKLMQKTQQYHKEREQPP
			RFAQPGTFEFEYASRWKALDEMEKQQREQVDRNIREAKEKLEAE
1			MEAARHEHQLMLMRQDLMRRQEELRRLEELRNQELQKRKQIQLR
6795	1740		HEEEHRRREBEMIRHREQEELRRQQEGFKDNYMENYVCHFLR
0,33	1740	1010	GPRRQTQVRDHELDSF*DWAAQETDCAQNSGERL*KGV/LENFS
1			TMSKSAVKISLDLLSNPLCEQDQDLLNMVTALDTAMKRMDAFNQ
1			EKVNQIQKTVIEPLKKFGSVFPSLNMAVKRREQALQDYRRLQAK
]	Ì		VEKYEEKEKTGPVLAKLHQAREELRPVREDFEAKNRQLLEEMPR
f			FYGSRLDYFQPSFESLIRAQVVYYSEMHKIFGDLSHQLDQPGHS
6796	48	683	DEQRERENEAKLSELRALSIVADD
		663	GKEIQIPTIKLAWLLFGLE*PVGALGKGVVSF**SHVALGQLGW
			LTRAVRSSWRWELCVSAQEVVSQRSA*SSPSPVGACPSLNPPET
1	I		SVQEGRDCWQR+LPRLFSALVGQPGCWPQGAPPERCV+PGRCKW
	<u>.</u>		HLQSQVLR*ERRRCCRCLPRFA*GWRRRHQRLGLGIHPAPLGST
6797	1620	211	SPPHPEGNSQQCRR*GWAAELRLPSSVVL*GKLGC*
1		211	TERMTPSQPTRGSSCTRFSSMLWTSTWRCLTCHWAGMRMSVVGV
]			TLGPMAQGLLSASGTTTEATWTRPTTHLTLIRWWLLTASRVDPP ERPPPPPSDDLTLLESSSSYKNL/DAQIPQ/DWSMSPSTSG*RP
			LTSRASSIMRSRTAIPSAS*SRLTTKHTVGGSPSAWRPRPTSRS
1			VSTPVSSSTETTASGSCLTWWSSSPAPCPSSSAPAHSFEASCCK
1		ļ	TSLWGSCGGSGDGSSACGSGWNLSMAGTSCSSPAMCSPSRAPS*
 		İ	RSASRPRTWRATTSAASSWAPRRCWCGWA*SAT*PSSTTTISSS
}	}		PHCGWPCPASCASAAAWLSSTWATASVAGSCWGPIM*SSAHSPW
]	1		CLSACSRSSMGTTCL*RSPP\SGASRAAAAWCGSSPSSTFTPSS
]	1		ASSSTWCSASSSRSSPAPTTPSSIPAAQAQRRASCRPTSHSART
	i		APPPASSAAGAARPAAFSAAAEGTPRRSIRCW
6798	3894	1696	
		2000	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
1 1	į		ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\PQIA
i . I	ŀ		VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLYSWTM
j 1	1	i	ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
]	İ	ļ	VFDDEEKSKLLAKLKSKNPDDLQEANKLIKSMVREDEARIQKV
1		į	TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC
		f	ENKRRTLFKLASETEDNDNSLGDILQASDNLSRVINSYKTIIEG
		İ	QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
			PAPTPPSSGIPILPPPPQASGPPRSRSSSQAEATLGPSSTSNAL
1			SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS
			PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPFPAPVVPASVP
			APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL
<u>_</u>			DQLLEEAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFQ
			

SEQ	Predicted	Predicted end	Amino agid aggress
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ļ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	WaTryptophan, YaTyrosine, XaUnknown, *aStop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
1		J	RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS
- {	1		MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK
		1	LTFALGEQLSTEVGEVDQFPPVEQWGNL
6799	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
İ			ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\PQIA
}	}		VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLYSWTM
ı			ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
1		1	VFDDEEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV
ļ	i		TKRLHTLEEVNNVRLLSEMLLHYSOEDSSDGDRRIMKELEDOG
1		1 .	ENKRYLFKLASETEDNDNSLGDILOASDNLSRVINSYKTITEG
	1	1	QVINGEVATLTLPDSEGNSQCSNOGTLIDLAELDTTNSLSSVI.A
1			PAPTPPSSGIPILPPPPQASGPPRSRSSCAEATIGPSSTSNAT.
		1	SWLDEELLCLGLADPAPNVPPKESAGNSOWHLLOREOSDIDERS
1			PRPGTAACGASDAPLLQPSAPSSSSSOAPLPPPFPAPVVPASVD
ı	1		APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL
1	İ		DQLLEEAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFQ
ŧ			PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
			RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS
			MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK LTFALGEQLSTEVGEVDQFPPVEQWGNL
6800	404	1646	RRSPSTGLSPVPQPSSPSLSDYSIPWSLLLSGTIAWATPGK*AG
	1		*POAW*LGLAPAIAFI/GLTRGRKQNKEKMAEGGSGDVDDAGDC
1			SGARYNDWSDDDDDSNESKSIVWYPPWARIGTEAGTRARARAR
· ·	,		RATRARRAVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILE
[[AALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKAL
İ			IVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLAGLRLL
ŀ	1		TNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQVLKLLLNLAE
			NPAMTRELLRAQVPSSLG\SLFNKKENKEVILKLLVIFENINDN
1	1		FKWEENEPTQNQFGEGSLFFFLKEFQVCADKVLGIESHHDFLVK
			VKVGKFMAKLAEHMFPKSQE
6801	2	1755	SAEEFESQQASVTMHDVDAESFEVLVDYCYTGRVSLSEANVERL
1 .			YAASDMLQLEYVREACASFLARRLDLTNCTAILKFADAFGHDKI.
1	1		RSQAQSYIAQNFKQLSHMGSIREETLADLTLAOLLAVLRIDSID
	İ		VESEQTVCHVAVQWLEAAPKERGPSAAEVFKCVRWMHFTEEDOD
	}		YLEGLLTKPIVKKYCLDVIEGALOMRYGDLLYKSLVPVPNSSSS
			/R*QQQLSCICSRXSTPETGYVCQGDGDLLWTPQRSLS\RYDPY
			SGDIYTMPSPLTSFAHTKTVTSSAVCVSPDHDIYLAAQPRKDLW
		ſ	VYKPAQNSWQQLADRLLCREGMDVAYLNGYIYILGGRDPITGVK
	}	İ	LKEVECYSVQRNQWALVAPVPHSFYSFELIVVQNYLYAVNSKRM
			LCYDPSHNMWLNCASLKRSDFQEACVFNDEIYCICDIPVMKVYN PARGEWRPISNIPLDSFTENVOIDENDOWN IN TOUR
]			PARGEWRRISNIPLDSETHNYQIVNHDQKLLLITSTTPQWKKNR VTVYEYDTREDQWINIGTMLGLLQFDSGFICLCARVYPSCLEPG
	1	1	QSFITEEDDARSESSTEWDLDGFSELDSESGSSSSFSDDEVWVQ
		ł	VAPQRNAQDQQGSL
6802	157	1341	ETFPLFFFLSKTPGKTASMAHFVQGTSRMIAAESSTEHKECAE
	1	ļ	PSTRKNLMNSLEQKIRCLEKQRKELLEVNQQWDQQFRSMKELYE
	1	Ĭ	RKVAELKTKLDAAERFLSTREKDPHQRQRKDDRQREDDRQRDLT
į		l l	RDRLQREEKEKERLNEELHELKEENKLLKGKNTLANKEKEHYEC
	•	İ	EIKRLNKALQDALNIKCSFSEDCLRKSRVEFCHEEMRTEMEVLK
	1		QQVQIYEEDFKKERSDRERLNQEKEELQQINETSQSQLNRLNSQ
1	J		IKACQMEKEKLEKQLKQMYCPPCNCGLVFHLODPWVPTGPGAVO
}		i	KQREHPPDYQWYALDQLPPDVOHKAN/DWCLAPPPVCCOAG/PP
1			TPGLK*SSCLWLPKC*NFRFILSKESPSVEVHTNRERQQATRER
<u> </u>			G [
6803	1	2203	KLSGRPYRHMGVLGTSKLYDIRKTIFTFTPQFIDQQQFYLALDN

SEQ Predicted beginning beginning nucleotide nucleotide location corresponding to first amino acid sequence residue of amino acid sequence Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence Sequence Sequence Requence Requence Representation acid sequence Representation acid sequence Representation acid sequence Representation acid sequence Representation acid sequence Representation acid sequence Representation acid sequence Representation acid sequence Representation acid sequence Representation acid sequence Representation acid sequence Representation acid sequence Representation acid segment containing signation (A=Alanine, C=Cysteine, D=Aspartic Glutamic Acid, F=Phenylalanine, G=Gutamic Acid, F=Phe	Acid, E= Elycine, e, .ne,
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence NO: nucleotide location corresponding to first amino acid residue of amino acid sequence NO: nucleotide location corresponding to first amino acid residue of amino acid sequence NO: nucleotide location corresponding to first amino acid residue of amino acid sequence (S-Evine, T-Threonine, V-Valine, W-Tryptophan, Y-Tyrosine, X-Unknown Codon, /=possible nucleotide deleti \=possible nucleotide insertion) NO: nucleotide location corresponding to first amino acid, F=Phenylalanine, G=G H=Histidine, I=Isoleucine, K=Lysine H=Histidine, I=Isoleucine, K=Lysine H=Histidine, I=Isoleucine, K=Lysine H=Histidine, I=Isoleucine, K=Lysine H=Histidine, I=Isoleucine, K=Lysine H=Histidine, I=Isoleucine, K=Lysine H=Histidine, I=Isoleucine, K=Lysine H=Histidine, I=Isoleucine, K=Lysine H=Histidine, I=Isoleucine, M=Methionine, N=Asparagi P=Proline, Q=Glutamine, R=Arginine, S=Gutomine, N=Asparagi P=Proline, Q=Glutamine, N=Asparagi P=Proline, Q=Glutamine, N=Asparagi P=Proline, Q=Glutamine, N=Asparagi P=Proline, Q=Glutamine, N=Asparagi P=Proline, Q=Glutamine, N=Asparagi P=Proline, Q=Glutamine, N=Asparagi N=Methionine, N=Asparagi P=Proline, Q=Glutamine, N=Asparagi P=Proline, Q=Glutamine, N=Asparagi N=Asparagi P=Proline, Q=Glutamine, N=Asparagi N=Asparagi P=Proline, Q=Glutamine, N=Asparagi N	lycine, , , , , *=Stop
location corresponding to first amino acid residue of amino acid sequence M=Histidine, I=Isoleucine, K=Lysine L=Leucine, M=Methionine, N=Asparagi P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown Codon, /=possible nucleotide deleti codon, /=possible nucleotide insertion XMIVEMLETDLSYLCSRWRMTGQPTITFPISHSML SILAALRKMQDGYFGGARVQTGKLSEFLTTSCCTH GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCGDE AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLV NVIMYLPTKLFQASRPSFNLLDSPHPRQENQVPSV QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKG	ne, .ne, ., *=Stop
corresponding to first amino acid residue of amino acid sequence	ne, 1, *=Stop
to first amino acid residue of sequence P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown Codon, /=possible nucleotide deleti sequence	ı, *=Stop
amino acid residue of serine, T=Threonine, V=Valine, residue of amino acid sequence Codon, /=possible nucleotide deleti (=possible nucleotide insertion) KMIVEMLRTDLSYLCSRWRMTGQPTITFPISHSML SILAALRKMQDGYFGGARVQTGKLSEFLTTSCCTH GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCGDE AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLV NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSV QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKG	ı, *=Stop
residue of amino acid sequence Codon, /=possible nucleotide deleti (=possible nucleotide insertion) KMIVEMLETDLSYLCSRWENTGOPTITFPISHSML SILAALRKMODGYFGGARVQTGKLSEFLTTSCCTH GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCGDE AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLV NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSV QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKG	ı, *=Stop
residue of amino acid sequence W=Tryptophan, Y=Tyrosine, X=Unknown Codon, /=possible nucleotide deleti	, *=Stop
amino acid sequence Codon, /=possible nucleotide deleti sequence \ =possible nucleotide insertion) KMIVEMLETDLSYLCSRWENTGQPTITFPISHSML SILAALRKMQDGYFGGARVQTGKLSEFLTTSCCTH GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCGDE AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLV NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSV QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKG	., -ocop
sequence \ \=possible nucleotide insertion\ KMIVEMLRTDLSYLCSRWRMTGQPTITFPISHSML SILAALRKMQDGYFGGARVQTGKLSEFLTTSCCTH GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCGDE AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLV NVINYLPTKLFQASRPSFNLLDSPHPRQENQVPSV QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKG	
KMIVEMLRTDLSYLCSRWRMTGQPTITFPISHSML SILAALRKMQDGYFGGARVQTGKLSEFLTTSCCTH GKLYSEDYDDNYDYLESGNWMDYDSTSHARCGDE AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLV NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSV QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKG	.011,
SILAALRKMQDGYFGGARVQTGKLSEFLTTSCCTH GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCGDE AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLV NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSV QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKG	
GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCGDE AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLV NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSV QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKG	
AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLV NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSV QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKG	LSFMDPGPE
NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSV QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKG	
NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSV QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKG	TKAKELHVQ
QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKG	RVEIHLPRD
	ואי. דייייותעורס
TDLLSHQKHLTVGLPPEPREKTISAPLPYEALTQL	
SISILTQEIMVYLAMYMRTQPGLFAEMFRLRIGLI	
HSLRCSAEEATEGLMNLSPSAMKNLLHHILSGKEF	
PTDSNVSPAISIHEIGAVGATKTERTGIMQLKSEI	
ISAESQSFGTSMTPSSGSFPSAYDQQSSKDSRQGQ	
ALNRVPVGFYQKVWKVLQKCHGLSVEGFVLPSSTT	REMTPGEIK
FSVHVES\VLNVLLRPEYRQLLVEAILVLTMLADI	EIHSIGSTT
AVEKIVHIANDLFLQEQKTLGP\DDTMLAKDPASG	\TCTT.P\VD
SAPSGRFGTMTYLS\RAA\ATYVQEFLP\HSICAM	
6804 1 951 GSPGKKEEKAKNKESLCMENSSNSSSDEDEBETKA	
GLEEKRKSLRTTGFYSGFSEVAEKRIKLLNNSDER	
KDVWSSIQGQWPKKTLKELFSDSDTEAAASPPHPA	
LQTVAEEESCSPSVELEKPPPVNVDSKPIEEKTVE	
SSGSNFSA*IPLPYLHLNRLHQSL*QKGSRQQSSV	
QEEVRSIKSETDSTIEVDSVAGELQDLQSERE*LA:	
KQ**SARTRTS*KSLYRSEKSERCSGRRKFIKKAE	KKP*SNSGK
QQKEGKRHK	
6805 1539 206 RQPDLKYFGKSFDVSVSESSSLLSNDLPKFADGIK	
VPSPVLRILDHTAFSTEKSADIVICDEECDSPESV	
IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLQI	DOTDEEPPA
KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCEL	CEFNSKYFS
DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAI	
CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDV	
LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEH	
KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRI	
AIEHTKIPPHVCDDCGKGFSSMLE\IAKHLNSHLSH	
EYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNE	
VHETT	SKELTSHPL
THE THOUSE WITHOUT IS CHIME IN OF THE PERIOD	
GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGM	
DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGST	
SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHG	SVLTSVMNR
MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRI	MHWSLLAO
RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQ	
ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGI	
TEEKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKT	
SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRE	Properto
FIGPDHLVFIVGKLDGLMVTGVRRHNADDVVATALA	
RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWM	
SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFL	
VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGK	
ELAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLI	
STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYF	PEVDLIAA
FYGCLYCGCVPVTVRPPHPQNLGTTLPTVKMIVEVS	
QAVTRLLRSKEAAAAVDIRTWPTILDTDDIPKKKIA	
DVLAYLDFSVSTTGILAGVKMSHAATSALCRSIKLQ	
IAICLDPYCGLGFALWCLCSVYSGHQSVLVPPLELE	
AVSQYKARVTFCCYSVMEMCTKGI.GAQTGVLRMKGV	
MVVAEERP\RIALTQSFSKLFKDIGLPARAVSTTFG	
, i prevendente en la militar de la marcia del marcia de la marcia del la marci	CKANANTC

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ľ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
l l	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	bedacues	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
Ĭ			LOGTAGPDPTTVYVDMRALRHDRVRLVERGSPHSLPLMESGKIL
1			PGVKVIIAHTETKGPLGDSHLGEIWVSSPHNATGYYTVYGEEAL
1			HADHFSARLSFGDTQTIWARTGYLGFLRRTELTDASGGRHDALY
ŀ			VVGSLDETLELRGMRYHPIDIETSVIRAHRSIAECAVFTWTNLL
1	1		VVVVELDGLEQDALDLVALVTNVVLEEHYLVVGVVVIVDPGVIP
6807	1444	606	INSRGEKQRMHLRDGFLADQLDPIYVAYNM
		000	VGHDTVHAMFTCFPKCLGFSPPVNVTVSPRSEESHTTTVSGGNG
1	1		SVFQAGPQLQALANLEARRGSIGAALSSRDVSGLPVYAQSGEPR
			RLTQAQVAAFPGENALEHSSDQDTWDSLRSPGFCSPLSSGGAE
	ļ		SLPPGGPGHAEAGHLGKVCDFHLNHQQPSPTSVLPTEVAAPPLE
	!		KILSVDSVAVDCAYRTVPKPGPQPGPHGSLLTEGCLRSLSGDLN
1			RFPCGMEVHSGQRELESVVAVGEAMA\LKFPMGAMSYCLRDRSR FLFRLPMGLSCPLQVQ
6808	2063	737	
			GVGSGAASALARSRPLASRLSSRRRTRAPRSGAMQRLAMDLRML
1			SRELSLYLEHQVRVGFFGSGVGLSLILGFSVAYAFYYLSSTAKK PQLVTGGESFSRFLQDHCPVVTETYYPTVWCWEGRGQTLLRPF\
1			ITSKPPVQYRNELIKTADGGQISLDWFDNDNSTCYMDASTRFTI
			LLLPGLTGTSKESYILHMIHLSEELGYRCVVFNNRGVAGENLLT
1			PRTYCCANTEDLETVIHHVHSLYPSAPFLAAGVSMGGMLLLNYL
			GKIGSKTPLMAAATFSVGWNTFACSESLEKPLNWLLFNYYLTTC
			LQSSVNKHRHMFVKQVDMDHVMKAKSIREFDKRFTSVMFGYQTI
1.			DDYYTDASPSPRLKSVGIPVLCLNSVDDVFSPSHAIPIETAKON
1 1			PNVALVLTSYGGHIGFLEGIWPRQSTYMDRVFKQFVQAMVEHGH
			BLS BLS
6809	939	65	DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ
1 1			TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF
1 1	į		GQFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKLNGTIV
1 1			EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA
1			VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG
l i	1		AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP
			TRTITPSGPRRPTALEPCETFHRFLLGP
6810	939	65	DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ
1	1	1	TUKAAQTUSQPLHPSDPTEKOOPKRLHVSNIPFRFRDPDT.ROME
1 1	İ		GQFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKLNGTIV
1 1		İ	EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVVGPREVA
1 1	1	1	VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPDDDTDTVG
1 1			AVVYQDGFYGAEI\LEATQPTDTLSPLORROPTATVTAESTOLD
6811	7.500		TRITTPSGPRRPTALEPCETFHRFLLGP
"""	1522	658	DLVTVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME
]	1	1	FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG
1		i	SVGQDTQLCLWDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN
1		1	GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGATASGV
1 1	1		SKFATLSLHDRKERHHEKDHKRNHSMGHTSSKSSDKLNTJUTUTE
1			TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI
6812	4001		VTACQEGFICTWGRPGKVVSFNP
	2001	1682	EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ
] [KGLQHRLILHAVKHQDSGALVGFSCPGVODSAALTTOES PURITI.
		1	SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGOKVERSELL.
1	ļ	1	VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVODPDV
!	1	11	HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGORVF
		1.3	ESDFVVLENEGPHRRLVLPATQPSDGGEFOCVAGDECAYFTVTT
	ļ	1 '	TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE
1		• 1	EVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT
1	l		VTVTEPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK
		ļ I	DGLEVEESEALVLERDGPRCRLVLPAAOPEDGGEFVCDAGDDSA
			FFTVTVTEPPVQFLALETTPSPLCVAPGEPVVLSCELSRAGAPV

SEQ	Predicted	Predicted end	Amino acid coment contains
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Ston
1	amino acid	aedneuce	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion
- 1			VWSHNGRPVQEGEGLELHAEGPRRVLCIOAAGPAHAGI.VTCOSC
1		1	AAPGAPSLSFTVQVAEPPVRVVAPEAAOTRVRSTPGGDLELAVH
1			LSGPGGPVRWYKDGERLASQGRVOLEOAGAROVT.RVOGARSGDA
1			GEYLCDAPQDSRIFLVSVEEPLLVKLVSDLTPLTVHEGDDATER
]	l .	1	CEVSPPDADVTWLRNGAVVTPGPQRQSCCSYGGCRMCGORKART
1	1	!	CVSKWRQAEWVQRGPCAGCEVGSPCPTTLACPWPRMGTSTASSS
6813	9		MVSYWPTRAPTAARATTIAPWPGSA
5515		836	SSTQQRPGVPAGPRPLDGYLGVADHKPLKMHCRDCALVTSSGHL
J	}		LHSRQGSQIDQTECVIRMNDAPTRGYGRDVGNRTSLRVIAHSSI
		1	QRILRNRHDLLNVSQGTVFIFWGFSSYMRRDGKGQVYNNLHLLS
1	1		QVLPRLKAFMITRHKMLQFDELFKQETGQ\NRKISNTWLSTGWF
1			TMTIALELCDRINVYGMGPPDFCRDPNHPSVPYHYYEPFGPDEC
ŀ		ĺ	TMYLSHERGRKGSHHRFITEKRVFKNWARTFNIHFFQPDWKPES LAINHPENKPVF
6814	3	737	KFRRQEAN/ARERNRMHGLNDALDNLRKVVPCYSKTQKLSKIET
1			LRLAKNYIWALSEILRIGKRPDLLTFVQNLCKGLSQPTTNLVAG
1			CLQLNARSFLMGQGGEAAHHTRSPYSTFYPPYHSPELTTPPGHG
			TLDNSKSMKPYNYCSAYESFYESTSPECASPQFEGPLSPPPINY
1	1		NGIFSLKQEETLDYGKNYNYGMHYCAVPPRGPLGQGAMFRLPTD
			SHFPYDLHLRSQSLTMQDELNAVFHN
6815	906	553	QGLDPASQTKVVELLKDGSGRRGDRRSSRDMAGGAGPRSESDLE
1			DVGPTAEWNGDGSGSLRRSGSFGKLRDALRRSSEMLVKKLOGGT
6816	1	0.00	PQEPPNPRMKRASSLNFLNKSVEEPTOPGG
1 5515	1 1	803	NLLKTHKF\LLGQDEDSLHSVPVAQMGNYQEYLKTLASPLREID
1			PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN
I			SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN
1	1 1		LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM
		i	TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF
	<u>l</u> .		GRSK
6817	1.72	3457	LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS
}			DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL
]		NNLISPDLEECHTPHKPOKRKSLESSYKDSIJJANSKKTPNYTA
Į.		;	IDGGKVLNSKHNGEVYDETSSNLPDSSGOONPIRTADSLERNEY
İ	1 1		LEADTVDMATTKDPATVDVSGTGRPSPONEGCTSKI.EMPLESKC
i	1	1	TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGT.CSKE
	ĺ		ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKL'TSEIFAEIET
1]]	CLNEVRDEIFISLOPOLRCTLGDMESPVFAFPLLLKLETHIEKL
Ì			FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF
]]	j	GPCNNCNSKSQIRKMVLEKVSPIFMLHFVEGLPQNDLQHYAFHF
i			EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH
			KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD
		1	HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV
		İ	AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ
			VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ
		.	LKQPLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ
		ł	SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS
		}	VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP
		ļ	SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH
	1		EDLVEGQIHKLRLKLRKKLKAEKKKLAALMSSPOSRTVRSENT.E
	1	ſ	QVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS
	•	. 1	QTHEBILAELLSPTPVSTELSENGEGDFRYLGMGDSHIPPPVPS
l		1	EFNDVSQNTHLRQDHNYCSPTKKNPCEVOPDSLTNNACVRTINI.
6818			ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY
0010	2	240	RGFDKVLWT/LSGAVK\CVQFSRISPDGEEGYPGELKVWVTYTL

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Trantonhan V-Transies Williams
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
-	sequence	004	\=possible nucleotide insertion)
	 		DGGE/LHS/ATTEHKP/VQATPVNLT\TILTSTWQARLPQI
6819	1	961	GIPCTEMGNFDNANVTGEIEFAIHYCFKTHSLEICIKACKNLAY
	_	301	GEEKKKKCNPYVKTYLLPDRSSQGKRKTGVQRNTVDPTFQETLK
	i		YQVAPAQLVTRQLQVSVWHLGTLARRVFLGEVIIPLATWDFEDS
	1		TTQSFRWHPLRAKADKYEDSVPQSNGELTVRAKLVLPSRPRKLQ
ľ			EAQEGTDQPSLHGQLCLVVLGAKNLPVRPDGTLNSFVKGCLTLP
ļ			DQQKLRLKSPVLRKQACPQWKHSFVFSGVTPAQLRQSSLELTVW
1			DQALFGMNDRLLGGT\RLGSKGDTAVGGDACSQSKLQWQKVLSS
			PNLWTDMTLVLH
6820	1014	340	GDMVYIVGHVPPGFFEKTQNKAWFREGFNEKYLKVVRKHHRVIA
			GQFFGHHHTDSFRMLYDDAGVPISAMFITPGVTPWKTTLPGVVN
1]		GANNPAIRVFEYDRATLSLKDMVTYFMNLSQANAQGTPRWELEY
			QLTEAYGVPDASAHSMHTVLDRIAGDQSTLQRYYVYNSVSYSAG
	1		VCDEACSMQHVCAMRQVDIDAYTTCLYASGTTPVPQLPLLLMAL
			LGLCT
6821	1088	518	EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN
1			RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT
1	l i		FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG
	l		GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI
	ļ		GSVIEVLORROEGLAS
6822	1088	518	EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN
			RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT
			FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG
1 1		•	GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI
			GSVIEVLQRRQEGLAS
6823	654	221	PPKLLSRWARMGHGDEIV\LSDLNFPGLLHLPVVGPWRSVQTAC
1 1			GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLOTPVWTE
1 1			YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL
6824			ILRKGVLALNPLL
0024	858	104	LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRG
] [{		ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV
1 1	Į.		NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS
	!		LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV
j /	}	}	WYFHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS
6825	3	1173	AALHICHAVILLQLWLGPQPFPKSTQHSKKAH
	_	11/2	SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL
1			PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ
j i			NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM
	1		KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI
			GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD
1	1		IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK
]	1	ł	TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF
1 1	1	i	PFGPLALPMDGYGDSLWEEHEYKFCLALVISTKLYHVRC
6826	2304	954	LKTESFKPW/VNIALAFHLLGERASPNSFWQPYIQTLPREYDTP
	- j		LYFEEDEVRYLQSTQAIHDVFSQYKNTARQYAYFYKVIQTHPHA
]	į.	ŀ	NKT.DI.KDCFTVBDVDUNIGGUMEDONA ZEMDDA AZZEMDA
	1		NKLPLKDSFTYBDYRWAVSSVMTRQNQIPTEDGSRVTLALIPLW
			DMCNHTNGLITTGYNLEDDRCECVALQDFRAGEQIYIFYGTRSN
l l			AEFVIHSGFFFDNNSHDRVKIKLGVSKSDRLYAMKAEVLARAGI
		ł	PTSSVFALHFTEPPISAQLLAFLRVFCMTEEELKEHLLGDSAID
			RIFTLGNSEFPVSWDNEVKLWTFLEDRASLLLKTYKTTIEEDKS
' 1		ł	VLKNHDLSVRAKMAIKLRIGEKEILEKAVKSAAVNREYYRQQME
		ļ	EKAPLPKYEESNLGLLESSVGDSRLPLVLRNLEEEAGVQDALNI
- 1			REAISKAKATENGLVNGENSIPNGTRSENESLNQESKRAVEDAK GSSSDSTAGVKE
			ODD ALG TIL

	SEQ	Predicted	Predicted end	l Amino acid
	ID	beginning	nucleotide	Amino acid segment containing signal peptide
	NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
		location	corresponding	Glutamic Acid, FaPhenylalanine, G=Glycine,
	Ĭ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
		to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1		residue of	amino acid	W-Trintonian V manager
		amino acid	sequence	W=Tryptopnan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		sequence	1	\=possible nucleotide insertion) .
	6827	1	779	SSVVEFGLSVLGGLFLLFVLENMLGLLRHRGLRPRCCRRKRRNL
		J		ETRNLDPENGSGMALQPLQAAPEPGAQGQREKNSQHPPALAPPG
ſ		İ	J	HQGHSHGHQGGTDITWMVLLGDGLHNLTDGLAIGAAFSDGFSSG
- 1		}		LSTTLAVFCHELPHELGDFAMLLQSGLSFRRLILLSLVSGALGL
J				GGAVLGVGLSLGPVPLTPWVFGVTAGVFLYVALVDMLPALFPSS
1				GAPAYA\HVLLQGLGLLLGGCLMLAITLLEERLLPVTTEG
- 1	6828	3	1654	KSQHG/WILQLMHSCKEGYVKDLKGNPGLHRAMLDLDNGTRPSE
1				LGHLSQTASLKRGSSFQSGRDDTWRYKTPHRVAFVEKLTKLVLS
ı				QLPNFWKLWISYVNGSLFSETAEKSGQIERSKNVRQRQNDFKKM
		i		IQEVMHSLVKLTRGALLPLSIRDGEAKQYGGWEVKCELSGQWLA
- 1				HAIQTVRLTHESLTALEIPNDLLQTIQDLILDLRVRCVMATLQH
- 1	i			TAEEIKRLAEKEDWIVDNEGLTSLPCOFFOCTUCGLOGLUCUT P
- 1				CKPGEASVFQQPKTOEEVCOLSINIMOVFTYCLEOLGTVDDDDT
-	1			DITHLSVDVSSPDLFGSIHEDFSLTSEORLLIVI.SNCCVI.EPUT
				FLNIAEHFEKHNFQGIEKITOVSMASLKELDORLFENVIELVAD
		İ		PIVGSLEPGIYAGYPDWKDCLPPTGVRNYLKEALWNTIAWAEW
	1			FILSKELVPRVLSKVIEAVSEELSRLMOCVSSFSKNGALOADID
1				ICALRDTVAVYLTPESKSSFKQALEALPQLSSGADKKLLEELLN
H	6829			: KIKSSMHLQLTCFQAASSTMMKT
	0025	1	782	MRMEAGEAAPPAGAGGRAAGGWGKWVRLNVGGTVFLTTRQTLCR
1	ŀ	Į		BQKSFLSRLCQGEELOSDRDETGAYLTDEDDTVFQDTLNELDUG
1	į	İ		KLVLDKDMAEEGVLEEAEFYNIGPLIRTIKDRMERKDVTVTOVD
1	i	1		PRHYYRVLQCQEEELTOMVSTMSDGWRFFOLWNIGSSYNVGERD
	ł			QAEFLCVVSKELHSTPNGLSSESSRKTKSTREOT.REOOODREET
1	6830	1	939	EBVEVEQVQVEADAQEK/CCYKPEAPGCEAPDHLQGLGVPI
1		_	,,,,	MEPGSVENLSIVYRSRDFLVVNKHWDVRIDSKAWRETLTLQKQL
ŀ	- 1			RYRFPELADPDTCYGFRFCHQLDFSTSGALCVALNKAAAGSAYR
	i	ľ		CFKERRVTKAYLALLRGHIQESRVTISHAIGRNSTEGRAHTMCI
ļ	- 1	1		EGSQGCENPKPSLTDLVVLEHGLYAGDPVSKVLLKPLTGRTHQL
1		i		RV\HCSALGHPVVGDLTYGEVSGREDRPFRMMLHAFYLRIPTDT
ł	j			ECVEVCTPDPFLPSLDACWSPHTLLQSLDQLVQALRATPDPDPE DRGPRPGSPSALLPGPGRPPPPPTKPPETEAQRGPCLQWLSEWT
L		ĺ		LEPDS
1	6831	3	1087	SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF
	ļ	j	İ	NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGQNVKEKSMILSN
ŀ				VEDLQQPKFISEVSREDYGKKEISGDSEEMNINSVVTSADGENL
1	1	· ·	ł	EIQSYSLIGEKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI
1	1		1	SIFKEEPRSDQKQKSLLSFDVVDKVPOOPKSASSNFASKNITKE
	1		j	SEKPESIILPVEESKGSLIDFSEDRIKKEMONDTSLKTSEFFTV
1	ĺ		•	DRSVSPTERKONLENR\SYTL\AEKKVLAEKONSV\ADT.FLDDC
ł	ł	1		NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG
-	6832	1000		SEKEKDEKKKK
		1809	412	MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV
1	ļ		į.	VSLKKKRSEDDYEPIITYOFPKRENLLRGOOFFFFFFI.KATBLE
ĺ	1			CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRIJ.RAGRC
l	ĺ			PRLPKVYCIISCIGCFGLFSKILDEVEKRHOISMAUTVDEMOGE
	- 1			KEAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHUDEGG
	1		ì.	LHCLSFEQILQIFASAVLERKIIFLAEGLSTT.SOCTUADADITY
1			Į ;	PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME
1	- 1	i		EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT
	1	I	1:	AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK
		ļ	1;	ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE
-	5833	1	1129	YBEQKKQ/TETKGKNCEIRAVVNKND
		_	1103	PLMTLSQCGGIPGHGHSHGGHGHGHGLPKGPRVKSTRPGSSDIN
			. [;	VAPGEQGPDQEETNTLVANTSNSNGLKLDPADPENPRSGDTVEV
				QVNGNLVREPDHMELEEDRAGQLNMRGVFLHVLGDALGSVIVVV

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
No:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
- [location	corresponding	H=H1SCldine, I=Isoleucine K-Tarrine
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
J	residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine.
Į.	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į	sequence	boquence	Codon, /=possible nucleotide deletion, \-possible nucleotide insertion)
			NALVFYFSWKGCSEGDFCVNPCFPDPCKAFVEIINSTHASVYEA
			GPCWVLYLDPTLCVVMVCILLYTTYPLLKESALILLQTVPKQID
	1		IRNLIKELRNVEGVEEVHELHVWOLAGSRIJATAHIKCEDDTGV
1		1	MEVAKTIKDVFHNHGIHATTIOPEFASVGSKSSVVDCELA CDTO
- 1	1		CALKQCCGTLPOAPSGKDAEKTPAVSISCLELSNNLEVEDDDDV
6834	78	1151	AENIPA\VVIEIKN\IPNK\QPESSL
			AGOERPAPIWRLLWLPTPSVSRKAEPAHIPINR*GA*E*RGGLP
		1	LCGSSASAYGWH*RLTPWSPGGS*HM*SSKAPVTQAREVLVAGD CSKLVLSGARGIVGTTVQVLVEAQQPLLLLFTGVWGLNLRAGEE
1			SRAL*LIBEVTQVRDAHLGNAVVGCAQCLSQGQVGSALAKALLE
			AAAAVRDCKEVLTVSGDKQQAEVSVRL*VRDVCVEEAGCVEFGQ
1			AHGRPGLALAKGRGGTNEVEEOVOVDGVOKLVLSAHECHELVAG
	1		QQDGEDQAARTRLLOAGAHSVAHGRROGOAPCRPHOEAGUSCUS
	,		LQQVVGDAL*ARE*APQIIVLLLLEDVAQLRTGKKA*DLVVDVE
6835	1	834	QLLRQL CIPAADO FACILITATION DE LA COMPANION DE
1		034	GIPAADR\EASLELIKLDISRTFPNLCIFQQGGPYHDMLHSILG AYTCYRPDVGYVQGMSFIAAVLILNLDTADAFIAFSNLLNKPCQ
1			MAFFRVDHGLMLTYFAAFEVFFEENLPKLPAHFKKNNLTPDIYL
1	ł		IDWIFTLYSKSLPLDLACRIWDVFCRDGEBFLFRTALGILKLFE
1			DILTKMDFIHMAQFLTRLPEDLPAEELFASIATIOMOSPNIKKWA
1	ĺ		QVLTALQKDSREMREGKSVPPTLRLQREFALGTNQSPMPRPLCC
6836	1	850	FRLTPGQPRRTDAL
	_	050	MSCGRPPPDVDGMITLKV\DNLTYRTSPDSLRRVFEKYGRVGDV
1			YIPREHTKAPRGFAFVRFHDRRDAQDAEAAMDGAELDGRELRV QVARYGRRDLPRSRQGRRHAAGPEAA/RYGRRSRSYGRRSRSPR
1 1			RRHRSRSRGPSCSRSRSRSRYRGSRYSRSPYSRSPYSRSRYSRS
1 1			PYSRSRYRESRYGGSHYSSSGYSNSRYSRYHSSRSHSVCGgcTe
[]			SKSASTSKSSSARRSKSSSVSRSRSRSRSRSSSMTRSPPRVSKRKS
6837	1	1265	KSRSRSKRPPKSPEEEGOMSS
	• •	1369	TDGAAVAGNPGSDYFPGGTAP/GGPRTRRP\SGTSSGSKASGP
1	1		PNPPAQGDGTSLSPNYTLESTSGNDGKPVSGGGGRGRGRRKRDS GHVSPGTFFDKYSAAPDSGGAPGVSPGQQQASGAAVGGSSAGET
1			RGAPTPHEKALTSPSWGKGAELLLGDQPDLIGSLDGGAKSDSSS
			PNVGEFASDEVSTSYANEDEVSSSSDNPOALVKASPEDL VTCCD
1			KLPPRGVGAGEHGPKAPPPALGLGIMSNSTSTPDSVGGGGGGGG
			PGTPGLEQVRTPTSSSGAPPPDETHPLETIOAOTOLOPOORETE
!!			EUQPLGLKGGKKGECAVGASGAONGDSELGSCCSEAVKSAMSTT
1			DLDSLMAEHSAAWYMPADKALVDSADDDKTLAPWEKAKPQNPNS
			KEAHDLPANKASASQPGSHLQCLSVHCTDDVGDAKARASVPTWR SLHSDISNRFGTFVAALT
6838	16	499	LTDTPPPKTHMIHHSISDYKATLRCWALGEYPMEITLTWOODER
	1	1	DQTRDMELVETRPAGDGTFOKWAAVVVPSGEE/O/RYMCHYOHE
		į	GLPEPLTLRWEQSSQPTIPIVGIVAGLVLLGAVVTGAVVSAVMC
6839	1		RKKNSDRVSYSEAASSDHAQGSDVSLTACKV
	-	1195	AAPAGGGPDPEALSAFPGRHLSGLSWPQVKRLDALLSEPIPIHG
			RGNFPTLSVQPRQIRAGGPQHPGGAG\IHVHRVRLHGSAASHVL
			HPESGLGYKDLDLVFRMDLRSEASFQLTKAVVLACLLDFLPAGV SRAKITPLTLKEAYVQKLVKVCTDSDRWSLISLSNKSGKNVELK
			FVDSVRRQFEFSIDSFQIILDSLLLFGQCSSTPMSEAFHPTVTG
	1		ESLYGDFTEALEHLRHRVIATRSPEEIRGGGLLKYCHLLVRGFR
	1	1	PRPSTDVRALQRYMCSRFFIDFPDLVEORRTLERYLEAHFGGAD
1	1	[-	AARRYACLVTLHRVVNESTVCLMNHERROTLDLIAALALOALAE
	I] '	QGPAATAALAWRPPGTDGVVPATVNYYVTPVQPLLAHAYPTWLP
6840	4254	'	CN
	-		ELQGDFSVPDVPKSMAWCENSICVGFKRDYYLIRVDGKGSIKEL
			FPTGKQLEPLVAPLADGKVAVGQDDLTVVLNEEGICTQKCALNW

SEQ	Predicted	Predicted end	Amino acid complete
10	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Stop
J	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
1			TDIPVAMEHQPPYIIAVLPRYVEIRTFEPRLLVQSIELQRPRFI
1			TSGGSNIIYVASNHFVWRLIPVPMATOIOOLLODKOFRIALOLA
1	1		EMKDDSDSEKQQQIHHIKNLYAFNLFCQKRFDESMQVFAKLGTD
-]			PTHVMGLYPDLLPTDYRKQLQYPNPLPVLSGAELEKAHLALIDY
1			LTQKRSQLVKKLNDSDHQSSTSPLMEGTPTIKSKKKLLQIIDTT
			LLKCYLHTNVALVAPLLRLENNHCHIEESEHVLKKAHKYSELII LYEKKGLHEKALQVLVDQSKKANSPLKGHERTVQYLQHLGTENL
į			HLIFSYSVWVLRDFPEDGLKIFTEDLPEVESLPRDRVLGFLIEN
ĺ			FKGLAIPYLEHIIHVWEETGSRFHNCLIQLYCEKVQGLMKEYLL
1			SFPAGKTPVPAGEEEGELGEYROKIJMFLEISSVVDDGBLIGDE
			PFDGLLEERALLLGRMGKHEOALFIYVHILKDTRMAREVCHKHV
1	i i		DRNKDGNKDVYLSLLRMYLSPPSIHCLGPIKLELLEDVANLOAR
			LQVLELHHSKLDTTKALNLLPANTOINDIRIFIRKYILFENAOKY
			RFNQVLKNLLHAEFLRV\QEERILHQQVKCIITEEKVCMVCKKK
6841	1	3206	IGNSAFARYPNGVVVHYFCS\KEVNPADT
	1		TPSTTGTKSNTPTSSVPSAAVTPLNESLQPLGDYGVGSKNSKRA REKRDSRNMEVQVTQEMRNVSIGMGSSDEWSDVQDIIDSTPELD
1			MCPETRLDRTGSSPTQGIVNKAFGINTDSLYHELSTAGSEVIGD
			VDEGADLLGEFSGMGKEVGNLLLENSQLLBTKNALNVVKNDLIA
			KVDQLSGEQEVLRGELEAAKOAKVKLENRIKELEERLVDIVCER
1			IIARREPKEEAEDVSSYLCTESDKIPMAORRRFTDVFMADVT.MD
1			RNQYKERLMELQEAVRWTEMIRASREHPSVOEKKKSTIWOFFSP
1			LESSSSSPPPAKRPYPSGNIHYKSPTTAGFSORRNHAMCDISAG
			SRPLEFFPDDDCTSSARREQKREQYRQVREHVRNDDGRLQACGW
[]			SLPAKYKQLSPNGGQEDTRMKNVPVPVYCRPLVEKDPTMKLWCA
1 1			AGVNLSGWRPNEDDAGNGVKPAPGRDPLTCDREGDGEPKSAHTS PEKKKAKELPEMDATSSRVWILTSTLTTSKVVIIDANQPGTVVD
1			QFTVCNAHVLCISSIPAASDSDYPPGEMFLDSDVNPEDPGADGV
	i		LAGITLVGCATRCNVPRSNCSSRGDTPVLDKGQGEVATIANGKV
1 1	l		NPSQSTEEATEATEVPDPGPSEPETATLRPGPLTEHVFTDDADT
	Į.		PSSGPQPGSENGPEPDSSSTRPEPEPSGDPTGAGSSAAPTMWI.G
1 [į		AQNGWLYVHSAVANWKKCLHSIKLKDSVLSLVHVKGRVLVALAD
1 1	İ	j	GTLAIFHRGEDGQWDLSNYHLMDLGHPHHSIRCMAVVYDRVWCG
1 1			YKNKVHVIQPKTMQIEKSFDAHPRRESQVRQLAWIGDGVWVSIR LDSTLRLYHAHTHQHLQDVDIEPYVSKMLGTGKLGFSFVRITAL
].]			LVAGSRLWVGTGNGVVISIPLTETVVLHRGQ\LLG\LRANKTSP
			TSGEG\ARPGG\IIHVYG\DDSSDRAARSFIPYCSMAQAQLCFH
		į	GHRDAVKFFVSVPGNVLATLNGSVLDSPAEGPGPAAPASEVEGO
1 1		ļ	KLRNVLVLSGGEGYIDFRIGDGEDDETEEGAGDMSOVKPVLSKA
6842	3		ERSHIIVWQVSYTPE
	-	926	RCQQLSATILTDHQYLERTPLCAILKQKAPQQYRIRAKLRSYKP
	}		RRLFQSVKLHCPKCHLLQEVPHEGDLDIIFQDGATKTPDVKLQN
1 1			TSLYDSKIWTTKNQKGRKVAVHFVKNNGILPLSNECLLLIEGGT LSEICKLSNKFNSVIPVRSGHEDLELLDLSAPFLIQGTVHHYGC
[KQWST*RSIQNLNSLVDKTSWIPSSVAEALGIVPLQYVFVMTFT
			LDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLQKSVDMIMDMFC
 			PPGIKIDAYPWLECFIKSYNVTNGTDNOICYOIFDTTVAEDVI
6843	2	821	NHRKVLSGAKRYECNECGKSFAYTSSLIKHRRIHTGERPVECSE
[1	CGRSFAENSSLIKHLRVHTGERPYECVECGKSFRRSSSLLOHOR
	1	1	VHTRERPYECSECGKSFSLRSNLIHHORVHTGERHECGOCGKSF
	1	1 '	SRKSSLIIHLRVHTGERPYECSDCGKSFAENSSLIKHLRVHTGE
J	İ	1 -	KPYECIDCGKSFRHSSSFRRHORVHTGMRPYK*SKFWKFSCDGF
ì	ĺ	1.2	LLLQGQRVHTGSRCYECDKWGIFFS*NASFFT*KSAPTEEVPFE
6844	244	642	CNECEKAFSPLSLVTTIFT
	:= = ::	416	EHQLAGFELRKTQTSMSLGTTREKTDRVKSTAYLSPQELEDVFY
		<u>\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ </u>	QYDVKSEIYSFGIVLWEIATGDIPFQGCNSEKIRKLVAVKRQQE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
f	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Doguesto	\=possible nucleotide insertion)
	1 - 1 - 1		PLGEDCPSELREIIDECRAHDPSVRPSVDEILKKLSTFSK*CIK
ı	İ		I I I I I I I I I I I I I I I I I I I
6845	3	1519	VAVRDECYWRHVFWDQDLWMLLFILMCHPETARARLBYRIRTLD
	1		GALENAQNLGYQGAKFAWESADSGLEVCPEDIYGVQEVHVNGAV
	İ		GLAFELYYHTTQDLQLFREAGGWDVVRAVAEFWCSRVEWSPREE
1]		KYHLRGVMSPDEYHSGVNNSVYTNVLVQNSLRFAAALAQDLGLP
1	i		IPSQWLAVADKIKVPFDVEQNFHPEFDGYEPGEVVKQADVVLLG
			ADADECT COURDANT STANFALMCDOCOURTHOUSEN
			YPVPFSLSPDVRRKNLEIYEAVTSPQGPAMTWSMFAVGWMELKD
1			AVRARGLLDRSFANMAEPFKVWTENADGSGAVNFLTGMGGFLQA
1	1	1	VVFGCTGFRVTRAGVTFDPVCLSGISRVSVSGIFYQGNKLNFSF
]		SEDSVTVEVTARAGPWAPHLEAELWPSQSRLSLLPGHKVSFPRS
ł	[AGRIQMSPPKLPGSSSSEFPGRTFSDVRDPLQSPLWVTLGSSSP
J	J		TESLTVDPASE*SGTGASETSLGPSLWPRLHPPLLGTLLACHPS
6846	212		PAARLSGKVHAAWPEFKAFCL
1 00-20	213	1258	LYFLKTIK*LNRLAEHP*YENEKLTKLRNTIMEQYTRTEESARG
			IIFTKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKP
			MTQNEQKBVISKFRTGKINLLIATTVAEEGLDIKECNIVIRYGL
1	1		VTNEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDFREKM
1			MYKAIHCVQNMKPEEYAHKILBLQMQSIMEKKMKTKRNIAKHYK
1 .			NNPSLITFLCKNCSVLACSGEDIHVIEKMHHVNMTPEFKELYIV
		•	RENKTLQKKCADYQINGEIICKCGQAWGTMMVHKGLDLPCLKIR
			NFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLFSDED
6847	1450	348	SMCWNSDRLEMPLIDLALILYPPSYVPYTGHLSDDSLSRKYCLT
]			WFEDALNGVL*RAEAIQPHCVNAGDRMEKFRQKYWNKLQTLRQQ
1			PFAYGTLTVRSLLDTREHCLNEFNFPDPYSKVKQRENGVALRCF
1			PGVVRSLDALGWEERQLALVKGLLAGNVFDWGAKAVSAVLESDP
			YFGFEEAKRKLQERPWLVDSYSEWLQRLKGPPHKCALIFADNSG
			IDIILGVFPFVRELLLRGTEVILACNSGPALNDVTHSESLIVAE
			RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR
			ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG
6848	19		GRLFSVIFKYEVPAE
0040	19	16	AMWWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND
1 8	1		LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH
			IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN
1 1	1		VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK
] [Í		VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA
6849	70		YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH
""	,,	821	SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC
1 1	į	ĺ	VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK
]]	Ī	}	PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM
]]			VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ
]]			YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG
6850			VIKVKGKGQLCTYFLNTDLTRTGPPSATLG
1 0000 [2	1235	ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD
[LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL
1			RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI
			GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT
j f			KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS
j l		ľ	NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL
	i	ļ	YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ
j	İ]	HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ
			LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK
			EALNQDINIPFANGI
6851	1765	660	VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD
		į	LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA
			CYCVYKLTIGRDDSEKLEEEGEEEWDDDQELDEEEPDIWFDFET

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, FaPhenylalanine, GaGlycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence .		\=possible nucleotide insertion)
1			MARPWTEDGDWTEPGAPGGTEDRPSGGGKANRAHPIKQRPFPYE
		1	HKNTWSAQNCKNGSCVLDLSKCLFIQGKLLFAEPKDAGFPFSQD
j			INSHLASLSMARNTSPTPDPTVREALCAPDNLNASIESQGQIKM
İ			YINEVCRETVSRCCNSFLQQAGLNLLISMTVINNMLAKSASDLK
ŀ			FPLISEGSGCAKVQVLKPLMGLSEKPVLAGELVGAQMLFSFMSL
6852	1	407	FIRNGNREILLETPAP
	1	307	RTRGEETYANFIKHNDGKNIFYAARTPATLFAVMFAMYIISGLT GFIGLNSIAVLCNLVMGLALIFLCTWAYVKYSGEFREIGTVIDQ
1			IAETLWEQVLKPLGDNLMEENIRQSVTNSIKAGLTDQVSHHARL
ĺ			KTD
6853	3	469	GDSCAVCIELYKPNDLVRILTCNHIFHKTCVDPWLLEHRTCPMC
1	1		KCDILKALGIEVDVEDGSVSLQVPVSNEIPNSASSHEEDNRSET
			ASSGYASVQGTYEPPLEEHVQSTNESLQLVNHEANSVAVDVIPH
			VDNPTFEEDETPNQETAVREIKS
6854	1148	585	HESYIGTFDPGELCVCAAIQWLQDNSASYFLNRKLVYEPSTQAK
			PVKNTFLRMWIYSHHIYQQDLRKKILDVGKRLDVTGFCMTGKPG
İ			IICVEGFKEHCEEFWHTIRYPNWKHISCKHAESVETEGNGEDLR
1	i		LFHSFEELLLEAHGDYGLRNDYHMNLGQFLEFLKKHKSEHVFQI
6855	1913	1148	LFGIESKSSDS
	4343	1140	GRVGGRVGRICSPLSGANEYIASTDTLKTEEVLLFTDQTDDLAK
			EEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALASRF YIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHI
			QLTYFSRWSEVEDSCDSDAIERMYCAPEVGAITEETEACDWWSL
1			GAVLFELLTGKTLVECHPAGINTHTTLNMPEWVSEEARSLIQQL
			LQFNPLERLGAGVAGVEDIKSHPFFTPVDWAELMR
6856	1617	997	VTQLYVSVDASTKDSLKKIDRPLFKDFWQOFLDSLKALAVKOOR
	1		TVYRLTLVKAWNVDELQAYAQLVSLGNPDFIEVKGVTYCGESSA
			SSLTMAHVPWHEEVVQFVRELVDLIPEYEIACEHEHSNCLLIAH
	-		RKFKIGGEWWTWINYNRFQELIQEYEDSGGSKTFSAKDYMARTP
6857	1		HWALFGASERGFDPKDTRHQRKNKSKAISGC
0037		617	KGPEATAMVCVCSHPNCRQNHIKPSHSAAQTWCGSPTPASAPNH
			KLMAMEQGKTLPSATEDAKEEGLEAQISRLABLIGRLESKALWF
1	1		DLQQRLSDEDGTNMHLQLVRQEMAVCPEQLSEFLDSLRQYLRGT TGVRNCFHITAVRLSDGFTFVIYEFWETEEAWKRHLQSPLCKAF
			RHVKVDTLSQPEALSRILVPAAWCTVGRD
6858	-2	669	RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA
1			LRCVQTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM
1 1	'		SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ
		i	IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAOLVR
			KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS
L			GN
6859	1	1150	GETMFKKAKTKAKKKPRKRSDSSGGYNLSDI1QSPSSTGLLKSG
	İ		KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE
]		į	AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT
1 1			SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT
			VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN
			SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM
			VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF
			YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC
6860	1889	1515	DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ
			DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP
		1	MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM
6861	1889	1515	DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ
<u> </u>			DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP
		· · · · · · · · · · · · · · · · · · ·	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1 " 1	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1 1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
<i>i</i> I	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
f 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	sequence	1.
	bequence	·····	\=possible nucleotide insertion)
			MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM
6862	2	471	EEIDREFHNKLKLKEDKLEKQEKPVNGEDKGDSGVDTQNSEGNA
1			DEEDPLGPNCYYDKTKSFFDNISCDDNRBRRPTWAEERRLNAET
1			FGIPLRPNRGRGGYRGRGGLGFRGGRGGGRGGTFTAPRGFRG
			GFRGGRGGREFADFEYRKTTAFGP
6863	2216	487	PQEPALKSEFSQVASNTIPLPLPQPNTCKDNGPCKQVCSTVGGS
			AICSCFPGYAIMADGVSCEDQDECLMGAHDCSRRQFCVNTLGSF
1			YCVNHTVLCADGYILNAHRKCVDINECVTDLHTCSRGEHCVNTL
1 1			GSFHCYKALTCEPGYALKDGECEDVDECAMGTHTCQPGFLCQNT
1 1			KGSFYCQARQRCMDGFLQDPEGNCVDINECTSLSEPCRPGFSCI
1 1			NTVGSYTCQRNPLICARGYHASDDGTKCVDVNECETGVHRCGEG
			QVCHNLPGSYRCDCKAGFQRDAFGRGCIDVNECWASPGRLCQHT
		,	CENTLGSYRCSCASGFLLAADGKRCEDVNECEAQRCSQECANIY
			GSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILCTFRCLNVPGS
			YQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIQGS
))			FRCLRFECPPNYVQVSKTKCERTTCHDFLECQNSPARITHYOLN
1			FOTGLLVPAHIFRIGPAPAFTGDTIALNIIKGNEEGYFGTRRLN
1 1			AYTGVVYLQRAVLEPRDFALDVEMKLWRQGSVTTFLAKMHIFFT
1 1			TFAL
6864	2	2933	LADSSPSNLQIIIKELLSMHHQPDPALTKEFDYLPPVDSRSSSG
	_		FVGLRNGGATCYMNAVFQQLYMQPGLPESLLSVDDDTDNPDDSV
			FYQVQSLFGHLMESKLQYYVPENFWKIFKMWNKELYVREQQDAY
			EFFTSLIDQMDEYLKKMGRDQIFKNTFQGIYSDQKICKDCPHRY
1 1			EREEAFMALNLGVTSCQSLEISLDQFVRGEVLEGSNAYYCEKCK
			EKRITVKRTCIKSLPSVLVIHLMRFGFDWBSGRSIKYDEQIRFP
1 1	ĺ		WMLNMEPYTVSGMARQDSSSEVGENGRSVDQGGGGSPRKKVALT
1 1			ENYELVGVIVHSGQAHAGHYYSFIKDRRGCGKGKWYKFNDTVIE
1			EFDLNDETLEYECFGGEYRPKVYDQTNPYTDVRRRYWNAYMLFY
1			QRVSDQNSPVLPKKSRVSVVRQEAEDLSLSAPSSPEISPQSSPR
1			PHRPNNDRLSILTKLVKKGEKKGLFVEKMPARIYOMVRDENLKF
1 1			MKNRDVYSSDYFSFVLSLASLNATKLKHPYYPCMAKVSLOLAIO
1 1			FLFQTYLRTKKKLRVDTEEWIATIEALLSKSFDACQWLVEYFIS
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL
1			HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL
1 1			LRHSALRHMISFLLGASRONNQIRRWSSAQAREFGNLHNTVALL
1 1			VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM
1 1	· · · · · · · · · · · · · · · · · · ·		
	l		SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH
1			
1 1			FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN
			fiknoletapphelkntfollheilviedpiovervkfvfbten Gllalmhhsnhvdssrcyocvkflvtlaokcpaakeyfkenshh
			FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFBTEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSBHYWTLQSNVSNETSTGKTFQRTISAQDTLA
6865	1820	1242	FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFBTEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP
6865	1820	1242	FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFBTEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS
6865	1820	1242	FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFBTEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV
6865	1820	1242	FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFBTEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQENVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDKHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDCKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ
6865	1820	1242	FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFBTEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDKHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDCKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS
6865			FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFBTEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDCKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGQSSVQTIQPKRDS
	1820	1242 495	FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFBTEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGQSSVQTIQPKRDS DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF
			FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFBTEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGQSSVOTIQFKRDS DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP
			FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFBTEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPFAS PFGQSSVQTIQPKRDS DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG
			FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFBTEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPFAS PFGQSSVOTIQPKRDS DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSR
			FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFBTEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQENVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPFAS PFGQSSVQTIQPKRDS DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF IIEGMEEAGSVALEELVEKEKDRFFSGVDYVISDNLWISQRKP ATTYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSR VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV
			FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFBTEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQENVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDCKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGQSSVQTIQPKRDS DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLBEYRNSSR VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTL
			FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFILV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGQSSVOTIOPKRDS DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP ATTYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSR VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIFGRV IGKFSIRLVPHMNVSAVEKQVTRHLEDVPSKRNSSNKMVVSMTL GLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMF
			FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFBTEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQENVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDCKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGQSSVQTIQPKRDS DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLBEYRNSSR VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ı	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
6867	2833	1704	GTRIMSQPKQKELAGFVRQKMLLDYSVYMGRCVPQESRSPQRSP
1			LQSAESSPTAGKKLPEVPPSEEEEQEAWVNALLGRIFWDFLGEK
}		ļ	YWSDLVSKKIQMKLSKIKLPYFMNELTLTELDMGVAVPKILQAF
			KPYVDHQGLWIDLEMSYNGSFLMTLETKMNLTKLGKEPLVEALK
1			VGEIGKEGCRPRAFCLADSDEESSSAGSSEEDDAPEPSGGDKOL
	ļ		LPGAEGYVGGHRTSKIMRFVDKITKSKYFQKATETEFIKKKIEE ,
1			VSNTPLLLTVEVQECRGTLAVNIPPPPTDRVWYGFRKPPHVELK
			ARPKLGEREVTLVHVTDWIEKKLEQEFQKVFVMPNMDDVYITIM
<u> </u>			HSAMDPRSTSCLLKDPPVEAADOP
6868	1	346	RPTRPPTRPEEIKNLILPYISDMNFVQDLCEDFYELFKTDKGFD
			KATFESQMSVMRGQILNLTQALRDGKSPFQLVQIPCVIVERSQG
			GSQGRIVHLSNSFTQTVNCRKPFFSSW
6869	3	1619	MYMERMDKRALISFWESVEHLKNANKNEIPQLVGEIYQNFFVES
1			KEISVEKSLYKEIQQCLVGNKGIEVFYKIQEDVYETLKDRYYPS
4			FIVSDLYEKLLIKEEEKHASQMISNKDEMGPRDEAGEEAVDDGT
			NQINEQASFAVNKLRELNEKLEYKRQALNSIQNAPKPDKKIVSK
			LKDEIILIEKERTDLQLHMARTDWWCENLGMWKASITSGEVTEE
1			NGEQLPCYFVMVSLQEVGGVETKNWTVPKRLSEFHNLHRKLSEC
1			VPSLKKDQLPSLSKLPFKSIDHTFMEKFENQLNKFLQNLLSDER
	i		LCQSEALYAPLSPSPDYLKVIDVQGKKNSFSLSSFLERLPRDFF
			SHQEEETEEDSDLSDYGDDVDGRKDALAEPCFMLIGEIFELRGM .
			FKWVRRTLIALVQVTFGRTINKQIRDTVSWIFSEQMLVYYINIF
			RDAFWPNGKLAPPTTIRSKEQSQETKQRAQQKLLENIPDMLQSL
			VGQQNARHGIIKIFNALQETRANKHLLYALMELLLIELCPELRV HLDQLKAGQV
6870	1	1566	MAAVVAATRWWQLLLVLSAAGMGASGAPQPPNILLLLMDDMGWG
1	_	2500	DLGVYGEPSRETPNLDRMAAEGLLFPNFYSANPLCSPSRAALLT
1			GRLPIRNGFYTTNAHARNAYTPQEIVGGIPDSEQLLPELLKKAG
			YVSKIVGKWHLGHRPQFHPLKHGFDEWFGSPNCHFGPYDNKARP
			NIPVYRDWEMVGRYYEEFPINLKTGEANLTQIYLQEALDFIKRQ
			ARHHPFFLYWAVDATHAPVYASKPFLGTSQRGRYGDAVREIDDS
]		IGKILELLQDLHVADNTFVFFTSDNGAALISAPEQGGSNGPFLC
1.			GKQTTFEGGMREPALAWWPGHVTAGQVSHQLGSIMDLFTTSLAL
1	1		AGLTPPSDRAIDGLNLLPTLLQGRLMDRPIFYYRGDTLMAATLG
1 1	ł		QHKAHFWTWTNSWENFRQGIDFCPGQNVSGVTTHNLEDHTKLPL
1			IFHLGRDPGERFPLSFASAEYQEALSRITSVVQQHQEALVPAQP
1			QLNVCNWAVMNWAPPGCEKLGKCLTPPESIPKKCLWSH
6871	209	1126	RMSLNPPIFLKRSEENSSKFVETKQSQTTSIASEDPLQNLCLAS
1	1	i	QEVLQKAQQSGRSKCLKCGGSRMFYCYTCYVPVENVPIEQIPLV
j	ĺ	1	KLPLKIDIIKHPNETDGKSTAIHAKLLAPEFVNIYTYPCIPEYE
	Ì		EKDHEVALIFPGPQSISIKDISFHLQKRIQNNVRGKNDDPDKPS
1 1			FKRKRTEEQEFCDLNDSKCKGTTLKKIIFIDSTWNQTNKIFTDE
, ,	ļ		RLQGLLQVELKTRKTCFWRHQKGKPDTFLSTIEAIYYFLVDYHT
6872	880	450	DILKEKYRGQYDNLLFFYSFMYQLIKNAKCSGDKETGKLTH
[""]	000	459	FGLLMVVLSLIFMKGNCVREDLIFNFLFKLGLDVRETNGLFGNT
]]	Ī		KKLITEVFVRQKYLEYRRIPYTEPAEYEFLWGPRAFLETSKMLV
1			LRFLAKLHKKDPQSWPFHYLEALAECEWEDTDEDEPDTGDSAHG
6873	1929	955	PTSRPPPR
	1,23	755	DEQAVLCSKDKTYDLKIADTSNMLLFIPGCKTPDQLKKEDSHCN
]			I IHTEIFGFSNNYWELRRRRPKLKKLKKLLMENPYEGPDSQKEK
]]		Í	DSNSSKYTTEDLLDQIQASEEEIMTQLQVLNACKIGGYWRILEF
		i	DYEMKLLNHVTQLVDSESWSFGKVPLNTCLQELGPLEPEEMIEH
			CLKCYGKKYVDEGEVYFELDADKICRAARMLLQNAVKFNLAEF
]		ļ	QEVWQQSVPEGMVTSLDQLKGLALVDRHSRPEIIFLLKVDDLPE
1		į	DNQERFNSLFSLREKWTEEDIAPYIQDLCGEKQTIGALLTKYSH SSMQNGVKVYNSRRPIS
		<u></u>	CINDACALANDACE

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence		\=possible nucleotide insertion)
6874	1	307	DSIADHVNSAAVNVEEGTKNLGKAAKYKLAALPVAGALIGGMVG
			GPIGLLAGFKVAGIAAALGGGVLGFTGGKLIQRKKQKMMEKLTS
1	ļ		SCPDLPSQTDKKCS
6875	1688	349	VIGTGERGNSASEKWEIMFNEELGDPFIIIHSISLLNAEEHSIA
			TLLLRIEKEELDMKGSGFYVSLEWVTISKKNQDNKKYEIIKRDI
1			LRGKSVPHYAAIEPDGNGLMIVSYKSLTFVQAGQDLEENMDEDI
			SEKIKEPLYYWQQTEDDLTVTIRLPEDNTKEDIQIQFLPDHINI
1			VLKDHQFLEGKLYSSIDHESSTWIIKESNSLEISLIKKNEGLTW
1	i		PELVIGDKQGELIRDSAQCAAIAERLMHLTSEELNPNPDKEKPP
			CNAQELEECDIFFEESSSLCRFDGNTLKTTHVVNLGSNQYLFSV
			IVDPKEMPCFCLRHDVDALLWQPHSSKQDDMWEHIATFNALGYV
1			QASKRDKKFFACAPNYSYAALCECLRRVFIYRQPAPMSTVLYNR
			KEGRQVGQVAKQQVASLETNDPILGFQATNERLFVLTTKNLFLI
1 :			KUNTEN
6876	41	1285	VGEMTLIWRHLLRPLCLVTSAPRILEMHPFLSLGTSRTSVTKLS
	3.4	1203	LHTKPRMPPCDFMPERYQVIFLVNSGSEANELAMLMARAHSNNI
			DIISFRGAYHGCSPYTLGLTNVGIYKMELPGGTGCQPTMCPDVF
1			RGPWGGSHCRDSPVQTIRKCSCAPDCCQAKDQYIEQFKDTLSTS
1			VAKSIAGFFAEPIQGVNGVVQYPKGFLKEAFELVRARGGVCIAN
1			EVQTGFGRLGSHFWGFQTHDVLPDIVTMAKGIGNGFPMAAVITT
1 1			PEIAKSLAKCLQHFNTFGGNPMACAIGSAVLEVIKEENLQENSO
			EVGTYMLLKFAKLRDEFEIVGDVRGKGLMIGIEMVQDKISCRPL
1			PREEVNQIHEDCKHMGLLVGRGSIFSQTFRIAPSMCITKPEVDF
1 1]		AVEVFRSALTOHMERRAK
6877	1	778	GTSPSPARAYAPPTERKRFYQNVSITQGEGGFEINLDHRKLKTP
	_	,,,	QAKLFTVPSEALAIAVATEWDSQQDTIKYYTMHLTTLCNTSLDN
ĺ			PTQRNKDQLIRAAVKFLDTDTICYRVEEPETLVELQRNEWDPII
i J			EWAEKRYGVEISSTSIMGPSIPAKTREVLVSHLASYNTWALQG
!			IEFVAAQLKSMVLTLGLIDLRLTVEQAVLLSRLEEEYQIQKWGN
1			IEWAHDYELQELRARTAAGTLFIHLCSESTTVKHKLLKE
6878	931	263	QTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN
			LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCODKEGNPAP
1	1		EYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLD
	i		TGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVIS
]	Į.		VCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSF
	!		II
6879	3	845	IRVIGESDIMQEFLSESDENYNGVSDVELRVALPDGTTVTVRVK
	ł		KNSTTDQVYQAIAAKVGMDSTTVNYFALFEVISHSFVRKLAPNE
	İ	İ	FPHKLYIQNYTSAVPGTCLTIRKWLFTTEEEILLNDNDLAVTYF
			FHQAVDDVKKGYIKAEEKSYQLQKLYEQRKMVMYLNMLRTCEGY
l l			NEIIFPHCACDSRRKGHVITAISITHFKLHACTEEGQLENQVIA
		İ	FEWDEMQRWDTDEEGMAFCFEYARGEKKPRWVKIFTPYFNYMHE
]		!	CFERVFCELKWRKEEY
6880	2110	1437	RKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISS
			MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRS
			NRDQIKNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMFH
			VLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNAS
			KPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDESD
			EDTF
6881	2638	2244	NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR
1			QRVAAVKDLIRQLPKPNQDTMQILFRHLRRVIENGEKNRMTYQS
			IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR
6882	-	850	
	^	050	GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN
[1	Ϊ	QEGNMVTARQEPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT
]]	İ	TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSQPYRLVHFEPH
			MRPRRPHQIADLFRPKDQIAYSDTSPFLILSEASLADLNSRLEK

SEQ	Predicted	Predicted end	Lamino and annual control of the con
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
10.	location	corresponding	Giddamic Acid, rephenylatanine, Geglycine,
}	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L-Leucine, M-Methionine, N-Asparagine, P-Proline, Q-Glutamine, R-Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	•
j	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1	sequence	sequence	\=possible nucleotide insertion)
	Jedaciico -		KVKATNFRPNIVISGCDVYAEDSWDELLIGDVELKRVMACSRCI
1			
1	1		LTTVDPDTGVMSRKEPLETLKSYRQCDPSERKLYGKSPLFGQYF VLENPGTIKVGDPVYLLGQ
6883	2794	2256	
0005	2/34	2230	NSKLKLNONLKLFITLTYQVLSLHGWGPGIHLQKEGAFPVTQNR
1	•		ALQLLYDLRYLNIVLTAKGDEVKSGRSKPDSRIEKVTDHLEALI
			DPFDLDVFTPHLNSNLHRLVQRTSVLFGLVTGTENQLAPRSSTF
	1		NSQEPHNILPLASSQIRFGLLPLSMTSTRKAKSTRNIETKAQYD ANC
6884	2	99	
6885	297		BFERVTAEAVKPRETSEPRAAAQRFCEKFPFL
8883	431	1554	STGQFWHVTDLHLDPTYHITDDHTKVCASSKGANASNPGPFGDV
			LCDSPYQLILSAFDFIKNSGQEASFMIWTGDSPPHVPVPELSTD
			TVINVITNMTTTIQSLFPNLQVFPALGNHDYWPQDQLSVVTSKV
	[YNAVANLWKPWLDBEAISTLRKGGFYSQKVTTNPNLRIISLNTN
1	1		LYYGPNIMTLNKTDPANQFEWLESTLNNSQQNKEKVYIIAHVPV
1	1		GYLPSSQNITAMREYYNEKLIDIFQKYSDVIAGQFYGHTHRDSI
			MVLSDKKGSPVNSLFVAPAVTPVKSVLEKQTNNPGIRLFQYDPR
İ			DYKLLDMLQYYLNLTEANLKGESIWKLEYILTQTYDIEDLQPES
}			LYGLAKQFTILDSKQFIKYYNYFFVSYDSSVTCDKTCKAFQICA IMNLDNISYADCLKQLYIKHNY
6886	2	1341	
""		1247	QCGGIPGREGGSSRPLEEGTGSSPACVRGAAPGSEDAFYPTRAK QARVSQELKKAAKRTVSISEGPDTLGDGMRERRETLALAPEPEP
i			LEKEACEKWKRPFRSASATSLTLSHCVDVVKGLLDFKKRRGHSI
1	1		GGAPEQRYQIIPVCVAARLPTRAQDVLDAHLSEVNAVRFGPNSS
1			LLATGGADRLIHLWNVVGSRLEANOTLEGAGGSITSVDFDPSGY
1			QVLAATYNQAAQLWKVGEAQSKETLSGHKDKVTAAKFKLTRHQA
1	l j		VTGSRDRTVKEWDLGRAYCSRTINVLSYCNDVVCGDHIIISGHN
			DQKIRFWDSRGPHCTQVIPVQGRVTSLSLSHDQLHLLSCSRDNT
į			LKVIDLRVSNIRQVFRADGFKCGSDWTKAVFSPDRSYALAGSCD
			GALYIWDVDTGKLESRLQGPHCAAVNAVAWCYSGSHMVSVDQGR
J	ļ .		KVVLWQ
6887	1047	116	WTARPSQKPFWEAGAVPGDPLSTGCSQAQLGGCCPRGPWGPQHG
		****	GOORAAGPTLPRGERGGPQQSGPGLAAQTPPTSKQVAWRAFLTG
i .			TYRSQSPRSPAGPFRGGTGWWPEPAVCLCVAVGPQRLSSPGLVY
1 .			NASGSEHCYDIYRLYHSCADPTGCGTGPDARAWDYQACTEINLT
1			FASNNVTDMFPDLPFTDELRQRYCLDTWGVWPRPDWLLTSFWGG
1			DLRAASNIIFSNGNLDPWAGGGIRRNLSASVIAVTIQGGAHHLD
			LRASHPEDPASVVEARKLEATIIGEWVKAARREQQPALRGGPRL
] .			SL SL
6888		992	FVAYVKKEIPHIVVTHCLLNPHALVIKTLPTKLRDALFTVVRVI
-	i	-	NFIKGRAPNHRLFQAFFEEIGIEYSVLLFHTEMRWLSRGOILTH
]			IFEMYEEINQFLHHKSSNLVDGFENKEFKIHLAYLADLFKHLNE
1 1			LSASMORTGMNTVSAREKLSAFVRKFPFWQKRIEKRNFTNFPFL
į l	1		EEIIVSDNEGIFIAAEITLHLQQLSNFFHGYFSIGDLNEASKWI
) 1]		LDPFLFNIDFVDDSYLMKNDLAELRASGQILMEFETMKLEDFWC
			AQFTAFPNLAKTALEILMPFATTYLCELGFSITFTFQNKVPEAA
			LILSDDIRVAISKKVPSFLGHH
6889	1	1534	LTLENQIKEEREQDNSESPNGRTSPLVSQNNEQGSTLRDLLTTT
]]		AGKLRVGSTDAGIAFAPVYSMGAPSSKSGRTMPNILDDIIASVV
l í	1		ENKIPPSKTSKINVKPELKEEPEESIISAVDENNKLYSDIPHSW
) l	1		ICEKHILWLKDYKNSSNWKLFKECWKQGQPAVVSGVHKKMNISL
! I	į	ļ	WKAESISLDFGDHQADLLNCKDSIISNANVKEFWDGFEEVSKRO
	į		KNKSGETVVLKLKDWPSGEDFKTMMPARYEDLLKSLPLPEYCNP
			EGKFNLASHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI
			EVSDVVNILVYVGIAKGNGILSKAGILKKFEEEDLDDILRKRLK
1 1	İ	ł	DSSEIPGALWHIYAGKDVDKIREFLOKISKEOGLEVLPEHDPIR
l			DQSWYVNKKLRQRLLBEYGVRTWTLIQFLGDAIVLPAGALHQVQ
		1	- 22 KARTINET O A KTH I HIGT DODGET A NEWGYNITÁ A Á

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ŀ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
1			NFHSCIQVTEDFVSPEHLVESFHLTQELRLLKEEINYDDKLQVK
			NILYHAVKEMVRALKIHEDEVDDMEEN
6890	3	667	THACGMWIPLYLHRALVVHKTAETCNSPPCGAKDSLIFGAITCF
1			TGFLGVDTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFV
1	1		AAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAV
į.			ALQSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYA
1			LMLCPFVVVLGGMFFLATALFFVSDRARAEQQVNQLAMPPASVK
6891	1980	3060	V
1 5551	T 200	1262	LRIHQELLSKELKLLRGITIESIIHIGLAAGKEQFMQDASNVMQ
1			LLLKTQSHLYNMEDNNPEVRQAAAYGLGVMAQFGGDDYRSLCSE
1	· ·		AVPLLVKVIKRAHSKTKKNVIATENCISAIGKILKFKPNCVNVD
1			EVLPHWLSWLPLHEDKERAIQTLSFLCDLIESNHPVVIGPNNSN
			LPKIISIIAEGKINETINYEDFCAKRLANVVRQVQTSEDLWLEC VSQLDDEQQEALOELLNFA
6892	3	876	RSVAAASGPGAWGTDHYCLELLRKRDYEGYLCSLLLPAESRSSV
1		0.0	FALRAFNVELAQVKDSVSEKTIGLMRMQFWKKTVEDIYCDNPPH
1			QPVAIELWKAVKRHNLTKRWLMKIVDEREKNLDDKAYRNIKELE
1			NYAENTQSSLLYLTLEILGIKDLHADHAASHIGKAQGIVTCLRA
1			TPYHGSRRKVFLPMDICMLHGVSQEDFLRRNQDKNVRDVIYDIA
} ·			SQAHLHLKHARSFHKTVPVKAFPAFLQTVSLEDFLKKIQRVDFD
			IFHPSLQQKNTLLPLYLYIQSWRKTY
6893	1	842	DGERKSMSVERTFSEINKAEEQYSLCQELCSELAODLOKERLKG
			RTVTIKLKNVNFEVKTRASTVSSVVSTABEIFAIAKELLKTEID
1			ADFPHPLRLRLMGVRISSFPNEEDRKHQQRSIIGFLOAGNOALS
1 1			ATECTLEKTDKDKFVKPLEMSHKKSFFDKKRSERKWSHODTFKC
1 1			EAVNKQSFQTSQPFQVLKKKMNENLEISENSDDCQILTCPVCFR
			AQGCISLEALNKHVDECLDGPSISENFKMFSCSHVSATKVNKKE
6894	1742	1463	NVPASSLCEKQDYEAH
	-,	1407	TTLCKPLVPREHQFYETLPAEMRKFTPQYKGKSQLLEGLPHWRG
1			DVRDRGHGRPWQPSLEPSLPPTLCFPSLSSFSSSWPSAQHLTPS VFNPW
6895	2379	478	VTYVELCDLASPTALLIMRTVLDLIVEDLQSTSEDKEQQYTSQT
{ }	1	1,0	TRLLALLYALASHKACKLAILHLINGTIKGDERYAEIFQDLLAL
	i		VRSPGDSVIRQQCVEYVTSILQSLCDQDIALILPSSSEGSISEL
1	ļ		EQLSNSLPNKELMTSICDCLLATLANSESSYNCLLTCVRTMMFL
1 !	ŀ	į	AEHDYGLFHLKSSLRKNSSALHSLLKRVVSTFSKDTGELASSFL
		1	EFMRQILNSDTIGCCGDDNGLMEVEGAHTSRTMSINAAELKOLL
j		1	QSKEESPENLFLELEKLVLEHSKDDDNLDSLLDSVVGLKOMLES
1 1		l	SGDPLPLSDQDVEPVLSAPESLQNLFNNRTAYVLADVMDDOLKS
1 1			MWFTPFQAEEIDTDLDLVKVDLIELSEKCCSDFDLHSELERSFL
			SEPSSPGRTKTTKGFKLGKHKHETFITSSGKSEYIEPAKRAHVV
1 1			PPPRGRGGGGGGGGRPHDIFRQRKQNTSRPPSMHVDDFVAAES
			KEVVPQDGIPPPKRPLKVSQKISSRGGFSGNRGGRGAFHSQNRF
			FTPPASKGNYSRREGTRGSSWSAQNTPRGNYNESRGGQSNFNRG
1 1	l		PLPPLRPLSSTGYRPSPRDRASRGRGGLGPSWASANSGSGGSRG
6896		. 555	KFVSGGSGRGRHVRSFTR
	- 1	. 333	GNIVIQKKKYNKQHIIPLENVTIDSIKDEGDLRNGWLIKTPTKS
[[1	. 1	FAVYAATATEKSEWMNHINKCVTDLLSKSGKTPSNEHAAVWVPD
]		J	SEATVCMRCQKAKFTPVNRRHHCRKCGFVVCGPCSEKRFLLPSQ
]	SSKPVRICDFCYDLLSAGDMATCQPARSDSYSQSLKSPLNDMSD DDDDDDSSD
6897	3	920	, and the second second second second second second second second second second second second second second se
'	-	727	GDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHY AGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVL
ļ	Ì	1	SLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLA
		İ	YLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDE
			DFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML
			TANA AND TANA TANA TANA TANA TANA TANA T

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Stor
Ī	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
ĺ			LRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGR
6898	0.00		LMVSEAVQGQVHPNYFWMVSGCVEPPPSWKPOOMPPPREDI.
0038	919	346	QKTVTAVASLLKGRQGIYTENERRMGAVIKTREEKTMING TICK
1	ļ		LSNIINESLLFYLEMQTDINGGSLKPVRTAAKTTWFTMGTINDA
			QGFLLSLAFYGWTGCSLGFOSPRKEIOWESLTTSAAFGAUDEDI
			MPHENPASGKVSQVGGQTSDEALSMLSEGSDASTIEIHTASESC
6899	120	827	NKNEGDPALPTHGDL
	-20	""	MKVRKNNDAYLLDKNKINMDCFISCFFKKMLTTLMFSHSGILSL
i			LEHGEEYTFSLPCAYARSILTVPWVELGGKVSVNCAKTGYSASI
			TFHTKPFYGGKLHRVTAEVKHNITNTVVCRVQGEWNSVLEFTYS
1			NGETKYVDLTKLAVTKKRVRPLEKQDPFESRRLWKNVTDSLRES
Í			EIDKATEHKHTLEERORTEERHRTETGTPWKTKYFIKEGDGWVY HKPLWKIIPTTQPAB
6900	3	451	TEVLGSKGIHELRSSTSALHHALEESASLLTMFWRAALPSTHIP
			VLPGKVGESTERELLELRTKVSQQEQLLQSTTEHLKNANQQKES
1	,		MEQFIVSQLTRTHDVLKKARTNLEVRKLLHQSEAPSLSPTHHHP
L			LADLVGDSWPALRFQEK
6901	1	201	DDNMVQRLETDFKMTLQQQSTLEQWAAWLDNVMMQALKPYEGRP
L			SFPKAARQFLLKWSFYRYHLGFS
6902	2	267	GAPPPPPSQPPRQPPQAAPSSHPHSDLTFNPSSALEGOAGACGA
6903			SDMPEPSLDLLPELTNPDELLSYLDPPDLPSNSNDDLLSLPPNN
0903	1	149	RINOVYROGPTGIHILVIDOMVONFODESCFLFSTVKAESSOCT
6904	464		HIILK
0501	707	2092	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC
1			VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA
1	1		DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF
1 1			SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD
1			TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN
			AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELUKQPPD VTENPYRKSGQBASIGKQILAPVEESACQFFFDLNEKQGRKRSS
1 1	[TGRDSKSSPHPKOPRKPPOPPGPCWFCLASPEVEKHLVVNIGTH
1	j		CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL
]]		i	RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF
1			ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR
]	j		IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEBTLARR
			FRKDFEPYDFTLDD
6905	1	226	VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI
6906			VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA
9999	3	611	SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKITDAT
	İ	ļ	ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVETET
	ļ		TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFTNAVKEKYGIE
- 1		1	PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV
6907			SFAPDIDGDEDLPGPPVRYYFSHDTD
1	-	2228	LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS
1	İ		SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS
1			DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT
ł			GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS
1	}	1	SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA
l	ľ		SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ
- 1	İ	j	TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHRD
1	1	1	TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE
1		1.	DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE
1	ŀ		DQLAGLQQELAALALKQSSVAEEVGLLPQQIQAVRDDVESQFPA
			WISQFLARGGGRVGLLQREEMQAQLRELESKILTHVAEMQGKS
			Z. Z. Zamanana matu Mana (CAC)

SEQ	Predicted	Predicted end	Daning and account contributes of such a
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
""	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	Labeucine, Mamethionine, NaAsparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Í	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
			AREAAASLSLTLQKEGVIGVTEEQVHHIVKQALQRYSEDRIGLA
1			DYALESGGASVISTRCSETYETKTALLSLFGIPLWYHSQSPRVI
1			LQPDVHPGNCWAFQGPQGFAVVRLSARIRPTAVTLEHVPKALSP
			NSTISSAPKDFAIFGFDEDLQQEGTLLGKFTYDQDGEPIQTFHF
•	ł		QAPTMATYQVVELRILTNWGHPEYTCIYRFRVHGEPAH
6908	3	780	QVPSAAWLMAVCGLGSRLGLGSRLGLQGCFGAARLLYPRFQSRG
ĺ			PQGVEDGDRPQPSSKTPRIPKIYTKTGDKGFSSTFTGERRPKDD
			QVFEAVGTTDELSSAIGFALELVTEKGHTFAEELQKIQCTLODV
l			GSALATPCSSAREAHLKYTTFKAGPILELEQWIDKYTSOLPPLT
			AFILPSGGKISSALHFCRAVCRRAERRVVPLVQMGETDANVAKP
ļ			LNRLSDYLFTLARYAAMKEGNQEKIYKKNDPSAESEGL
6909	3	409	GRLLAVGTDLYGQRSSAPEQELLVQDATPVSNSLLPEKAFSDIP
ļ			SPYLRGTIKMMQAVRQAFQDQDDRRTWDGRPLTMAATFDDCLYA
1			LCVVDTIKRSSQTGEWQNIAIMTEEPELSPAYLISEAMRRSRMS
Ì			LYC
6910	1	1068	LVPVVVIDSYYYGKLVIAPLNIVLYNIFTPHGPDLYGTEPWYFY
1	}		LINGFLNFNVAFALALLVLPLTSLMEYLLQRFHVQNLGHPYWLT
	1		LAPMYIWFIIFFIQPHKEERFLFPVYPLICLCGAVALSALQHSF
			LYFQKCYHFVFQRYRLEHYTVTSNWLALGTVFLFGLLSFSRSVA
1		•	LFRGYHGPLDLYPEFYRIATDPTIHTVPEGRPVNVCVGKEWYRF
			PSSFLLPDNWQLQFIPSEFRGQLPKPFAEGPLATRIVPTDMNDO
	[NLEEPSRYIDISKCHYLVDLDTMRETPREPKYSSNKEEWISLAY
j		•	RPFLDASRSSKLLRAFYVPFLSDQYTVYVNYTILKPRKAKQIRK
			KSGG
6911	1184	966	GEDAEEMETGNVANLISIFGSSFSGLLRKSPGGGREEEEGEESG
			PEAAEPGQICCDKPVLRDMNPWSTAIVAF
6912	1	844	AMKPVETHSFQMLFTILSTGSALKAQSYEDAYRCIKSSILLGSI
1	'		SGGTDIISCFMGHNFSLPVYKGEIQARNLGMAVEAWNEEGKAVW
			GESGELVCTKPIPCQPTHFWNDENGNKYRKAYFSKFPGIWAHGD
			YCRINPKTGGIVMLGRSDGTLNPNGVRFGSSEIYNIVESFEEVE
			DSLCVPQYNKYREERVILFLKMASGHAFQPDLVKRIRDAIRMGL
			SARHVPSLILETKGIPYTLNGKKVEVAVKQIIAGKAVEQGGAFS
			NPETLDLYRDIPELQGF
6913	1643	. 1558	KKSHEESHKEELSYGAQASLPLPCSDFR
6914	1251	615	ELAAECKSAGYPGTLIPYRCDLSNEEDILSMFSAIRSQHSGVDI
			CINNAGLARPDTLLSGSTSGWKDMFNVNVLALSICTREAYQSMK
1			ERNVDDGHIININSMSGHRVLPLSVTHFYSATKYAVTALTEGLR
	!		QELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMK
C01E			CLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT
6915	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
			ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
	·		VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6916	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
[ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
 _			VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6917	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
	[ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
			VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6918	28	921	PEAGTRSWREPDPEDLRRFLLSAACRSFPQWLPGGGGGQVSSCS
	1		DTDVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRLLFLLGSP
	į		VGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAW
	ļ		LGRHCPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLGE
	I		VFTQAMPLRKPGGPFYVPESFFEGGYPAYASGGGYVIAGRLAPW
			LLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADRT
			ADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC

SEQ	Predicted	Predicted end	L'amino
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
- 1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	Walling, Tainreonine, Vavaline,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	pedacuce	Codon, /=possible nucleotide deletion,
6919	850	41	\=possible nucleotide insertion)
	1	4.1	QGRRELSGSVFCPFIQQEPKEMLTLSEYHERVRSQGQQLQQLQA
İ			ELDKLHKEVSTVRAANSERVAKLVFQRLNEDFVRKPDYALSSVG
1	ſ		ASIDLQKTSHDYADRNTAYFWNRFSFWNYARPPTVILEPHVFPG
	1		NCWAFEGDQGQVVIQLPGRVQLSDITLQHPPPSVEHTGGANSAP
			RDFAVFFLLSFFTHQGLQVYDETEVSLGKFTFDVEKSEIQTFHL
1			QNDPPAAFPKVKIQILSNWGHPRFTCLYRVRAHGVRTSEGAEGS
6920	1418		AQGPH
6921		591	EAQGPSKVHLTLKKKK
0321	2	1711	MNATRSEEQFHVINHAEQTLRKMENYLKEKQLCDVLLIAGHLRI
1			PAHRLVLSAVSDYFAAMFTNDVLEAKQEEVRMEGVDPNALNSLV
			QYAYTGVLQLKEDTIESLLAAACLLQLTQVIDVCSNFLIKQLHP
1			SNCLGIRSFGDAQGCTELLNVAHKYTMEHFIEVIKNQEFLLLPA
			NEISKLLCSDDINVPDEETIFHALMQWVGHDVQNRQGELGMLLS
	·		YIRLPLDPPQLLADLETSSMFTGDLECQKLLMEAMKYHLLPERR
Į			SMMQSPRTKPRKSTVGALYAVGGMDAMKGTTTIEKYDLRTNSWL
1			HIGTMNGRRLQFGVAVIDNKLYVVGGRDGLKTLNTVECFNPVGK
			IWTVMPPMSTHRHGLGVATLEGPMYAVGGHDGWSYLNTVERWDP
			EGRQWNYVASMSTPRSTVGVVALNNKLYAIGGRDGSSCLKSMEY
			FDPHTNKWSLCAPMSKRRGGVGVATYNGFLYVVGGHDAPASNHC
1			SRLSDCVERYDPKGDSWSTVAPLSVPRDAVAVCPLGDKLYVVGG
6922	1075	369	YDGHTYLNTVESYDAQRNEWKEEVPVNIGRAGACVVVVKLP
"""	10/3	369	LTPPAGIRHEVRDREREREREREREKFPLDSTGSELKONIHSIT
			GLPPAMQKVMYKGLAPEDKTLREIKVTSGAKIMGGGSTINDVLA
1			VNTPKDAAQQDAKAEENKKEPLCRQKQHRKVLDKGKPEDVMPSV
1 1			KGAQERLPTVPLSGMYNKSGGKVRLTFKLEQDQLWIGTKERTEK
1	1		LPMGSIKNVVSEPIEGHEDYHMMAFQLGPTEASYYWVYWVPTQY
6923	2469	1660	VDAIKDTVLGKWQYF
1	1.05	1000	LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ
))	}		LPVTFGNKQKVLGKALSLIRFPLMTIEEFAAGPAQSGILSDREV
	j		VNLFLHFTVNPKPRVEYIDRPRCCLRGKECCINRFQQVESRWGY
1	į		SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDYQVNIQIIEYEKK
1 1	1		QTLGQNDTGFSCDGTANTFRVMFKEPIEILPNVCYTACATLKGP
	i		DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT
6924	2210	1235	
		1233	PEERVICEVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP
[ł		KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP
1	į.		ISCFYCECEEKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE
1 1	j		HGEEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF
	i		HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG
			ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI
1 1			DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ
6925	2	1653	SPLESTLMGLEVQSFPV
	- 1	1033	RGGAAGAAMBPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL
]]	.		SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF
			DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP
}	İ		EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI
, ,			ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI
		[IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG
[[1	LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS
		. 1	TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV
			WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW
1	ļ	i	STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC
į į		İ	GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP
		ļ	RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL
6926			NVPPSAQNETRSPSRTYTYISR
0000	1	733	SGRVAMDGLGLQFPEQGFPAGPPLLPPHMGGHYRDCQSLGAPPL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ĺ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
· I	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			DGYPLPTPDTSPLDGVDPDPAFFAAPMPGDCPAAGTYSYAQVSD
1		i	YAGPPEPPAGPMHPRLGPEPAGPSIPGLLAPPSALHVYYGAMGS
İ			PGAGGGRGFQMQPQHQHQHQHQHHPPGPGQPTPPPEALPCRDGT
J]	DPSQPAELLGEVDRTEFEQYLHFVCKPEMGLPYQGHDSGVNLPD
			SHGAISSVVSDASSAVYYCNYPDV
6927	2	1484	LTLCGDIQLMLAQNANNRAAHLEEFHYQTKEDQEILHSLHRESS
}			CQGFAWATDLSTDLESQLSVSCKCYEAANRILOFRDLKSONPEH
ļ			YVQVLKRMGNIRNEIGVFYMNQAAALQSERLVSKSVSAAEOOLW
]		KKSFSCFEKGIHNFESIEDATNAALLLCNTGRLMRICAOAHCGA
			GDELKREFSPEEGLYYNKAIDYYLKALRSLGTRDIHPAVWDSVN
F	1		WELSTTYFTMATLQQDYAPLSRKAQEQIEKEVSEAMMKSLKYCD
1			VDSVSARQPLCQYRAATIHHRLASMYHSCLRNOVGDEHLRKOHR
1	Į .		VLADLHYSKAAKLFQLLKDAPCELLRVQLERVAFAEFOMTSONS
ſ	(ı	NVGKLKTLSGALDIMVRTEHAFQLIQKELIEEFGQPKSGDAAAA
			ADASPSLNREEVMKLLSIFESRLSFLLLQSIKLLSSTKKKTSNN
!			IEDDTILKTNKHIYSQLLRATANKTATLLERINVIVHLLGQLAA
6020	1000		GSAASSNAVQ
6928	1086	777	EAIDLINNLLQVKMRKRYSVDKTLSHPWLQDYQTWLDLRELECK
			IGERYITHESDDLRWEKYAGEQGLQYPTHLINPSASHSDTPETE
6929	7540		ETEMKALGERVSIL
0929	1749	607	RDQRGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG
1 1			NLHQHDPQDLRHNGNVVVAGRPSCSRGPRRAIQKPQPAGGRRSG
			RGPAAGGLCLQPPDGGTCVPEEPPVPPMDWEALEKHLAGLQFRE
1 1			QEVRNQGQARTNSTSAQKNERESIRQKLALGSFFDDGPGIYTSC
1 1			SKSGKPSLSSRLQSGMNLQICFVNDSGSDKDSDADDSKTETSLD
1 . !			TPLSPMSKQSSSYSDRDTTEEESESLDDMDFLTRQKKLQAEAKM
1	1		ALAMAKPMAKMQVEVEKQNRKKSPVADLLPHMPHISECLMKRSL
1 1	ļ		KPTDLRDMTIGQLQVIVNDLHSQIESLNEELVQLLLIRDELHTE QDAMLVDIEDLTRHAESQQKHMAEKMPAK
6930	131	545	FKDTANVFVSLFQMRNNFRHYFIEPSQLKLFYDVITWIVTQVAI
1 1		313	SYTVVPFVLLSIKPSLTFYSSWYYCLHILGILVLLLLPVKKTOR
1	f		RKNTHENIQLSQSKKFDEGENSLGQNSFSTTNNVCNQNQEIASR
}			HSSLKO
6931	2	659	FVERLPNRPACLLVASGAAEGVSAQSFLHCFTMASTAFNLQVAT
; I	ŀ	-	PGGKAMEFVDVTESNARWVQDFRLKAYASPAKLESIDGARYHAL
			LIPSCPGALTDLASSGSLARILQHFHSESKPICAVGHGVAALCC
)	}		ATNEDRSWVFDSYSLTGPSVCELVRAPGFARLPLVVEDFVKDSG
			ACFSASEPDAVHVVLDRHLVTGQNASSTVPAVQNLLFLCGSRK
6932	2	1131	FVDSPGQGEQAEEEEGGIQMNSRMRAHSPAEGASVESSSPGPKK
		ļ	SDMCEGCRSLAAGHPGYISHDKETSIKYVSHQHPSHPQLFSIVR
		İ	QACVRSLSCEVCPGREGPIFFGDEQHGFVFSHTFFIKDSLARGF
1	ì	ļ	QRWYSIITIMMDRIYLINSWPFLLGKVRGIIDELOGKALKVFEA
			EQFGCPQRAQRMNTAFTPFLHQRNGNAARSLTSLTSDDNLWACI.
		Ì	HTSFAWLLKACGSRLTEKLLEGAPTEDTLVOMEKLADLEEESES
	i		WDNSEAEEEEKAPVLPESTEGRELTQGPAESSSLSGCGSWOPRK
1	Ī		LPVFKSLRHMRQVGGRGTAHHELRRRANHGLCLPTRLASGPSTL
			KTLQEVTDSLLGGWLMAQGVGGII
6933	1431	890	SLNLHCTLPPPPHQYPAGYPSDKEGKKPKGQSKKQPSGTTKRPI
	Ì	i	SDDDCPSASKVYKASDSAEAIEAFQLTPQQQHLIREDCONOKLW
į	1	İ	DEVLSHLVEGPNFLKKLEQSFMCVCCQELVYQPVTTECFHNVCK
J			DCLQRSFKAQVFSCPACRHDLGQNYIMIPNEILQTLLDLFFFGY
L			SKGR
6934	3030	2588	DRDHSQCGGIRRVALARVSSVKLISKAKIRTVKMTFIIVLAFIV
1		ļ	CWTPFFFVQMWSVWDANAPKBASAFIIVMLLASLNSCCNPWIYM
j		·	LFTGHLFHELVQRFLCCSASYLKGRRLGETSASKKSNSSSFVLS
			HRSSSQRSCSQPSTA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
αı	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Í	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
6935	886	543	NSALYVAGGNDGTSCLNSVBRYSPKAGAWESVAPMNIRRSTHDL
Į.			VAMDGWLYAVGGNDGSSSLNSIEKYNPRTNKWVAASCMFTRRSS
	ĺ		VGVAVLELLNFPPPSSPTLSVSSTSL
6936	1347	567	RSHRRQFLSRALLEFFGKSHPPPHRLFRKSLNVGLHYSHIPFLT
i	".		TCLHFLRKRLQKGEVGLSVETSKPQVPVGGLSRKKVPQEPWATV
1	ì		MEKRLQEAQLYKEEGNQRYREGKYRDAVSRYHRALLQLRGLDPS
i			LPSPLPNLGPQGPALTPEQENILHTTQTDCYNNLAACLLQMEPV
ŀ			NYERVREYSQKVLERQPDNAKALYRAGVAFFHLQDYDQARHYLL
			AAVNRQPKDANVRRYLQLTQSELSSYHRKEKQLYLGMFG
6937	1	727	AVEFRCCPGRDPACFARGWRLDRVYGTCFCDQACRFTGDCCFDY
1	-	· • ·	DRACPARPCFVGEWSPWSGCADQCKPTTRVRRRSVQQEPQNGGA
			PCPPLEERAGCLEYSTPQGQDCGHTYVPAFITTSAFNKERTRQA
			TSPHWSTHTEDAGYCMEFKTESLTPHCALENRPLTRWMQYLREG
			YTVCVDCQPPAMNSVSLRCSGDGLDSDGNQTLHWQAIGNPRCQG
1			TWKKVRRVDQCSCPAVHSFIFI
6938	3	719	NSRKLELAERVDTDFMQLKKRRQSSEKENDSGTLDTVGAVVVDH
}	-	, = 5	EGNVAAAVSSGGLALKHPGRVGQAALYGCGCWAENTGAHNPYST
1 .			AVSTSGCGEHLVRTILARECSHALQAEDAHQALLETMQNKFISS
1			PFLASEDGVLGGVIVLRSCRCSAEPDSSQNKQTLLVEFLWSHTT
!			ESMCVGYMSAQDGKAKTHISRLPPGAVAGQSVAIEGGVCRLGEP
1			SELTLQAECEASQRHFRT
6939	3	810	KVTAPRRPORYSSGHGSDNSSVLSGELPPAMGRTALFHHSGGSS
!			GYESLRRDSEATGSASSAPDSMSESGAASPGARTRSLKSPKKRA
[]			TGLQRRRLIPAPLPDTTALGRKPSLPGQWVDLPPPLAGSLKEPF
			EIKVYEIDDVERLQRPRPTPREAPTQGLACVSTRLRLAERRQQR
			LREVQAKHKHLCEELAETQGRLMLEPGRWLEQFEVDPELEPESA
1			EYLAALERATAALEQCVNLCKAHVMMVTCFDISVAASAAIPGPQ
1			EVDV
6940	1188	496	GKMAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQ
i i			VVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAV
	,		LADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFLVGIEGSLKGS
] }			TYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLL
1 1	ĺ	I	KTKAIVNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILS
		i	EVTPDQSKPEN
6941	1	713	SLSRADSDPHGPHTCGHVLNVIIGSNVLALAEAQRQAEALGYQA
l I	1		VVLSAAMQGDVKSMAQFYGLLAHVARTRLTPSMAGASVEEDAQL
	İ		HELAAELQIPDLQLEEALETMAWGRGPVCLLAGGEPTVQLQGSG
		j	RGGRNQELALRVGAELRRWPLGPIDVLFLSGGTDGQDGPTEAAG
1 1			AWVTPELASQAAAEGLDIATFLAHNDSHTFFCCLQGGAHLLHTG
L i			MTGTNVMDTHLLFLRPR
6942	1	246	GDYVERYDPKTDTWTMGAPLSMPTNAVGGCLLGDRLYADGGYDG
/	{		QTYLNTMESYDPQTNEWTQMASLNIGRAGACVVVIKQP
6943	. 1	739	PMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWLRLG
			HSPAGGSITETLVQGDKTEYLLTALEPKPTYIICMVTMETTNAY
[VADETPVCAKAETADSYGPTTTLNQEQNAGPMASLPLAGIIGGA
			VALVFLFLVLGAICWYVHQAGELLTRERAYNRGSRKKDDYMESG
	1	Ì	TKKDNSILBIRGPGLQMLPINPYRAKEEYVVHTIFPSNGSSLCK
1			ATHTIGYGTTRGYRDGGIPDIDYSYT
6944	960	156	VANILLNGVKYESELTGSSERAEQPLSVGRLCSTICNMPKALRT
1	į		LCVNHFLGWLSFEGMLLFYTDFMGEVVFQGDPKAPHTSEAYOKY
	•	1	NSGVTMGCWGMCIYAFSAAFYSAILEKLEEFLSVRTLYFIAYLA
		}	FGLGTGLATLSRNLYVVLSLCITYGILFSTLCTLPYSLLCDYYQ
	. 1		SKKFAGSSADGTRRGMGVDISLLSCQYFLAQILVSLVLGPLTSA
]	ļ	}	VGSANGVMYFSSLVSFLGCLYSSLFVIYEIPPSDAADEEHRPLL
L	[j	TWA.

	SEQ	Predicted	Predicted end	1 min
	ID	beginning	nucleotide	
	NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
-		location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ı		amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence		\=possible nucleotide insertion)
١	6945	2067	179	EGEDRGLPRTMGAALGTGTRLAPWPGRACGALPRWTPTAPAQGC
1		i		HSKPGPARPVPLKKRGYDVTRNPHLNKGMAFTLEERLQLGIHGL
-		1	1	IPPCFLSQDVQLLRIMRYYBRQQSDLDKYIILMTLQDRNEKLFY
-				RVLTSDVEKFMPIVYTPTVGLACQHYGLTFRRPRGLFITIHDKG
J				HLATMLNSWPEDNIKAVVVTDGERILGLGDLGCYGMGIPVGKLA
		1		LYTACGGVNPQQCLPVLLDVGTNNEELLRDPLYIGLKHQRVHGK
- (1		AYDDLLDEFMQAVTDKFGINCLIOFEDFANANAFRIINKYPNKY
				CMFNDDIQGTASVAVAGILAALRITKNKLSNHVFGFOGAGFAAM
-1				G\IAHLLVMALE\KEGVPKA\EATRKIW\MVDF\KGLTVOGPDH
				LNHEKEMFAQD\HPEVNSLEEVVRLVKPTATIGVAATARA\ ETR
1				QILRDMASFHERP\IIFALSNPTSKAECTA\EKCYRVTEGDDGR
1				FAS GSPF*GVLIWEMGKTFIPGGRGNNA*RVPRGWOLGVHSDG
1				GDPGHIP\DEIFLPDSRAKLPQEVSEOHLSOGRLYP\ PI.ST\ TP
1				NVFLRIAIKVFD*GYKHNLV\SYYPEPKD\KEAFCKTPGSYTDD
H	6946	122		YDSFYT/VDSYIWAQGKAMNVOTV [
1	0,740	133	2551	SCEYSGITVAPGDPCPGVAHLLAPSMASDTPESLMALCTDFCLR
				NLDGTLGYLLDKETLRLHPDIFLPSEI\CDRIANEVVELAMAAC
ı				NF\EPHE\SFFNPLFRDPRKQPASRRIHL\RED\LVQD\QD\LE
1	1			AIRKQDL\VEL\YLTN\CEKLSAKSLOTLRSFSHTT.GVD+AFRG
	ŀ	1		C\TNILLERKENPGGL/CEDEYLFNPTCQVLVKDFTFEGFSRLR
1	1	1		F\LKLGRMIDWVPVES\LLRPLNSLAALDLSGIQTSDAA\FLTQ
ı	1			WKDSL\VSLVL\YNMDLSDDHIR\VIVQLHKLRHLDISRDRLSS
L	- 1	1		YYKFKLTREVLSLFVQKLGNLMSLDISG\HMILENCSISKIGKR
L	ľ	į		EAGQTSI\EPSK\SSIIPFRGFEGGPLQF\LGVF*GIFCGRLTH
		1		IPAYKVSGDKNEEQVLNAIEAYTEHRPEITSRAINLLFDIARIE
1				RCNQLLRALKLVITALKCHKYDRNIQVTGSAALFYLTNSEYRSE
	1	ļ		QSVKLRRQVIQVVLNGMESYQEVTVQRNCCLTLCNFSIPEELEF QYRRVNELLLSILNPTRQDESIQRIAVHLCNALVCQVDNDHKEA
ŀ	I			VGKMGFVVTMLKLTQKKLLDKTCDQVMEFSW\SALWNITDETPD
	į			NCEMFLNFNGMKLFLDCLNEFPEKQELHRNMLGLLGNVAEVKEL
				RPQLMTSQFISVFSNLLESKADGIEVSYNACGVLSHIMFDGPEA
ĺ	ł			WGVCEPQREEVEERMWAAIQSWDINSRRNINYRSFEPILRLLPQ
	1			GISPVSQHWATWALYNLVSVYPDKYCPLLIKEGGMPLLRDIIKM
L				ATARQETKEMARKVIEHCSNFKEENMDTSR
	6947	2	1682	TSVSTIPRGLASARPOSRSWRCCPVWRRSPGRARGRGLKMINVP
	1	l l		SQSFPAPRSQQRVASGGRSKVPLKOGRSLMDWIRLTKSGKDI.TG
	Ì			LKGRLIEVTEEELKKHNKKDDCWICIRGFVYNVSPYMEYHPGGE
	1			DELMRAAGSDGTELFDQVHRWVNYESMLKECLVGRMATKPAVIK
	l		:	DYREEEKKVLNGMLPKSQVTDTLAKEGPSYPSYDWFOTDSLVTT
	i			/EHIY*TEGYQFRLNNS*SSE*FLYSRNNY*GLLTSYTYW/P*A
				MRFRKIFLCGL/CESVGKIEIVLQKKENTSWDFLGHPLKNHNSL
	<u> </u>		ĺ	IPRKDTGLYYRKCQLISKEDVTHDTRLFCLMLPPSTHLQVPIGQ
	l			HVYLKLPITGTEIVKPYTPVSGSLLSEFKEPVLPNNKYIYFLIK
	ļ	ì		IYPTGLFTPELDRLQIGDFVSVSSPEGNFKISKFQELEDLFLLA
	[ľ	AGTGFTPMVKILNYALTDIPSLRKVKLMFFNKTEDDIIWRSQLE
		}		KLAFKDKRLDVEFVLSAPISEWNGKQGHISPALLSEFLKRNLDK
	6948	104	58	SKVLVCICGPVPFTEQGVRLLHDLNFSKNEIHSFTA
	i			PDGAHSFFPDEYFTCSSLCLSCGVGCKKSMNHGKEGVPHEAKSR
		[ĺ	CRYSHQYDNRVYTCKACYERGEEVSVVPKTSASTDSPWMGLAKY
	1		1	AWSGYVIECPNCGVVYRSRQYWFGNQDPVDTVVRTEIVHVWPGT
]	j		DGFLKDNNNAAQRLLDGMNFMAQSVSELSLGPTKAVTSWLTDQI
	- 1	1	ł	APAYWRPNSQILSCNKCATSFKDNDTKHHCRACGEGFCDSCSSK TRBUPFRGWGDAPUPCCNCVFAP (MD NAGONGEGFCDSCSSK
		ł		TRPVPERGWGPAPVRVCDNCYEAR/TRPVSCYRGTSGR*RRRT QETVB
-	5949	152	4656	GLRLCLSRPLTRPGDDSVGGSAMASGAGGVGGGGGGKIRTRRCH
		•		QGPIKPYQQGRQQHQGILSRVTESVKNIVPGWLQRYFNKNEDVC
				F FFAKKWKDAGTTOKA LEDAVIATA BEATTOK I LUKUKDAG

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	\n-n-duine, C=CVSCeine, D-Aspartic x=/1 m
- 1	location	corresponding	Johnson Color Pappenvialaning Colors
- 1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
i	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- 1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan V=Try
- 1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
- 1			SCSTDTSEVPRWPENKEDHLVYADEESSNITDGRITPEPAVSNT
ł	1	İ	BEPSTTSTAST\YPDVLTRVSLYRSHLNFSMLESPALHCQPSTS
ł	1 .		SAFPIGSSGFSLVKEIKDSTSQHDDDNISTTSGFSSRASDKDIT
	1	i	VSKNTSLPPLWSPEAERSHSLSQHTATSSKKPAFNLSAFGTLSP
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- 1	location	corresponding	Caucamic Acid, Febbenvialaning C-Closein-
ı	corresponding	to first	1 montactuatio, letsoleucine volvaire
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ſ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
i	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
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1			CLYCRKGDNDEFLLLCDGCDRGCHIYCHRPKMEAVPEGDWFCTV
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		1	TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAAIT
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regidue of amino acid and acid sequence solver the stryptophan, YeTyrosine, XeUnknown, *=Stop Codon, /=possible nucleotide deletion, \				P=Proline, Q=Glutamine, R=Arginine
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equance Codon, /-possible nuclectide insertion	1		1	W=Tryptophan, Y=Tyrosine, X=Unknown *-c+
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ARWARKENDEP\TASFF\RGRPDLSTLTHSTVRRRYLAHSGRS HLBEBERGALKALUSEEPLIKMYDEARSERDELDITKRGKRPPT PCSDPERKBFRNGSESGBEASSPDYPGPPAKNOVASRSHTHP KENPFRRA)SKAVEESSDEERGRDAGGEESSEEESKYKKK TRKFVVKKOAPGKASVSRKOAREESSEESEEEKYKKK TRKKPVVKKOAPGKASVSRKOAREESSEESEEEKYKKK KTKSLKESEGEESEELILAGKKROREESVEESKEADENGOK PRIKSNGRKSAREERSCKKSKOARELLGDSSEEGKEADSKO DDSGROREPPVQRKSEDRTCLKGGKRLGGSGEBEDEGGKGEPTA KGSRKWARLGSTSGEEDDLERGEGDLEREVSDEAGGGPGGERINGSSKES SRKORTRSSSSSSOSPEAKGGAGSGGRGEDHAVWRLKRYTR ACGAIRMYKKLIGSCSCHKERLSIABAELALGMKGTPSLGKKR ALKEQREBABVASLDVANI ISGSGRPRRTAMMPLGEAAPPGE LYRRILDSDEERPRAPPVDMSHMGI ISSDGEN RPWSSPTMKPMFSIGRIE ISMLAKWGTPYLSKHRADBMRRLGDFL NGESPDLALLEEVWSGDPGYLTKKLSTYTAAHHFRSGI IGSG LCVFSKHPIGELICHIYTLMGYPYMHHGDMFSGKAVGLUVHL SGMVLNAVYTHLHAEVNROKDTYLAHRVAQAWELAGPTHTSKK ADVULLCGDLMMHPEDLGCCLLKEWICHDAYLETRDFKGSEEG NTMVPKNCYJSQOELKFPPFGVEIDYVLYKAVSGFFISCKSFET TTOFDPHGTPLSDHEALMATLFVHRSPPCOMPSSTHGF\ARRS PL/MCVCLKEALDGSLGLGMA\QARWA\TFA\SYVIGLGL\LI LLALCVLAAGGGAGEAAILLWTFSVGLVLALL\LGGGEDRTKEQ NGSSPLALEEWWSGDPGYLTGKYLALL\LGGGEDRTKEG NEWSSPTMKNFSLRLRIFINLKWGIPYLSKHRADBMRRLGDFL NGSSPLALEEWWSGDPGYLTGKYLALL\LGGGEDRTKEG NEWSSPTMKNFSLRLRIFINLKWGIPYLSKHRADBMRRLGDFL NGSSPLALEEWWSGDPGYLTGKYLALL\LGGGEDRTKEG LCVFSKHPIGELTGHTYTLNKGWIPYLSKHRADBMRRLGDFL NGSSPLALEEWWSGDPGYLTGKYLALL\LGGGERTKEG NEWSSPTMKNFSLRLRIFINLKWGIPYLSKHRADBMRRLGDFL NGSSPLALEEWWSGDPGYLTGKYLALL\LGGGERTKEG NTWPKNCYJSQOELKPPFGGRIDYJLYKAVSGFYISCKSFET TTGFDPHGTPLSDHEALMATLFYRHYPQNWSGFYISCKSFET TTGFDPHGTPLSDHEALMATLFYRHYPQNWSGFYISCKSFET TTGFDPHGTGTPLSDHEALMATLFYRHYPQNWSGFYISCKSFET TTGFDPHGTGTLSCHARATLFYRHYPQNWSGFYISCKSFET TTGFDPHGTGTLSCHARATLFYRHYPQNWSGFYISCKSFET TTGFDPHGTGTLSCHARATLFYRHYPQNWSGFYISCKSFET TTGFDPHGTGTLSCHARATLFYRHYPQNWSGFYISCKSFET TTGFDPHGTGTLSCHARATLFYRQDPYTYRHYRGWSGFE PL/MCVCLKEALDGSLGLGMA\QARWA\TFA\SYVIGLGLALL LLHALCSLAAGGAGEAAILLWTPSCVCLUWAGGAPLIFYNGVNSGF PL/MCVCLKEALDGSLGLGMA\QARWA\TFA\SYVIGLGLALL LHNGNSVLETLINGCRNGHFCDVTVRIHGRANGROCHARG PFFQNKLLLATAGGGGGSTEGSGCGSTGSTGSTGTDFDSV DCGGGGAARDSQAEPTQFRQAAFAGGGFTNALTGGRASPE EAVLSPDPALLTTREGCTSDSCVSLGGGTBEDDSV D	6960			RHTTAT
HILBERGALKELVBEEPLINGVDEAASREDILITKKGKRPPT PCSDPERKFRFNESESGSEASPDYFOP PAKNGVARSHTHEI KEEMFRRA\SKAVEESDEERGRDLPAQRGEESSEEEEKGYKGK TRKFVVVKOADGKASVSRKOAREESSESEEEKGYVGK TRKFVVVKOADGKASVSRKOAREESSESEEEKGYKGK RGTKSLKESEGESEEELAGKKRGAREEVSEEKEEEDEEKGDKK PRITKSNGRKSARSERSCKGKSGAKELLGDSDSEEGKEAASSG DDSGROREPPVQRKSEERTCLKGKGREEVSEEKEEEGKEAASSG DDSGROREPPVQRKSEGSTEDLEGGSEDEDEGKGEPTA KGSRKMARLGSTSGEEDLEREVSDSEAGGGPGERKNRSSKKS SRKORTKSSSSSIGSSEPARGGRAGEGSEEDEDEGKGEPTA KGSRKMARLGSTSGEEDLEREVSDSEAGGGPGERKNRSSKKS SRKORTKSSSSSIGSSEPARGGRAGERGEDHPAVMRLKRYIR ACGAIRNYKKLLGSCCSHKERLSILPAELEALGKKGTPSLGKER ALKEQREEAAEVASLDVANIISGSGPRRTAMPLGEAAPPOR ALKEQREEAAEVASLDVANIISGSGPRRTAMPLGEAAPPOR LINRTLDSDEERPRAPPDWSHMGGISSDGESN ALKEQREEAAEVASLDVANIISGSGPRRTAMPLGEAAPPOR LINRTLDSDEERPRAPPDWSHMGGISSDGESN NGSSPDLALLEEVWSGDFOYLRGKLSFTYPAAHHFRSGIIGSG LCVFSKHPIGELTGHTYTLNGYPYMIHGDMFSGKAVGLLVLHL SGMVLLNAVYTHLHAEVARQXDIYJVLYKAVSGFYISCKSFET TTGFDPHGTPLSCHERAHATLFYHAPQONDSTHEYKSEEG NTWVERNCYVSQCELKFFFGWIDYVLYKAVSGFYISCKSFET TTGFDPHGTPLSCHERAHATLFYHAPQAWGAFTLAFFWQEVMS LVRAQAELGHVLGRAREAGDLGPEPQLVALL\LGQGGGDRTKEG PPSSFTWKPFFSLRLIFFNLCWGTFYLSKHRDRMRRLGDFL NGESPDLALLEEVWSRODPQYLRGKLSFTYPAAHHFRSGIIGSG LCVFSKHPIGELTCHTYTLNGFYPMIHHGDWFSGRAVGLLVLHL SGMVLLNAVYVHLHAEVRRQKDIYLAKAGAFTLAFFWQEVMS ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETTDPKGSEEG NTMVFKNVYVGLGELKFPFFGWIDYVLAVAVSGFYISCKSFET TTGFDPHGTPLSDHEAMATLFVRHSPFQONDSTHEFO\AERS PL/MCVCLKEALDGSLGLGMA\QARWA\TFA\SVYIGLGI\LL LLALLCVLAAGGGGGEAALLLHTPSCVJAWGAFTLFHYOSVMG LYRAQAELGHVLYGARGRAGAETTTDFGGGSAKFGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSDCDISCKGMTERHSIN LHNFSNSVLETHURGRNSGHFTOPGGSSAKFGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSDCDISCKGMTERHSIN LHNFSNSVLETHURGRNRSHFTOPGGSSAKFGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSDCDISCKGMTERHSIN LHNFSNSVLETHURGRNRSHFTOPGGSSAKFGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSDCDISCKGMTERHSIN LHNFSNSVLETHURGRNRSHFCOVTVIHIGRGNDFOTQDGROPT PRSGTGSGSSTETSGTGSGSSTETSGTGDSVSSTGTEPDSV EQGGGGAARDSQAEPTQFRQAAEAGGGFGTNOLETGASSPE EQGGGGGGAARDSQAEPTQFRQAAEAGGGFGTNOLETGASSPE EQGGGGGGAARDSQAEPTQFRGAAEAGGGGTNOLETGASSPE	6,560	387	2068	AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRS
### REENPERA SKAVESESDERAGEN PORTOR GERSES EES KGYKKE KEENPERA SKAVESESDERAGEN PAGGESSES EES KGYKKEN KTKKPVVKKOAPGKAS VSRKOAREES EES KGYKKEN KGTKSLKES BEGESEEL LAGKKEOREES EES KEEDEE KGOKK KGTKSLKES BEGESEEL LAGKKEOREES EES KEEDEE KGOKK KOTKSLKES BEGESEEL LAGKKEOREES EES KEEDEE KEEDE KEEDE KEEDE KEEDE KEEDE KOTKSLKKS DE BODGENGE POR VORKER STEEL KEEDE	1	ľ		HLEPEEKQALKRLVEEEPLKMOVDEAASREDKI.DI.TKKGKPBDT
KEENFRRA SKAVESSSDEERGRDLPAORGEESSEEBEKGYKGK TRKKPVVKKOAPGKAVSSKOKAPSEN ESTERSAREPOKPATAKVEON KGYKSLKESEGESEELLAGKKEQREES EEEKEEDEEKGOWK PRTKSNORRKSARERSCKOKSQAKRLLGDSDEEEGKEAASSG DDSGRDREPPVGRKSEDKTOLKGGKRLGGSEEEBOSGKGEPTA KGSRKMARLGSTSGEESDLEERVSDEERGGFQGERNRRSKKS SRKGRTASSSSSDSDESPAKGGKAGSGRGEDHPAWRIKRYTR ACGAINNYKKLLGSCCSKKERLSILRAELEALGMKGTPSIGKCR ALKEGREBAEVASLDVANIISGERPRRTAMPLGBAAPFGE LYRRTLDSDEEPPRAP PDWSHMRGIISSGEESN EYRRTLDSDEEPPRAP PDWSHMRGIISSGEESN LYRRTLDSDEEPPRAP PDWSHMRGIISSGEESN LYRRTLDSDEEPPRAP PDWSHMRGIISSGEESN NGESPDLALLEEVWSEQDFOYLROKLSFTYPAAHHFRSGIIGSG LCVFSKHPIQELTOHIYTLNGYPYMIHHGDWFSGKAVGLUVHL SGRVUNAVYTHLHAFYNROKDIYAKAVAGAFTLAAPIHHTSKI ADVULLCGDLMMHPEDLGCCLLKSWTGLHDAYLETHAEKSEE NTMVPKNCYVSQELKPFPFGVRIDVULYKAVSGFYISCKSFET TTGFDPHRGTEISDHEALMATLFVRHSPPCQMPESTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWAYTFA\STYVIGLGIL\LL LALLCULAAGGGAGAAILLWTPAYTHSPCQMPESTHGP\AERS PL/MCVLCKEALDGSLGLGMA\QARWAYTA\STYVIGLGIL\LL LALLCULAAGGGAGAAILLWTASTYLFHVOEVMG LYRAQAELQHVLGRARRAQDLGPEPQLVALL\LGQGEGDRTKEQ NTMVPKNCYVSQELKFPFFGVRIDYLJKKAVSGFYISCKSFET TGFDPHRGTISCHLTHITTINGYYPYMIHHGDWFSGKAVGLUVHH SGMVLINAVTHLHAPYNROKDIYJKKAVSGFYISCKSFET TTGFDPHRGTISCHLTHITTINGYYPYMIHHGDWFSGKAVGLUVHH SGMVLINAVTHLHAPYNROKDIYJKKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWAYTAA\STYLGLG\LLVHL SGMVLINAVTHLHAPYNROKDIYJKKAVAGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWAYTAA\STYLGLG\LLVHL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYIFHVQSVNG LYRAQAELQHVLGRAREAQDLGPEPQLVALL\LGCGGGDRTKEG NTWVFKNCYVSQGELKFPFFGWATENVALKAGEENFTTDFGGSSAKFGLDFCLMF EAVLSPDFALLTHSTHSLTNSHAHTGSSDCDISCKGMTERHSIN LHNFSNSVLETLNEQRNGHFCDVTVRHSBMRAQRCVLAAGS PFFQDKLLLGYSDIETPSVGVVQSVQKLDFMYSGVLRVSQSER LQIITAASSLQIKTVIDECTRIVSONGOWYPGIQDSQDTPRG TPESGTSGGSSTEESTGJGSFDTSGVSSSIGGTEPDSV BQQFGYGAARDSQAEPTGPEGAAEAPABGGGPTNQLETGASSPE BQGGGGGAARDSAAGGGPTGDGAACAAAPABGGGFTNQLETGASSPE BQGGGGGAARDSGAEPTGDEGAACAAAPABGGGFTNQLETGASSPE BQGGGGGAARDSGAEPTGDEGAACAAAPABGGGFTNQLETGASSPE	1			PCSDPERKRFRFNSESESGSEASSPDYFGPPAKNGVASPSHTUD
TRKKPVKKQAPCKASYSKQAREESEEAEPUQRTAKKUEGN KGTKSILKESGUSESEEEILAQKGEEVEEBEEKGDMK PRTESNIGRKSAREERISCKOKSQAXRILGDSDSEEQKEAASSG DDSGORDEPPUQRKSEDRTQLKGGKIGSSEDEEDGGKGEPTA KGSRKMARIGSTSGEESDLERVSDSEAGGGPGERNRSSKKS SRKGRTSSSSSDGSPFAKGGKAGSGRGEDHPAMRIKRYTR ACQAINNYKKLIGSCSHKERLIARELEALMKGTPSLGKCR ALKEQREEAAEVASLDVANITSGSGRPRRTAWNPLGEAAPPGE LYRRTLDSDEEPRPAPPDWSHMKGIISSGESN 6961 340 1646 RPWSSPTMKPMFSIRLETFMLNCGIPYLSKHRADDMRRLIGDFL NQESPDLALLEEVWSEQDPGVLRCKLSFTYPAAHHFRSGIIGGG CLVFSKHPIQELTCHIYTLNGVHINHENDMPSGRAVGLLVUHL SGMVLNAYVTHLHABYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETTDFKGSEG NTMVPRNCYVSQQELKFPPFGVRIDYVLYKAVAGFYISCKSFET TTGFDPHRGTFLSDHEALMATLFVRHSPPGQNFSSTHGP\AREA PL/MCVCLKEALDGSLGGMA\GARWA\TFA\SVVIGLGV\LL LALLCULAAGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPPPQLVALL\LGQDGGDRTKEQ NOESFDLALLEEVWSEQDFGYLRQKLSFTTPAAHHFRSGI IGGG CLVFSKHPIGELTGHTYLTINGYPTJSKHRADMRRLGOFL NGESFDLALLEEVWSEQDFGYLRQKLSFTTPAAHHFRSGI IGGG LCVFSKHPIGELTGHTYLTINGYPTJSKHRADMRRLGOFL NGESFDLALLEEVWSEQDFGYLRQKLSFTTPAAHHFRSGI IGGG NTMVPKNCYVSQGLKFPFGVRIDYVLYKAVAGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNSSTHGP\AREA ADVVLLCODLNMHPEDLGCCLLKWTGHAVLTSTLTSKGSEG NTMVPKNCYVSQGLKFFFFGVRIDYVLYKAVAGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONSSTHGP\AREA ADVVLLCODLNMHPEDLGCCLLKWTGHAVLTSTLTSKGSEG NTMVPKNCYVSQGLKFFFFGVRIDYVLYKAVAGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONSSTHGP\AREA LYRAQAELQHVUGRARRAQDLISCHGMAYATPA\SVTICKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONSSTHGP\AREA LYRAQAELQHVUGRARRAQDLISCHGMAYATPA\SVTICKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQDARSTHGP\AREA LYRAQAELQHVUGRARRAQDLISCKGMTERHSIN LHNFSNSVLETINGENNGHFCTVYRHGSMLARQRCVLAAGS PFFQDKLLLGYSDIEIPSVUSVQSVQKLIDFMYSGVLRVSQSSA LQILTAASTLQIKTVUDECTRIVSONVGBVPFGIDDSGODTPRG TPESGTSGQSDTESGYQGHPGNVDHFTYRHGRSQVLRVSQSSA LQILTAASTLQIKTVUDECTRIVSONVGBVPFGIDDSGODTPRG TPESGTSGGSDTESGYQGHPGNVDHFTYRHERSQOMERYL STTPETTHCRKQPREDGYDYTYGGRVQ ILERNESECTEDTDQABGTBEFGGFFDSGVSSIGTEPDSV DQGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1			KEENPRRA\SKAVEESSDEERORDLPAORGEESSEEEEKGVKGV
RGTKSLKESGQSSEEILAGKKEQREEKEENDEKGDMK PRTESNORKSARERSCKOKSOAKRILGDSDSEEGKEAASSG DDSGRREPPYQRKSEDRTQLKGGKRLSGSSEDEERGDKGEPTA KGSRKMARLGSTSGESDLEREVSDSEKGGGPGGERNRSSKKS SRKGRTKSSSSSDSPBAKGGKAGSGRGEDHPAWRIKRYIR ACGAIRNYKKLIGSCCSKKERLSILRAELEALGMKGTPSLGKCR ALKEGREAAEVASLDVANIISGGPRPRRTAWNPLGEAAPPGG LYRRTLDSDEERPRPAPPDWSHMKGISSDCESN 6961 340 1646 RPWSSPTNKPNFSLRLRIFNLCKGIFPYLSKHRADDMRRLGDFL NQSSPDLALLEEVWSGQDFOYLROKLSFTYPAAHHRGGIIGGG LCVFSKHPIGELTCHITTLNCYGIFYLSKHRADDMRRLGDFL NGSSPDLALLEEVWSGQDFOYLROKLSFTYPAAHHRGGIIGGG LCVFSKHPIGELTCHITTLNCYGIFYLSKHRADDMRRLGDFL SGWYLNAYYTHLHAEYNRQKDIYLAKRVAQAMELAQFIHHTSKK ADVVLLCGDLMMHPEDLGCCLLKEWTGLHDAYLETTDFKGSEG NTMVPRNCYVSQQELKFPFFGVRIDYVLYKAVGGFYISKKSFET TTGFDPHKGTFLSDHEALMATLFVRHSPPQONFSSTGGP \AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCYLAAGGGAGEAAILLWTBSVCLIVWAGAFYLFHVQEVNG NGSSPDLALLEEVWSEQDFOYLAVLAGGGGGDTKEQ RWSSPTMKFNFSLRLRIFNLCKGTPYLSKHRADDMRRLGDFL NGSSFDLALLEEVWSEQDFOYLAVLAGAFYLFHVQEVNG LCVFSKHPIQELTCHIYTLNGYPYMLHHCDWSGGAVGLLVHLH SGMVLNAYVTHLHAENNRCDIYLLARRVAQAMELAQFIHHTSKK ADVVLLCGDLMMHPEDLGCCLLKWTGLHDAYLETTDPKGSEGE NTMVPKNCYVSQQELKFFPFGVRIDHAVLFTDPKGSEGE NTMVPKNCYVSQQELKFFPFGVRIDHAVLFTDPKGSEGE NTMVPKNCYVSQQELKFFPFGVRIDHAVLFTDPKGSEGE NTMVPKNCYVSQQELKFFPFGVRIDHAVLFTDPKGSEGE NTMVPKNCYVSQQELKFFPFGVRIDHAVLFTDPKGSEGE NTMVPKNCYVSQQELKFFPFGVRIDHAVLFTDPKGSEGE NTMVPKNCYVSQQELKFFPFGVRIDHAVLFTDPKGSEGE NTMVPKNCYVSQQELKFFPFGVRIDHAVLFARGYLYARGS PL/MCVCLKBALDGSLGLGMA\QARWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTBSVQLVLWAGAFYLFHVORVMG LYRAQAELGHVLGARRAGADLAFGYLVALKAGGGAGGTFRG PSFGQALGHRINGRHGHFCYVTRHGSMLAAGQCVLAAGG PFFFGDKLLLGYSDIETPSWVSVQSVQKLIDFMYSGVLRVSQSGA LQILTAASILQIKTVIDECTRIVSQNVGSVFRIGDPCTLMF EAVLSPDPALIHSTHSITMSHAHTGSSDCDISCGMMTERHSIN LHNFSNVELTIMEQRNGHFFCYVTRHGSMLAAGQCVLAAGG PFFFGDKLLLGYSDIETPSWSVQSVQKLIDFMYSGVLRVSQSGA LQILTAASILQIKTVIDECTRIVSQNVGBVPTGIODSGGDTPRG TFESGTSGGSDTESGYLQSHPGHSVDRIVSQDWRYLGCDPTYGG GCGGGARADSQAFFTQEGAARAPABGGGFTNQLETGRSPE EQGGGGGAGAARAPABGAGFTORGFTPRDPSV GCGGGGAARABAGAAFPTGEGGFTNGLETGRSPE	1]		TRKKPVVKKQAPGKASVSRKOAREESEESEAEPVORTAKKURGN
DDSGRDEPPVQVKSEDRTZLKGGKALGSDSEEDGKRAASSG DDSGRDEPPVQKKSEDRTZLKGGKKLGGSSEDEBDSGKGEPTA KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS SRKGRTRSSSSSSDGSPEAKGGKAGGGSGRGEDHPAWRIKKRYIR ACCAHRNYKKLLGSCCSHERESIIRAELEALGMKGTPSLGKCR ALKEQREEAAEVASLDVANIISGSGRPRRTTAWNPLGBAAPPGB LYRRTLDSDEERPRAPPDWARGIISSDGESD 6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL NQESPDLALLEEVWSEQDFQYLRQKLSTYPAAHHFRGGIIGSG LCVFSKHPLQELTQHIYTLNGYPYMHHGDWSGKAVGLUVHL SGWVLMAYVTHLHAEVRGKDIYLAHRVAQAMELAQPIHTTSKK ADVVLLCGDLINHHPEDLGGCLKEWTGLTDAYLETRDFKGSEEG NTWVPRNCYVSQOELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPQCNPSSTHGP\AERS PI/MCVCLKEALDGSLGJMAA QARWMA\TFA\SYVLIGLIV,LL LALLCVLAAGGGAGEAAILLWTPSVGLUWAGAFYLPHVQEVMG LVRAQAELQHVUGARREAQDLGPEPQLVALL\AGQGCBRTKEQ RPWSSPTMKPMFSLRIFINLNCWGIFYLSKHRADRMRRLGDFL NQESPDLALLEEVWSEQDFQYLRGKLSFYPAAHHFRSGIIGSG LCVFSKHPIQEITCHTYTLNGYFYMHHGDWFSGKAVGLLVHL SGMVLNAVYTHLHAEYNGKDIYLAHRVAQAWELAQPIHTYSKK ADVVLLCGDLMMHPSDLGCCLKEWTGLDAYLETRDFKGSEEG NTMVPKNCVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPQQNBSSTHGP\AERS PL/MCVCLKEALDGSLGJGMA\QARWMA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQBVMG LYRAQAELQHVLGBAREAQDLGPPGQLYALL\LLGQQBGDRTKEQ FL/MCVCLKEALDGSLGJGMA\QARWMA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQBVMG LYRAQAELQHVLGBAREAQDLGPPGQLYALL\LGQQBGDRTKEQ FL/MCVCLKEALDGSLGJGMA\QARWMA\TFA\SYVIGLGL\LL LLHNESSECTEDTGGAGGAGEAAILLWTPSVGLVLWAGAFYLFHVQBVMG LYRAQAELQHVLGBAREAQDLGPPGQLYALL\LGQQBGDRTKEQ FPFGDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGULVAGGSEA LQUITAASILQIKTVIBGCRNTGROFFOVTVRIHGBMRAQRCVLAAGS PFFGDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGULRVGGERA LQUITAASILQIKTVIBGCRNTGROFFOTOVTRIHGRAGAGGGAGTEA LQUITAASILQIKTVIBGCRNTGROFFOTOVTRIHGRAGAGGGAGGAGEA LQUITAASILQIKTVIBGCRNTGROFFOTONEGGERGE RSFYSGAVNSHHETALGLPRDHIMEDPSWITTAHERSQOMERYL STTPETTHCRKQPRPWRICTILVGCNNTGCREVQ ILERNESEECTEDTDQAEGTESSFKGESFDSGVSSSIGTEPDSV EQOFGGAARDSQAFTQFGQAAEAPAEGGFGTONGLETGASSPE EQOFGGAARDSQAFTQFGQAAEAPAEGGFGTONGLETGASSPE	}	[[KGTKSLKESEQESEEILAOKKEOREEVEEERKEEDEEKGDWV
DDSGNDREPPVQRKSEDTICLKGKRLGGSEDEBDGKGEPTA KGSRKMARLGSTSGESDLEREVSDEBAGGGPGERKNRSSKKS SRKGRTRSSSSSDGSPEAKGGKAGGRRGEDHPAVMRLKRYIR ACGAIRNYKKLLGSCCSHKERISIIRABLEALGMKGTPSLGKCR ALKEQREBABEVASLDVANI ISGSGRPRRTAMPLGEBAPPGB LYRRILDSDERPRPAPPDWSHMGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRIRIFNLNCWGIPYLSKHRADRMRRLGDFL NQESPDLALLERVWSEQDPSVLRQKLSTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMHHHDWSGKAVGLLUJHL SGMVLLAVYTHLHAEVNRQNJYLARRVAQAWELAQPIHHTSKK ADVULLCGDLNMHPEDLGCCLLKEWTGLHDAYLETTPFKGSEGE NTMVPKNCYVSQOELKFPFFGWRIDYVLYKAVSGFYISCKSFET TTGFPDFHRSTFLSDHEALMATHVRHSPQONPSSTHGP\AERS PL/MCVCLKEALDGSLGIGMA\QARWMA\TFA\SVVIGLGI\LL LALLCVLAAGGAGERAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRARREAQDLGPEPQLVALL\LGQQEGDRTKEQ RWSSFTMKFMFSIRLRIFNLNCWGIPYLSKHRADRWRRLGDFL NGESFDLALLEEVWSEQDFYVLRQKLSFTYFAAHHFRSGI IGSG LCVFSKHPIQELTQHIYTLNGYPYMHHRGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQXDIYLARRAPHRSGI IGSG LCVFSKHPIQELTQHIYTLNGYPYMHHRGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQXDIYLARRAPHTPSGI IGSG LCVFSKHPIQELTQHIYTLNGYPYMHRGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQXDIYLARRAPHTPSGI IGSG NTMVPKNCYVSQQELKFPFFGWRIDYVLYKAVSGFYISCKSFET TTGFPPHRGTFLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSLGGMA\QARWMA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQSVNG LYRAQAELQHVLGARREAQDLGPPPQUYALL\GQQEGDRTKEQ RYPAQAELQHVLGARREAQDLGPPPQUYALL\GQQEGDRTKED EAVLSPDPALHSTHSLTNSHAHTGSSDCIISCKGMTERHSIN LHNENSVLETIJMEQRNRGHFCDVTVRIHGMRAQRCVLAAGS PFFCDKLLLGYSDIEFSVVSVQSVQXLDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQVVSQVFPGIQDSQDTPRG TPESGTSGSSDTESGYLGSHPCDVTVRIHGRAGRCVLRAGS PFFCDKLLLGYSDIEFSVVSVQSVQXLDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQVVSGVPFGIQDSQDTRTSQ STFTETTHCKQPFPRFIGTLOTHINKEPSFCWSSSIGTEPDSV STFTETTHCKGPPRFIGTLOTHINKEPSFCWSSSIGTEPDSV STFTETTHCKGPPRFIGTLOTHINKEPSFCWSSSIGTEPDSV EQOFGFGAARDSQAETTGPEQAAEDARGEGFOTNOLETGASSPE EQOFGFGAARDSQAETTGPEQAAEDARGEGFOTNOLETGASSPE	1	1		PRIKSNGRRKSAREERSCKOKSOAKRLLGDSDSEEEOKEAAGGG
RGSRKMRILGSTSGEESDLEREVSDSEAGGGPQERKNRSSKKS SRKGRTESSSSSSSGSPGSPAGKAGKAGSGRGEDHPAVMRIKRYIR ACGAIRNYKKLLGSCCSHKERLSILRAELEALGKKGTESLGKCR ALKEQREBAAEVASLDVANIISGSGPRRETTAWPLGEBAPPGB LYRRTLDSDEERPPRAPPDWSHWRGIISDGESN RPWSSPJMKRDFSLRLRIFNLNCWGJPYLSKHRADRWRRLGDFL NQESPDLALLEEVWSRQDFQYLRKLSFTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLMGYPYMIHHGDDFSGKAVGLUUHL SGWLJAAVYHLHAEYNRQKDIYLAHRVAQAWELAQPIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCVVSQGELRFPFGVRIDYVLYKAVSGFYISCKSPFT TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSSLGMA\QARWA\TFA\SYVIGLGL\LL LALLCYLAAGGGAGEAAILLWTPSVGLVWAGAFYLEHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ PL/MCVLKABLDGSSLGMA\QARWA\TFA\SYVIGLB\LL LALLCYLAAGGGAGEAAILLWTPSVGLVWAGAFYLEHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ PL/MCVLKEALDGSSLGHAA\QARWA\TFA\SYVIGLBCL\LL SGMVLNAVYTHLHAEYNRQKDIYLAGWELAQFIHTSKK ADVVLLCGDLNHHPBELGCCLLKKBWTGLHDAYLETRDFKGSEEG LCVFSKHPIQELTQHIYTLNGYFYMHHGDWFSGKAVGLLVLHL SGMVLNAVYTHLHAEYNRQKDIYLAGWELAQFIHTSKK ADVVLLCGDLNHHPBELGCCLLKKBWTGLHDAYLETRDFKGSEEG NTMVPKNCVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFFT TTGFDPHRGTFLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSSLGIGMA\QARWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVUMAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGGPTKRQ LYRAQAELQHVLGRAREAQDLGPEPQLYALLL\LGQQEGGPTKRQ LYRAQAELQHVLGRAREAQDLGPEPQLYALLL\LGQQEGGPTKRQ LYRAQAELQHVLGRAREAQDLGPEPQLYALLL\LGQQEGGPTKRQ LYRAQAELQHVLGRAREAQDLGPEPQLYALLL\LGQQEGGPTKRQ LYRAQAELGHVLGRAREAQDLGPEPQLYALLLYRAGGSGEA LUITAASILGIKTVIDECTURNHHKDDFSWTTRIHERSCQMERYL LHNFSNSVLETLNEQRNRGHCDVTVVRHGSMLRAQRCVLAAGS PFFGQKULLGYSDIEIPSVUSVGSVQKLIDHYSGVLRVSQESA LQILTAASILGIKTVIDECTURNHINGDFSMDYDYVGQRVQ TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALVACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWTTRIHERSQQMERYL STTFETTHCRKQRPPVRLGTURNHINGEMEDDYDYYGQRVQ TLERNESECTEDTDQAEGTESEPKGESFDSGVSSSIGTEEPDSV EQQFGGAARDSQAEPTQPEQAARBGGFGTNQLETGASSPE EQUFGGAARDSQAEPTQPEQAARBGGFGTNQLETGASSPE				DDSGRDREPPVQRKSEDRTOLKGGKRLSGSSEDEEDSGKGEDTA
SKAGKTRSSSSDSPERAGGKAGGREGDHPAVMLIKRYIR ACCAIRMYKRLIGSCCSHKERLSILARALERLGMKGTPSLGKCR ALKEQREAAEVASLDVANIISGGRPRRTTAMPLGEAAPPGE LYRRTLDSDERRPRAPPDWSHWRGIISSDCESN RPWSSPTMKPNFSLRLRIFNLNCGTPYLSKHRADRMRRLGDFL NQSSPLALLEEVWSEQDFQYLRQKLSFTYPAAHHFRSGIIGSG LCVPSKHPIQELTQHIYTLMGYPYMIHHGDWFSGKAVGLLVLHL SGMVLMAYVTHHHAEVNRGKDIYLAHRVAQAWELAQFIHHTSKK ADVULLCGDLMMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYSQOELKFPGVRIDTYVLYKAVSGFYISCKSPET TTGFDPHRGTPLSDHEALMATLFVRHSPPQCNPSSTRGP\AERS PL/MCVLKEALDGSIGCMA\QARWWA\TFA\SYVIGLGI\LL LALLCVLAAGGGAGEAAILLWTSVGLIVWAGAFYLHVOENNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ RPWSSPTMKFNFSLRLRIFNLNCWGIPYLSKRABEMRRLGDFL NQESPDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHHABEYNRGDYJVLKAVAGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS NTMVPKNCYVSQQELKPFPFGVRIDYVLKKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS NTMVPKNCYVSQQELKPFFFGVRIDYVLKAVAGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGIGL\LL LALLCVLAAGGGAGEAAILLWTSVRHVAQAWELAQFIHTTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDPKGSEG NTMVPKNCYVSQQELKPFFFGVRIDYVLKAVAGFYLFHVQBVMG LYRAQAELQHVLGRAREAQDLGPEPQLVALL\LGQQEGGDTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLVALL\LGQQEGGTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLVALL\LGQQEGGTKEG LYRAQAELQHVLGRAREAQDLGPEPQLVALL\LGQQEGGTKEG LUTAASILQITYJDECTRIVSQNVGDVFPGQDSQDTFRG EAVLSPDPALHSTHSLTNSHAHGSDCDISCKGMTERIHSIN LHNPSNSVLETINSQRNNGHFCDVTVRIHGSMLRAQRCVLAAGS PFFGDKLLLGYSDIEIPSVVSQOSVGKLDDMYSGQLRVGSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGQDSQDTFRG TPESGTSGQSSDTESGYLQSHQHSVDRIVSGLRVACSGMERYL STTPETTHCRKQRPPVRICTURNHIKQEMEDDYDYYQQRVQ ILERNESECTEDTDQAEGTESEPKGESFDSGVSSSIGTEDDSV EQQFGFGAARDSQAEPTQSEQAARGGFTNGLETGASSPE EQGFGFGAARDSQAEPTQFRQAAEGPGTNQLETGASSPE	j	j		KGSRKMARLGSTSGEESDLEREVSDSEAGGGPOGERKNESSKKG
ACAGINYKKLLGSCCSHKERLSILRABLEALGMKGTPSLGKCR ALKEQREBAABVASLDVANISGIGRPRRTAWNPLGEAAPPGB LYRRTLDSDEERPRAPPDWSHMKGIISSDGESN RFWSSPTMKPNFSLRLFIFMLNCKGIFYLSKHRADRMRRLGDFL NQSSPTMKPNFSLRLFIFMLNCKGIFYLSKHRADRMRRLGDFL NQSSPTMKPNFSLRLFIFMLNCKGIFYLSKHRADRMRRLGDFL NQSSPTMKPNFSLRLFIFMLNCKGIFYLSKHRADRMRRLGDFL SGNVLNAYVTHHHABVNRQKDIYLANKVAQAWELAQFIHHTSKK ADVULLGDINMHPEDIGCCLLKEWTGHHDAYLETRPFKGSEG NTWPKNCYVSQOELKFFPGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONBSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWA\TPA\SYVIGIGL\LI LALLCVLAAGGGAGEAAILLMTFSVGLULWAGAFYLFHVQEVNG LVRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQOEGDRTKEQ PMSSPTMKFNFSLRLFIFNLNCWGIFYLSKHRADRMRRIGDFL NGESFDLALLESWSGODFQYLKQKLSPTYPAAHHFRSGIIGSG LCVFSKHPJCBETQGHLYTHLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAFYNRQKDIYLAHRVAQAWELAGFIHTSKK ADVVLLCGDLAMHFBELGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQOELKFPFURIPVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQPSSSTHGF\AERS PL/MCVCLKEALDGSLGLGMA\QARWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQOEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQOEGDRTKEQ LYRAQAELQHTLGRAREAQDLGPEPQLYALL\LGQOEGDRTKEQ LYRAQAELQHTLSTHSLTNSLTNGAFYLFHVQEVNG LYRAQAELQHTLSTHSLTNSLTNGAFYLFTALSVYIGLGL\LL LALLCVLAAGGAGEAAILLWTSVGLUKAGAFYLFHVQEVNG LYRAQAELQHTLSTHSLTNSLTNGAPTLFTALSVGLUKAGAFYLFHVQEVNG LYRAQAELQHTLSTHSLTNSLTNGAFYLTGSDLGCKGMTERISIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSNLRAQRCVLAAGS PFFQDKLLLGYSDLEIPSVUSVQSVQKLJDMYSGQURQCVLAGGSGE RYSYSGAVSHHETALGLPRDHHMEDSSWITRIHERSQOMERYL STTTETTHCRKQRPPVRICTURNHINGDEMDDYDYYGQQRVQ ILERNESEGCTEDTDQAEGTESEPKGESFDSGVSSIGTEDPSV EQOFGGAARDSQAEPTQPEQAARGGGFOTNQLETGASSPE ROMEVEMDSTVITTUSNSSUKSVLOOPSVNTEIGGPLEPGTOLVLD EQOFGGAARDSQAEPTQPEQAARGGGFOTNQLETGASSPE	1			SREGRITESSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRIKDVID
ALKEGREEAAEVASLUVANI ISGGEPRRRANPLGEAAPPGB LYRRTLDSDEERPRPAPPDWSEMRGI ISSGGESN RFWSSPTMKPNFSLRLRIFNLNCWGTPYLSKHEADRWRRLGDFL NGESFDLALLEEVWSEQDFQYLRQKLSFTYPAAHHFRSGI IGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLUVLHL SGMVLNAYVTHLHAEYWRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHFEDLGCCLLKEWTGLHDAYLETDFKGSEEG NTWPPKNCYVSQGELKFPFFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQORPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLUTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ RWSSPTMKPNFSLRLRIFFILLWGSPYLISKHRADRWRRLGDFL NGESFDLALLEEWWSEQDFQYLRQKLSPTYPAAHHFRSGI IGSG LCVFSKHPIQELTQHIYTLRGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQKDIYLJAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPBEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKFFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFYRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQGEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQGEGBTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQGEGDRTKEQ EAVLSPDPALHSTHSLTTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNGRHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNYGDVPFGLOGAGDPTRG TPESGTSGOSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVSHHETALGLPRDHHMEDPSWITTHERSQQMRRYL STTPETTHCRKQPRPVRIQTLVVNIHIKQBMEDDSWITTHERSQQMRYL STTPETTHCRKQPRPVRIQTLVVNIHIKQBMEDDSWITTHERSQQMRYL STTPETTHCRKQPRPVRIQTLVVNIHIKQBMEDDFDLTDLYLD RSMEVEMDSTVITTVSNSSDKSVLQOPSVYNSIGOPLBSTOLYLD				ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCP
6961 340 1646 RPMSSPJMKNPTSLRLRIFNLMCWGIPYLSKHRADRMRRLGDFL NQESPDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTCHIYTLMGYPYMTHHGBWFSGKAVGLLULHL SGMYLNAYVTHLHAEVRRQKDIYLAKWAQAWELAQPIHHTSKK ADVULLCGDLNMHPEDLGCCLLKEWTGHDAYLETRDFKGSEEG NTMVPKNCYVQDELKFPFFGVRIDYULYKAVGGFYISCKSPET TTGFDPHRGTPLSDHEALMATLFVRHSPQCNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTBSUGLVULWAGAFYLFHVQEVNG LTRAQAELQHVLGRARSQUGJFFPFGVALL\LGQQEGDRTKEQ APWSSPTMKNPFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL NQESPDLALLESVWSEQDFGYLRQKLSFTYPAAHHFRSGIIGSG LCVFSKHPIQEITCHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPBDLGCCLLKKWTGLHDAYLETTDFKGSEEG NTMVFKNCTVSQQELKFPFFGVRIDYVLYKAVSGFYISCKSFFT TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWMA\TFA\SVVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVYKAVSGFYISCKSFFT TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWMA\TFA\SVVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEWNG LYRAQAELQHVLGRAREAQDLGPPPQLVALL\LGQQEGDRTKEQ 6963 374 2618 RVTPLILKLLKKPTAENQKASEENETTOPGGSSAKFGLPCLNF EAVLSPDPALHISTHSLTHSHAHTGSSDCIISCKGMTREHSIN LHNFSNSVLETINBGRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIETPSVSVQSVQKLIDFMYSGVLRVSQSEA LQUITAASILQIKTVIDECTRIVSQNVGDVPFGLOGAGDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVSHHETTALGLPRDHHMDPPSWITTHERSQQMRRYL STTPETTHCRKQPRPVRIQTLVUNIHIKGEMEDDFSUTTHERSQQMRYL STTPETTHCRKQPRPVRIQTLVUNIHIKGEMEDDFSUTPLGPROVPQFQCRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEDSV EQQFGPGAARDSQAEPTQFEQAAEDAEGGPOTNQLETGASSPE EQGFGGAARDSQAEPTQFEQAAEDAEGGPOTNQLETGASSPE EQGFGGAARDSQAEPTQFEQAAEDAEGGPOTNQLETGASSPE	ı			ALKEQREEAAEVASLDVANIISGSGRPRRRTAWNPIGEAADDGR
RPWSSPYMKPNFSLRIRIPMINCWGIPFLSKHRADRMRRLGDFL NQSSPDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIGELTCHIYTLNGYPYMIHHGDWFSGKAVGLLVHL SGMVLNAYVTHLHABYNRQKDIYLAHRVAQAMELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLDAYLETRDFKGSEGG NTMVPKNCYYSQGELKPFFFGVRIDYVLYKAVSGFYISCKSPET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSLGMA\QARWWA\TFA\SYVJGLGL\LL LALLCVLAAGGGAGEAAILLWTBSVGLVLWAGAFYLFHVQEVNG LYRAQAELCHVLGRAREAQDLGBEPQLYALL\LGQQEGDRTKEQ RPWSSPTMKPNFSLRLRIFNINCWGIPFYLSKHRADDRMRRLGDFL NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTCHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRGKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKFPFFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWA\TFA\SYVIGLGL\LL LALLCYLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ RVFPLIKLLKKFFATARNGKASEENEITQPGGSSAKFGLFCLNF EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETINEQRNRGHFCDVTVRIHSSMLRAQRCVLAAGS PFFFGDKLLGYSDIFIPSVUSVQSVQKLIDFMYSGVLRVSGSEA LQILTAASILQIKTVIDECTRIVSGNVGDVFFGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHMEDPSWITRIHERSQMERYL STTPETTHCRKQPRFVRIQTLVGNHIKQEMEDPVYYGQQRVQ ILGRNESBECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQFEQAAEAPARGGFTNOLETGASSPE ESKEVENDSTVITYSNSSKKVLOOPSVNTSIGOPLFTGASSPE	6961	340		LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN
INGESPOLALLEEVWSGOPPGYLRGKLSFTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLUVLHL SGMVLNAYVTHLHAEYNRGKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLGGDLNMHPEDLGCCLLKEWTGLHDAYLETTDFKGSEEG NTMVPKNCYVSQGELKFPFFGVRIDYVIYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLEVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTSVGLVLWAGAFYLFHVQEVNG LAPAGAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ RPWSSPTMKFNFSLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESFDLALLEEVWSEQDFQYLRQKLSPTYFAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKFPFFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGAGEAAILLWTSYGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRARBAQDLGPEPQLYALL\LGQQGEGDRTKEQ EAVLSPDPALHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGFLOVTVRIHGSMLRAQRCVLAAGS PFFGDKLLLGYSDIEIPSVVSVQSVQKLDFNYSGVLRAGSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPCHVTVTHRISMLRAQRCVLAAGS PFFFGDKLLLGYSDIEIPSVVSVQSVQKLDFNYSGVLROVSGEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPCHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQMERYL STTPETTHCRKQPRPVRIQTLVGNHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGGAARDSQAEPTQDEQAAEAPABEGPTNOLETGASSPE EQQFGGAARDSQAEPTQDEQAAEAPABEGPTNOLETGASSPE EQQFGGAARDSQAEPTOGDEQAAEAPABEGPTNOLETGASSPE	0,01	340	1646	RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADPMPDICDET
LCVFSKHPIQELTQHITHIGSTPYMIHHGDWFSGKAVGLIVLHL SGMVLNAVYTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSPET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLG\LL LALLCVLAAGGGAGERAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQOEGDRTKEQ 6962 340 1646 RPWSSPTMKENFSIELRIFNLNCWGIPYLSKHRADRMRRLGDFL NQES FDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLMGYPYMIHHGDWFSGKAVGLLVLHIL SGMVLINAVYHLHABYNRQKDIYLAHRVAQAMELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGIGMA\QARWM\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LQQGEGDRTKEQ 6963 374 2618 RVTPLILKLKKPKTAENQKASEENEITOPGGSSAKFGLPCINF EAVLSPDPALITSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLSTLINEQRNKGHFCDVTVXIHGSMLRAQRCVLAAGS PFFCDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVPFGIQDSGQDTPRG TPESGTSGQSSTTESGYLQSHPCHSVDRIYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVPFGIQDSGQDTPRG TPESGTSGSSSTESGYLQSHPCHSVDRIYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVPFGIQDSGQDTFRG TPESGTSGSSTTESGYLQSHPCHSVDRIYSGVLRVSQSEA STTPETTHCRKQPRPVRIQTLVGNIHIKQEWEDDDYYYGQQRVQ ILERNESECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPAARDSQAEPTQPBQAAEAPAEGGPQTNQLETGASSPE EQGFGPGAARDSQAEPTQPBQAAEAPAEGGPQTNQLETGASSPE EQGFGPGAARDSQAEPTQBGAAEAPAEGGPQTNQLETGASSPE				NQESFDLALLEEVWSEQDFQYLROKLSPTYPAAHHERSGTTGCG
SGMVLMAYVTHLHAEYARQKDIYLAHRVAQAMELAQFIHHTSKK ADVULCGDLMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKFFPFGVRIDYVLYKAVSGFYISCKSPET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARMWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLUVMAGAFYLFHVQEVNG LYRAQABLQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EYRAQABLQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ NGSSFDLALLEBVWSEQDFQYLRQKLSPTYPAAHHFRSGI IGSG LCVFSKHPIQELTQHTYTLNGYPYMTHHGDWFSGKAYGLLVLHL SGMVLMAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKBWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYULYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWMA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQGGDRTKEQ EXPROAECHVLGRAREAQDLGPEPQLYALL\LGQGGDRTKEQ RVTPLILKLLKKPKTAENQKASEENEITQPGGSSAKFGLPCLNF EAVLSPDPALIHSTHSLTMSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEGRRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRTYSALYACSMQNGSGE RSFYSGAVVSHHSTALGLPRDHIMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNHHIKQEMEDDYDYYGQGRVQ ILERNESEECTEDTDQAEGTESBEKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQFEQAAEAPAEGGGTNQLETGASSPE RSSMVEMDSTVITVSNSSDKSVLOOPSVMTSIGOPLPSTOLYLB		!		LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLUI
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PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQBVNG LYRAQAELQHVLGGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETINEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRHERSQQMEXYL STTPETHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSTVITVSNSSDKSVLOOPSVNTSIGOPLPSTOLVLP				TTGEDDURGTDI COURT IN THE TOTAL CONTROL OF THE TOTA
LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVIGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVIGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ RVTPLILKLKKPKTAENQKASEENEITDPGGSSAKPGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETINEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNRVEMDSTVITVSNSSDKSVLOOPSVNTSIGOPLPSTOLYLP	1	ľ		PL /MCVCL YEAR DOOL OF CALL AND
EYRAQAELQHYLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ RVTPLILKLLKKPKTAENQKASEENEITQPGGSSAKPGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSIGTEPDSV EQQFGPGBARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNRVEMDSTVITVSNSSDKSVLOOPSVNTSIGOPLPSTOLVLP	i	:	l	LALLOW ANGGOOGRAPHIC TO THE PROPERTY OF THE PR
RVTPIILKLLKKPKTAENQKASEENEITOPGGSSAKPGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETILNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKILLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSIGTEPDSV EQQFGPGBARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLOOPSVNTSIGOPLPSTOLVLP	1		l	LYPACARI OUR GRADES ON GRADES OF THE CONTROL OF THE
EAVLSPDPALIHSTHSLIKRYAENQKASEENEITOPGGSSAKFGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSIGTEPDSV EQQFGPGABARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLOOPSVNTSIGOPLPSTOLVLP	6963	374	2618	PVTBLILLY LYNDY BY STORY OF THE PURISH STORY O
LHNYSNSVLETINEQRNRGHFCDVTVR HGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALVACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMEXYL STTPETHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGYSSSIGTEPDSV EQQFGPGAARDQAEPTQFEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLOOPSVNTSIGOPLPSTOLVLD		j		FAMI SEDERI THORWAY MANAGEMENT TOPOGGSSAKPGLPCLNF
PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALVACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLOOPSVNTSIGGPLPSTOLVLD	ļ			LUNESHELL STHELTHSLITHSHAHTGSSDCDISCKGMTERIHSIN
LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKGEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLOOPSVNTSIGGPLPSTOLVLD	l l	1	1	DEFORM I GARRIAGE TO THE OWNER OF THE OWNER O
TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLOOPSVNTSIGGPLPSTOLYLP				FFFQDALLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA
RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSIGTEPDSV EQQFGPGBARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLOOPSVNTSIGOPLPSTOLVLD	.	ł	1:	DQIDIAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG
RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSIGTEPDSV EQQFGPGBARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLOOPSVNTSIGOPLPSTOLVLD	j]	1	PERSONAL PROPERTY OF THE PROPE
ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLOOPSVNTSIGOPLPSTOLYLD	1	1	1.	RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSOOMERY:
ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLOOPSVNTSIGOPLPSTOLYLD	İ		13	STIPETHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ
RSNEVEMDSTVITVSNSSDKSVLOOPSVNTSIGOPLPSTOLVLD	- 1	}	1.	1LERNESEECTEDTDQAEGTESEPKGESFDSGVSSSTGTEPDSV
RSMKVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR QTETLTSNLRMPLTLTSNTQVIGTAGNTYLPALFTTQPAGSGPK	ľ		1:	EQUIFGPGAARUSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE
QUETETSNLRMPLTLTSNTQVIGTAGNTYLPALFTTQPAGSGPK			1 !	KSNKVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR
				WILLIAM THE TRANSPORT OF THE PROPERTY OF THE P

SEQ	Predicted	Predicted end	Amino agid company
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
[location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ı	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	-	\=possible nucleotide insertion)
			PFLFSLPQPLAGQQTQFVTVSQPGLSTFTAQLPAPQPLASSAGH
1			STASGQGEKKPYECTLCNKTFTAKQNYVKHMFVHTGEKPHQCSI
ļ)		CWRSFSLKDYLIK\HMVTHTGVRAYQCSICNKRFTQKSSLNVHM
			RLHRGEKSYECYICKKKFSHKTLLERHVALHSASNGTPPAGTPP
		i	GARAGPPGVVACTEGTTYVCSVCPAKFDQIEQFNDHMRMHVSDG
6964	1	178	SGRPFFFFFSNTDVYFIKKVTNRWTAGSSYKMTRMKSIGKILLL
			QIFIG\NCSMFVLVI
6965	757	208	NVFIEPRIQGFMKTSAHPGQKHPDFSMGLLFPLLAALEVCSCGS
		i	SGSLGYNLPQNH\GLLGRNTLVLLGQMRRISPFLCLKDRSDFRF
İ	1		PQEKVEVSQLQKA\QAMSFLYDVLQQVFNFSHKALL\CCMEHDL
İ			PGPTPHFTSSAAGTPGDLLGAGDGRRRSWGQWVIEGSTLALRRY
6000	 		FQESISTLE
6966	820	1867	IITALGVRGMPGCPCPGCGMAGPRLLFLTALALELLGRAGGSQP
i			ALRSRGTATACRLDNKESESWGALLSGERIDTWICELLGELMIC (
			LSGVFPLLVIPLEMGTMLRSEAGAWRLKOLLSFAT.cct.t.cnupt
1			HLLPEAWAYTCSASPGGEGOSLOOOOLGLWVTAGTI.TEL.ALEV
1			/HVPGQQGGDQPGPQORPHCCCRRAOWRPI.SGDAGCDADDCD
			GP\DIKVSGYLNLLANTIDNFTHGLAVAASFLVSKKTGI.T.TTMA
1			ILLHEIPHEVGDFAILLRAGFDRWSAAKLQLSTALGGLLGAGFA
6967	162	633	ICTQSPKGVEETAAWVLPFTSGGFLYIALVNVLPDLLEREDPW
		633	GFLPFKYWILDLSASSRMETDCNPMELSSMSGFEEGSELNGFEG
1		•	TDMKDMRLEAEAVVNDVLFAVNNMFVSKSLRCADDVAYINVETK
L			ERNRYCLELTEAGLKVVGYAFDQVDDHLQTPYHETVYSLLDTL\ SPAYREAFGKR\LLQRLEALKRDGQS
6968	1	2265	RGGGGGRGGPGARERERPGEPERTMEAAAGGRGCFQPHPGLQKT
Í	ļ		LEQFHLSSMSSLGGPAAFSARWAQEAYKKESAKEAGAAAVPAPV
1]		PAATEPPPVLHLPAIQPPPPVLPGPFFMPSDRSTERCETVLEGE
1			TISCFVVGGEKRLCLPQILNSVLRDFSLQQINAVCDELHIYCSR
			CTADQLEILKVMGILPFSAPSCGLITKTDAERLCNALLYGGAYP
			PPCKKELAASLALGLELSERSVRVYHE\CFGKCKGL\TAUPELVC
1	İ		SPSAACIQCLD\CRLMYPPHKFVVHSHKALENRTCHWCF\Dea\
	[NWRAYILLSQDYTGKEEQARLGR\CLDDVKEKFDYGNKYKPRUD
1 1			RVSSEPPASIRPKTDDTSSOSPAPSEKDKPSSWI,pti.accenve
1 1			LGCVHPRQRLSAFRPWSPAVSASEKELSPHLPALTRDSEVGVKG
] [FETAVAPNVALAPPAQOKVVSSPPCAAAVSRAPEDI.ATCTODDV
			RKLTVDTPGAPETLAPVAAPEEDKDSEAEVEVESREEFTSSLSS
1			LSSPSFTSSSSAKDLGSPGARALPSAVPDAAAPADADGGLPAPI.
1 1			EHLROALEGGLDTKEAKEKFLHEVVKMRVKQEEKLSAALQAKRS
1 1	}		LHQELEFLRVAKKEKLREATEAKRNLRKEIERLRAENEKKMKEA
{	1		NESRLRLKRELEQARQARVCDKGCEAGRLRAKYSAQIEDLQVKL
/	1	1	QHAEADREQLRADLLREREAREHLEK\VVK\ELQEQLWPRARPE AAGSEG\AAELEP
6969	1855	118	AGTMAGRLKVKTSEEQAEAKRLEREQKLKLYQSATQAVFQKRQA
		· 1	GELDESVLELTSQILGANPDFATLWNCRREVLQQLETQKSPEEL
	ł	l	AALVKAELGFLESCLRVNPKSYGTWHHRCWLLGRLPEPNWTREL
1 1	ļ	ſ	ELCARPLEVDERNFHCWDYRRFVATQAAVPPAEELAFTDSLITR
1 1	ì	J	NFSNYSSWHYRSCLLPQLHPQPDSGPQGRLPEDVLLKELELVQN
1			AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF
			SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLD
		1	AASLNDQLPQHTFRVIWTAGDVOKECVLLKGROEGWCRDSTTDF
	•		QLFRCELSVEKSTVLQSELESCKBLQELEPENKWCL\LTTTLLM
	1	i	RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS
1		j.	VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTI.
J	ŧ	į	PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLOELLI.
1	ļ	i ·	CNNRLQQPAVLQPLASCPRLVLLNLQGNPLCQAVGILEOLAELI.
	<u></u>		PSVSSVLT

	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence	1	\=possible nucleotide insertion)
- 1	6970	3	1528	SFPPLLSSPSAVGEGKVAVAAPCPGRSECARAKMAYIQLEPLNE
ı		1		GFLSRISGLLLCRWTCRHCCQKCYESSCCQSSEDEVEILGPFPA
- 1			İ	QTPPWLMASRSSDKDGDSVHTASEVPLTPRTNSPDGRRSSSDTS
]		KSTYSLTRRISSLESRRPSSPLIDIKPIEFGVLSAKKEPIQPSV
- 1		1	ļ	LRRTYNPDDYFRKFEPHLYSLDSNSDDVDSLTDEEILSKYQLGM
ı				LHFSTQYDLLHNHLTVRVIEARDLPPPISHDGSRQDMAHSNPYV
١				KICLLPDQKNSKQTGVKRKTQKPVFEERYTFEIPFLEAQRRTLL
- 1				LTVVDFDKFSRHCVIGKVSVPLCEVDLVKGGHWWKALIPSSQNE
- 1		1		VELGELLLSLNYLPSAGRLNVDVIRAKQLLQTDVSQGSDPFVKI
1				QLVHGLKLVKTKKTSFLRGTIDPFYNESFSFKVPQEELENASLV
- 1				FTVFGHNMKSSNDFIGRIVIG\QYSSGP\SEPNHWRRMLNTHRT
L				AVEQWHSLRSRAECDRVSPASLEVT
-1	6971	37	3702	ACFYVPGSRSFKLIPRHGLVNMGRSGKLPSGVSAKLKRWKKGHS
-				SDSNPAICRHRQAARSRFFSRPSGRSDLTVDAVKLHNELQSGSL
-				RLGKSEAPETPMEEEAELVLTEKSSGTFLSGLSDCTNVTFSKVQ
1		ļ		RFWESNSAAHKEICAVLAAVTEVIRSQGGKETETEYFAALIRKA
				AQHGVCSVLKGSEFMFEKAPAHHPAAISTAKFCIQEIEKSGGSK
1				EATTTLHMLTLLKDLLPCFPEGLVKSCSETLLRVMTLSHVLVTA
1	- 1			CAMQAFHSLFHARPGLSTLSAELNAQIITALYDYVPSENDLQPL
Т	-			LAWLKVMEKAHINLVRLQWDLGLGHI,PRFFGTAVTCII.SDUSOV
ļ	1	,		LTAATQSLKEILKECVAPHMADIGSVTSSASGPAGSVAKMEDAY
				EEGLTYKFHAAWSSVLQLLCVFFEACGROAHPVMRKCLOSLCDT
1	l	1	ı	RLSPHFPHTAALDQAVGAAVTSMGPEVVLOAVPLEIDGSRETLD
1	ĺ	ŀ		FPRSWLLPVIRDHVQETRLGFFTTYFI.PI.ANTI.KSKAMDI.AOAG
1		Ì		STVESKIYDTLQWQMWTLLPGFCTRPTDVAISFKGLAPTLGMAT
1	-	İ		SERPOLRVIVÇQALRILITKGCOAEADRAEVSREAKNRI.DII EN
1		i		LYGQPVAAGDTPAPRRAVLETIRTYLTITDTOLVNSLLEWASEV
1				VLDPASSDFTRLSVLDLVVALAPCADEAATSKI,VSTTDDVI.Egv
1	Ì	ļ		AHGVQKKAYRVLEEVCASPOGPGALFVOSHLEDLKKTLLDGLEG
1				TSSPAKRPRLKCLLHIVRKLSAEHKEFITALIPEVILCTKEVSV
ļ	1			GARKNAFALLVEMGHAFLRFGSNOEEALOCYLVI.TVPGI.VGAVT
	- 1			MVSCSILALTHLLFEFKGLMGTSTVEQLLENVCLLLASRTRDVV
ı	j			KSALGFIKVAVTVMDVAHLAKHVQLVMEAIGKLSDDMRRHFRMK
	į			LRNLFT\KFIPK\FGILTWGKKAVGPKEYHRVLVNIRKAEARAK
	1	1		RHRALSQAAVEEEEEEEEEEPAQGKGDSIEEILADSEDEEDNE
ı	1	i		EEERSRGKEQRKLARQRSRAWLKEGGGDEPLNFLDPKVAQRVLA
	1	l l	1	TQPGPGRGRKKDHSFKVSADGRLIIREEADGNKMEEEEGAKGED
	i	1	1	EEMADPMEDVIIRNKKHQKLKHQKEABEEELEIPPQYQAGGSGI
L		j	ĺ	HRPVAKKAMPGAEYKAKKAKGDVKKKGRPDPYAYIPLNRSKLNR RKKMKLQGQFKGLVKAAQRGSQVGHKNRRKDRRP
Г	6972	2179	973	PGGAILLPLWRRTRPREATVPRGAAQRGRARSAEGRIPSSQSPS
	ļ		I	PAEAGGATRSPPPRPPRPARPPGPSAPPLLRSDAGPGATVSAAA
l	1			AAATERARRGATMGAQLSTLGHMVLFPVWFLYSLLMKLFQRSTP
		j	İ	AITLESPDIKYPLRLIDREIISHDTRRFRFALPSPQHILGLPVG
			i	QHIYLSARIDGNLVVRPYTPISSDDDKGFVDLVIKVYFKDTHPK
		1	1	FPAGGKMSQYLESMQIGDTIEFRGPSGLLVYQGKGKFAIRPDKK
	i	1	1	SNPIIRTVKSVGMIAGGTGITPMLQVIRAIMKDPDDHTVCHLLF
	1	1	İ	ANQTEKDILLRPELEELRNKHSARFKLWYTLDRAPEAWDYGQG\
	1	i		FUNEENT DOUG DDDE \ PEDI UT MOOD DOUT ON A CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF T
		1	i	FVNEEMIRDHLPPPE\EEPLVLMCGPPPMIQYACLPNL\DHVGH PTERCFVF
	6973	1		
		!		LQPRCAHRGLRAQKCGRPAPGVDAMVLCPVIGKLLHKRVVLASA
	-		;	SPRROEILSNAGLRFEVVPSKFKEKLDKASFATPYGYAMETAKQ
	f	İ	;	KALEVANRLYQKDLRAPDVVIGADTIVTVGGLILEKPVDKQDAY
	1	j	1;	RMLSRFE/SGREHSVFTGVAIVHCSSKDHQLDTRVSEFYEETKV
			1;	KFSELSEELLWEYVHSGEPMDKAGGYGIQALGGMLVESVHGDFL
				NVVGFPLNHFCKQLVKLYYPPRPEDLRRSVKHDSIPAADTFEDL

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	,	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	b=Leucine, M=Methionine N=Asparagine
- 1	to first amino acid	amino acid	P=Proline, O=Glutamine P=Arginine
	residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine
1	amino acid	sequence	Welryptophan, Yelvrosine Yellnknown + cha-
Ĺ	sequence	Dequence	Codon, /=possible nucleoride deletion
		T	\=possible nucleotide insertion)
- 1		j	SDVEGGGSEPTQRDAGSRDEKAEAGEAGQATAEABCHRTRETLP PFPTRLLELIEGFMLSKGLLTACKLKVFDLLKDEAPQKAADIAS
1			KVDASACGMERLLDICAAMGLLEKTEQGYSNTETANVYLASDGE
į.			ISLAGE IMHNNDLTWNLFTYLEFAIREGTNOHUDALCKVAEDIR
	1		QUALIUS PETRLREMRAMHGMTKI, TACOVATA ENT. CD DCCA CDU
ì			GGCIGALARELAREYPRMOVTVFDI.PDTTRIAAUROPPCDONIO
1			INPAGED FROM PERSON INPAGE
L	. [KPGAGLLLVETLLDEEKRVAQRALMQSLNMLVQTEGKERSLGEY
6974	3082	2172	QCLLELHGFHQVQVVHLGGVLDAIL\PPKWPPEAQAACSL RSCAAFASFASRPPLELFAPPGSHRSPPGRGVATSAQCALSVRK
1			LLAARPGLGTKYQATMVYKTLFALCILTAGWRVQSLPTSAPLSV
1			SEPINIVEPTITIWTSSPONTDADTASPSNGTHWNGVI DIWN CAR
			TSLLPKNISIESREEEITSPGSNWEGTNTDPSPGGEGGGGGG
1			LITTLEEHSLGTPEAGVAATLSOSAAEPPTI,ISDOADASCROCT
Ĺ		ļ	SISPENISASVITNHSSTVTSTOPTGAPTAPPEDTPPEGGOVER
6975	2	500	PTSHATAEPVPQEKTPPTTVSGKVMCELIDMET\PPPPG RPRTVHCCKWALKLETAMETLINVFHAHSGKEGDKYKLSKKEL
	ĺ		KELLQTELSGFLDVKELML*ATEALKTFEEA*KSPIIQCSSSRS
1	1		Suprangippy L*LSAVPFPIHI.PI.PI.I.DPOAOKDYDAYDVA
6976	1216		BLDENGUGEVDFQEYVVLVAALTVACNNFFWFMC
	1210	970	GCQL*VAYGTTENSFVTFAHFPEDTVEOKAESVCPTMDVDED DE
1			MINIEAGTLAKLNTPGELCIRGYCVMI.GVWGEDOVTEPA VDODVA
İ			YWTGDVATMNEQGFCKIVGRSKDMIIRGGENIYPAELEDFFHTH
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7004 121 2285 FLEFULTSRSLRGPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG/YYCRVRPLGFPDQECCIEVINNTTVQLHTPE GYRLNRNGDYKETGYSFKQVFGTHTTQKELFDVVANPLIVNDLIH GKNGLLFTYGVVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQBFCKABEVDEDSVYGVFVSYIBIYNNYIYDLL EEVPPDPINPNLHNLNCFVKIKNHMYVAGCTEVEVKSTEKAFE	1		1	EDBADCIVDETHIR CONFIDENCE
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GYRLARNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQBFCKABEVDEDSVYGVFVSYIBIYNNYIYDLL EEVPFDPINPNLHNLNCFVKIKNHMYVAGCTEVEVKSTBRAFE	1			CA PROTESTED OF THE PROTEST OF THE P
GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQBFCKABEVDEDSVYGVFVSYIBIYNNYIYDLL EEVPFDPINPNLHNLNCFVKIKNHMYVAGCTEVEVKSTERA FE	ŀ	ĺ		GYPL NEW CONTROL OF THE CONTROL OF T
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EEVPFDPINPNLHNLNCFVKIKNHNMYVAGCTEVEVKSTERAFE		1		QAKRYVFKSNDRNSMDIQCEVDALLEROKREAMPNPKTSSSKRO
EEVPFDPINPNLHNLNCFVKIKNHNMYVAGCTEVEVKSTERAFE	[VDPEFADMITVQEFCKABEVDEDSVYGVFVSYIBIYNNYIYDLL
VFWRGQKKRRIANTHLNRESSRSHSVFNIKLVQAPLDADGDNVL	- 1			EEVPFDPINPNLHNLNCFVKIKNHNMYVAGCTEVEVKSTERAFE
				VFWRGQKKRRIANTHLNRESSRSHSVFNIKLVQAPLDADGDNVL

SEQ	Predicted	Predicted end	1 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
D	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
. [corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			QEKEQITISQLSLVDLAGSERTNRTRAEGNRLREAGNINQSLMT
			LRTCMDVLRENOMYGTNKMVPYRDSKLTHLFKNYFDGEGKVRMI
i	Ì	l	VCVNPKAEDYEENLOVMRFAEVTQEVEVARPVDKAICGLTPGRR
			YRNQPRGP\IGNEPLVTDVVLQSFPPLPSCEILDINDEQTLPRL
1			IEALEKRHNLRQMMIDEFNKQSNAFKALLQEFDNAVLSKENHMQ
ľ			GKLNEKEKMISGQKLEIERLEKKNKTLEYKIEILEKTTTIVEED
1			KRNLQQELETQNQKLQRQFSDKRRLEARLOGMVTETTMKWRKRC
			ERRVAAKQLEMQNKLWVKDEKLKQLKAIVTEPKTEKPERPSRER
7005			DREKVTQRSVSPSPVPVSYL
7003	63	876	RNMALYQRWRCLRLQGLQACRLHTAVVSTPPRWLAERLGLFEEL
1]		WAAQVKRLASMAQKEPRTIKISLPGGOKIDAVAWNTTDVOTADO
1	ł		ISSTLADTAVAAQVNGEPYDLERPLETDSDLRFLTFDSPECKAV
1]		FWHSSTHVLGAAAEQFLGAVLCRGPSTEYGFYHDFFLGKERTIR
1			GSELPVLERICQELTAAARPFRRLEASRDOLROLFKDNPFKT.HT.
ı			IEEKVTGPTATVYGCGTLVDLCQGPHLRHTGQIGGLKLLSNSSS LWRSSG
7006	22	898	
1			NAFGRHSTAVKMAAAAWLQVLPVILLLIGAHPSPLSFFSAGPAT VAAADRSKWHIPIPSGKNYFSFGKILFRNTTIFLKFDGEPCDLS
			LNITWYLKSADCYNEIYNFKAEEVELYLEKLKEKRGLSGKYQTS
1			SKLFQNCSELFKTQTFSGDFMHRLPLLGEKQEAKENGTNLTFIG
		•	DKTAMHEPLQTWQDAPYIFIVHIGISSSKESSKENSLSNLFTMT
1			VEVKGPYEYLTLEDYPLMIFFMVMCIVYVLFGVLWLAWSACYWR
7000			DLLRIQFWIGAVIFLGMLEKAVFYAGFO
7007	2	1001	AMTVSGPGTPEPRPATPGASSVEOLRKEGNELFKCGDVGGALAA
i i	1		YTQALGLDATPQDQAVLHRNRAACHLKLEDYDKAETFASKATRK
	1		DGGDVKALYRRSQALEKLGRLDOAVLDLORCVSLEPKNKVEGEA
1	. [LRNIGGQIQEKVRYMSSTDAKVEQMFQILLDPEEKGTEKKQKAS
	j		QNLVVLAREDAGABKIFRSNGVQLLQRLLDMGETDLMLAALRTL
1 1	1		VGICSEHQSRTVATLSILGTRRVVSILGVESQAVSLAACHLLQV
	j		MFDALKEGVKKGFRGKEGAIIVGEWKQVWGLLDVTVMEGMGLSQ PGQFFGDQTCSCRLFGIRFGDIILL
7008	70	1478	CPSALCHER DRDAUT DACCORT OFFICE CONTROL CONTRO
1 1	·		CRSALGHERPPPAHLPAGGRRLQTCPRSCRWLGRPPSGLPPGPR SPPPLAGPGQKMVQKKPABLQGFHRSFKGQNPFELAFSLDQPDH
, ,	j		GDSDFGLQCSARPDMPASQPIDIPDAKKRGKKKKRGRATDSFSG
			RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH
			IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG
		j	SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE
1	İ		NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS
	1	1	AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG
l l	ł	1	RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHTSCAA
			KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR
· 7009	1		WDSHFLLPPHPCRIHVRPGGLVRTVTVNE
	*	626	ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG
į	•	1	RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKOGFVVA
		l	LRLVACAQSGHEVTLSNLNLSMPPPKFHDTSSPLMVTPPSAEAH
			WAVRVEEKAKPDGIFESLLPINGLLSGDKVKPVLMNSKLPLDVL
7010	79	571	GRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE
	}		SHTRRAVVPETLLSPLCPLLGGGTAMSGGEQKPERYYVGVDVGT GSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAACC
}			VVTKKVVQGIDLNQIRGLGFDATCSLVVLDKQFHPLPVNQEGDS
		1	HRNVIMWLDHRAVSQVNRINETKHSVLQYVGG
7011	3	994	RIQTLPNQNQSQTQPLLKTPPAVLQPIAPQTTFGVQTQPQPQSL
ļ	ŀ	1	LQAQISAASITPLLQTQPQPLLQQPQQKAGLLQPPVRIVSQPQP
	ļ	1.	ARRLDPPSRFSGRNDRGDQVPNRKDDRSRERERRRSRERSPQ
}	}	13	RKRSRERSPRRERERSPRRVRRVVPRYTVOFSKFSLDCPSCDMM
			ELRRRYQNLYIPSDFFDAQFTWVDAFPLSRPFQLGNYCNFYVMH

SEC	Predicted		
ID		Predicted end	
NO:		nucleotide	Incording, C=CVSteine, D=Nengueia Nain =
1.0		location	Gracemite Acid, Febbenylalanine C.Cl/
- 1	location	corresponding	A=nistidine, l=isoleucine K-tunine
}	corresponding	to first	L=Leucine, M=Methionine N-Asparagina
İ	to first	amino acid	F=FFOLINE, O=Glutamine, D=Arginine
J	amino acid	residue of	S=Serine, T=Threonine, V=V=line
1	residue of	amino acid	W=Tryptophan, Y=Tvrosine, Y-Whitneym + G-
- 1	amino acid	sequence	Codon; /=possible nucleofide deletion
<u> </u>	sequence		\=possible nucleotide insertion\
1	ł		REVESLEKNMAILDPPDADHLYSAKVMLMASPSMEDLYHKSCAL
	İ		AEDPQELRDGFQHPARLVKFLVGMKGKDEAMAIGGHWSPSLDGP
7012			DFERDPSVEIRT\AIRCCKALTG
/ / / / /	1	2661	RRAGSVKRGEARLFGPTEROSERDURDSAADDDDMICOVKAAA
l l			PARAMETER GENERAL PROPERTY OF THE PROPERTY OF
ı			**************************************
- 1	į		1 ************************************
J	1		WARAGABAALPPPPPPOAPPEENESEDEEDECUPCAREGES
1	1		DAMISUSAACEPDIISGPOOTOKVFI, FIRNDIT OLWI DADKEO
ı	i		1 1 CALLQUEAR INSUTVLVHRVHQVI.FDUCT.TNEGTVVDT
1	ł		FIREIGRALITIESGVSGLAAAROLOSECMDUTILEARDRUTGER
1	1		ATTACOM I VALUGAMV VIGI GCNDMAINIQUOTAMENT TUTTORE
1]		I DIEMIGUAVEREKDEMVEOEFNRIJEATSVI SUOT DENTE STORES
1		1	A STOCKARD A LOTOR KHAKDEOLEHMKKLAKADEDI ABLI AMBARA
1		į	A MARKATABURQQYKEASEVKPPRDTTAEET.VVCVVDDT TAY OVER
1			1 DELIGITUGE LEKA QELEAN PPSDVVI SSPDPOTI DWIED NOT TO
j]	ł	FARALPESTESDEHWDODDDFRFTGSHT.TUDWGVGGUDUAL DEG
J	1	ľ	DDIADNIAVKQVRYTASGCEVIAVNTPSTCOTPTVVODAUT CTT
I	1	1	FIGVENOUPPAVOEVEPENKTSAVORMGEGNI NIVIAG GERRI.
1	ŀ		THOPSVILLEGHVGSTTASRGELFI.FWNT.VKADIII.XI.VAGDAAG
J	,		THENTSDDVIVGRCLAILKGIFGSSAVDODKEMATCDWD & DDVI
1			ROSISIVAAGSSGNDYDIMAOPTTPGDGTDGADODTDDT DDS
1			HITKNIPATVHGALLSGLREAGRIADOFLGAMVTLDBOATDOVD
7013	1	366	755252M
İ] -	2661	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKAAAA
	J -		HAMAMAAAIGIEAGPGTAGGSENGSEVAAADAAA GGAAAVAA
i	1		VGERIFRAREPPRASPPGGLAEPDGGACDOACDTRITTGGATTT
1	1		1G1AE1PEG \KKISKKKAKVEYREMDEGIAMI ODDERWARDE
	1		MANAGRANDPPPPPPDAPPEERNEGEDEPPCCTPCT > management
1	ļ		DIMITS OF PARCEPUL ISGPOOTOKVELET DND TELL DND WEST
ł	1		
!	[FIRM GRALL LGSGVSGLAAAROLOGEOMDUTT TEXTENTIONS
l	[ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP
}	1	İ	LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP
	1	ľ	VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV
1	1		NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE
}		ĺ	YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG
	1 1		LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL
		ļ	PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV
] [FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG
	1		IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA
		.	RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE
l	1		HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP
7014		I.	AQQSPSM
1014	3	3950	DFEVGDKIRILATLEDGWLEGSLKGRTGIFDVPFUKI GDDWDVG
]	! :	ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEAEEPD
]	ļ.	CIISEAPTSPLGHLTSEYDTDRNSYQDEDTAGGPPRSPGVEWEM
			PLATDSPTSDPTEVVNGISSQPQVPFHPNLQKSQYYSTVGGSHP
		1 1	HSEQYPDLLPLEARTRDYASLPPKRMYSQLKTLQKPVLPLYRGS
		1 8	BVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSISERLEMKPG
		1 1	PQAQGLVMEAATHSQGDGSTDLDSKLTQQLIEFEKSLAGPGTEP
		1 1	DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR
		1 1	PCTPVSTSPHLLVDQNLKPAPPLVVRPSRPAPLPPSAQQRTNAV
1		S	SPKLLSRHRPTCETLEKEGPGHMGRSLDQTSPCPLVLVRIEEME
		R	DLDMYSRAQEELNLMLEEKQDESSRAETLEDLKFCESNIESLN
			- TOPODATE TOPODAT CESNIESIN

SEQ	Predicted	Predicted end	Drive said second
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Į.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	}	\=possible nucleotide insertion)
			MELQQLREMTLLSSQSSSLVAPSGSVSAENPEQRMLEKRAKVIE
ı	1	1	ELLQTERDYIRDLEMCIERIMVPMQQAQVPNIDFEGLFGNMQMV
İ	j		IKVSKQLLAALEISDAVGPVFLGHRDELEGTYKIYCQNHDEAIA
			LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFLIKP
1	1		VQRVMRYPLLLMELLNSTPESHPDKVPLTNAVLAVKEINVNINE
-	1		YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKKSNRVSSHLKH
1			LTGFAPQIKDEVFEETEKNFRMQERLIKSFIRDLSLYLQHIRES
i			ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNFKER
}			TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAEKLK
1			DKKTLEELQSARNNYEALNAQLLDELPKFHQYAQGLFTNCVHGY
ı			AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSPVIO
i]		QLQVFTFFPESLPATKKPFERKTIDRQSARKPLLGLPSYMLOSR
].		ELRASLLARYPPEKLFQAERNFNAAODLDVSLLEGDLVGVIKKK
			DPMGSQNRWLIDNGVTKGFVYSSFLKPYNPRRSHSDASVGSHSS
]		TESENGSSSPRFPRQNSGSTLTFNPN\S\MAVSFTSGSCOKOPO
	1		DASPPPKEWDQGTLSASLNPSNSESSPSRCPSDPDSTSOPRSGD
1			SADVARDVKQPTATPRSYRNFRHPEIVGYSVPGRNGQSQDLVKG
1]		CARTAQAPEDRSTEPDGSEAEGNQVYFAVYTFKARNPNELSVSA
7015	1842	513	NQKLKILEFKDVTGNTEWWLAEVNGKKGYVPSNYIRKTEYT
1		213	RQAWHE\VAAPSWRGARLVQSVLRVWQVGPHVARERVIPFSSLL
1			GFORRCVSCVAGSAFSGPRLASASRSNGQGSALDHFLGFSQPDS
1			SVTPCVPAVSMNRDEQDVLLVHHPDMPENSRVLRVVLLGAPNAG
			KSTLSNQLLGRKVFPVSRKVHTTRCQALGVITEKETQVILLDTP
1 .	1		GIISPGKQKRHHLELSLLEDPWKSMESADLVVVLVDVSDKWTRN QLSPQLLRCLTKYSQIPSVLVMNKVDCLKQKSVLLELTAALTEG
			VVNGKKLKMRQAFHSHPGTHCPSPAVKDPNTQSVGNPQRIGWPH
			FKEIFMLSALSQEDVKTLKQYLLTQAQPGPWEYHSAVLTSQTPE
1	!		EICANIIREKLLEHLPQEVPYNVQQKTAVWEEGPGGELVIQQKL
1			LVPKESYVKLLIGPKGHVISQIAQEAGHDLMDIFLCDVDIRLSV
			KLLK
7016	167	2513	ILNAPKPPPPRDSVEAVAAKRDTGGGSWGTGMDVSGQETDWRST
]	}		AFROKLVSQIEDAMRKAGVAHSKSSKDMESHVFLKAKTRDEVLS
		1	LVARLIIHFRDIHNKKSQASVSDPMNALOSLTGGPAAGAAGTGM
1			PPRGPGQSLGGMGSLGAMGQPMSLSGOPPPGTSGMAPHSMAVVS
) i	İ	1	TATPOTOLOLOGVAAAAAATARSSSSSSRRRYSSSSSSSSSSS
1	1	ľ	FQAQQSAMQQ\QFQA\VVQQQQQL\QQQQOOQOOHLIKLHHONOO
i 1			QIQQQQQLQRIAQLQLQQQQQQQQQQQQQQQQALQAQPPIQQP
	j	1	PMQQPQPPPSQALPQQLQQMHHTQHHQPPPQPQQPPVAQNQPSQ
,		[LPPQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQP
	ì	1	QVQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQVQTP
! 1			QSMPPPPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPF
			\QSPVTARTPQNFSVPSPGPLNTPVNPSSVMSPAGSSQAEEQQY LDKLKQLSKYIEPLRRMINKIDKNEDRKKDLSKMKSLLDILTDP
ĺ			SKRCPLKTLQKCEIALEKLKNDMAVPTPPPPPVPPTKQQYLCQP
		1	LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR
			RLEDDERQSIPSVLQGEVARLDPXFLVNLDPSHCSNNGTVHLIC
		į.	KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSV
			HRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA
7017	1	1785	INLGNTCYMNSVI*ALFMATDFRROVLSLNLNGCNSLMKKLOHL
Ì	1		FAFLAHTQREAYAPRIFFEASRPPWFTPRSOODCSEYLRFLLDR
	ļ	1:	LHEEEKILKVQASHKPSEILECSETSLOEVASKAAVLTETPRTS
1		[]	DGEKTLIEKMFGGKLRTHIRCLNCRSTSOKAEAFTDLSLAFWPS
		1.3	YSLEYMSCPDCSQSPSIQDGGLMQASVPGPSEEPVVYNPTTAAF
1) :	ICDSLVNEKTIGSPPNEFYCSENTSVPNESNKILVNKDVPOKPG
		[(GETTPSVTDLLNYFLAPEILTGDNQYYCENCASLONAEKTMOIT
		1	SEPEYLILTLLRFSYDQKYHVRRKILDNVSLPLVLELPVKRITS

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
No:	nucleotide	location	I Warmanile, CECVSCEING Dentandia and a
1 1	location		TOTAL CALLA REPRENVISION C. C. C.
	corresponding	corresponding	1 "-"-OCTUING, ISISO(P))Cina V-tycata-
	to first	to first	1 b=beucine, M=Methionine N-Asparagine
	amino acid	amino acid	Percoline, OsGlutamine Debraining
	residue of	residue of	S=Serine, T=Threonine, V=V=7; no
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, Y=Tlpknown + Change
	sedneuce	sequence	Codon, /=possible nucleofide delotion
<u> </u>	seduence		\=POSSIBLE Nucleotide insertion\
1 1			FSSLSESWSVDVDFTDLSENLAKKLKDSGTDEASCTRELEDITE
]			DVVVIGGESGRIYSYARNITSTDSSVOMVUOGENINT NA NOOG
			DELIGROSPSAVEEQDLENKEMSKEWFI.FMDQDtvppmppActyor
1 1]	I I SKEPKUTAYVLLYKKOHSTNGI SCHNIDTSCI MINGROOM
			DEDATTRUNKLYLQEQELNARARALQAASASCSEDBMGEDDWDD
7018	40.		PGSCGPIGGGGGGFNTVGRLVF
7010	484	1066	SLVFRGNTWSGEAGHHCSALFNI, AAVHOLEVGTERIDA DET VEG
			PSDIGECAGIAETLOYILDRYPKOVOEMIJONRIET POCAMILIA
- 1		}	GMKARMEKELLEMRPFRSSFQVQLASNPVLDAWYGARDWALNHL
1 1			DDNEVWITKEYEEKGGEYLKEHCASNIYVPIRLPKQASRSSDA
7070			QASSKGSAAGGGGAGEQA
7019	1048	335	APGGFLVTMVFPAPSPPWMLGCCSHEVTAGPPTLCKDMSALVAA
	,		RMRHIPLAFGSDWRDLPNIEVRLSDGTMARKLRYTHHDRKNGRS
			SSGALRGVCSCVEAGKACDPAARQFNTLIPWCLPHTGNRHNHWA
1 1			GLYGRLEWDGFFSTTVTNPEPMGKQGRVLHPEQHRVVSVRECAR
1 1			SQGFPDTYRLFGNILDKHRQVGNAVPPPLAKAIGLEIKLCMLAK
7000		_	ARESASAKIKEERAAKD
7020	1	2154	FADSKRKSVLLDKIKNLQVALTSKQQSLBTAMSFVARNTFKRVR
			NGFLMRKVAVFFSNTPTRASPQLREAVLKLSDAGITPLFLTRQE
]			DRQLINALQINNTAVGHALVLPAGRDLTDFLENVLTCHVCLDIC
1	1	•	NIDPSCGFGSWRPSFRDRRAAGSDVDIDMAFILDSAETTTLFQF
1 1	f		NEMKKYIAYLVRQLDMSPDPKASQHFARVAVVQHAPSESVDNAS
			MPPVKVEFSLTDYGSKEKLVDFLSRGMTQLQGTRALGSAIEYTI
i	1		ENVFESAPNPROLKIVVLMLTGEVPEQQLEEAQRVILQAKCKGY
			FFVVLGIGRKVNIKEVYTFASEPNDVFFKLVDKSTELNEEPLMR
1			FGRLLPSFVSSENAFYLSPDIRKQCDWFQGDQPTKNLVKFGHKQ
1 1	į.		VNVPNNVTSSPTSNPVTTTKPVTTTKPVTTTTKPVTTTTKPVTI
	 		INOPSVKPAAAKPAPAKPVAAKPVATKTATVRPPVAVKPATAAK
1 1	1		PVAAKPAAVRPPAAAAAKPVATKPEVPRPQAAKPAATKPATTKP
1			MVKMSREVQVFEITENSAKLHWERPEPPGPYFYDLTVTSAHDQS
1	l		LVLKQNLTVTDRVIGGLLAGQTYHVAVVCYLRSQVRATYHGSFS
1 1			TKKSOPPPPOPARSASSSTINLMVSTEPLALTETDICKLPKDEG
1.			TCRDFILKWYYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCA
7022			PVLAKPGVISVMGT
7021	2	338	VNAVSFFPNGYAFATGSDDATCRLFDLRADOFLI LVCUDVITCO
	f		ITSVAFSKSGRLLLAGYDDFNCNVWDTLKGDRAGVLAGHDNRVS
7022			CLGVIDLGMAVATGSWDSFLRIWN
1022	2	856	VYIGSFWSHPLLIPDNRKLFEAFEODLEDDYOGLDDNAAA
1 1	. [i	DUIKRAKLAKVHAYIISSLKKEMPSVFGKDNKKVELIDINI A TITU
			GRIEREROISPGDEPNLKRMODOLOAODESKEODI. KCVI I DIRTE
1 1		i	DELIMINATION OF THE PROPERTY O
ĺ		1	EGAGEGIDDAEWVVARDKPMYDETFYTT, SPVDGYTTC AND YVDA
1	į.	1	VRSKLPNSVLGKIWKLADIDKDGMLDDDEFALANHLIKVKLEGH
			ELPNELPAHLLPPSKRKVAR
7023	2	748	AMVFGGVVPYVPQYRDIRRTQNADGFSTYVCLVLLVANILRILF
	}	I '	WE GREE ESPLENOSAIMILT MLLMIKI, CYPTODIANIET MADDON
		ļ.	TAADSKDEEVKVAPRRSFLDFDPHHFWQWSSFSDYVQCVLAFTG
	1	,	VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST
:]			EGMSIKMVLMWTSGDAFKTAYFLLKGAPLQFSVCGLLQVLVDLA
7024		:	ILGQAYAFARHPQKPAPHAVHPTGTKAL
7024	1207	190	RTGVTGVVAQVWMFGGGGVLSSGEQLQMPVKPERGLGPSDGWLV
l		١	SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS
ł		18	QLKPPVLPGTLGGQALHLRSWLLSRQGPAETGGQGQPQGPGLRT
		, ,	
ı		F	LLITGLEGAGI.GGAWI.AI.PARKERI ACAMONICA
		1 2	ULLIGUEGAGLGGAWLALRAEKERI,OOOKRTEAT.DOAAMOOOD
		F	RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV RQLEAEPGLPPVQPVFITVDPERDDVEAMARYVQDFHPRLLGL

SEQ	Predicted	Predicted end	l bring gald
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
- [location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j	residue of	amino acid	WaTryptophan, YaTyrosine, XaUnknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
1			TGSTKQVAQASHSYRVYYNAGPKDEDQDYIVDHSIAIYLLNPDG
-			LFTDYYGRSRSAEQISDSVRRHMAAFRSVLS
7025	232	832	ERNSPIGNNENL*K\HSLDCLCFRGDWEGNTOFOTT ODVOTTOR
j	i		AQVIKICEKRPTFNOHTVFNLHORINTGDKINFEVELOVABLOG
1	į.	1	SDHTQHQLIHTSEKFCGDKECGNTFI.PDSEVIOVOTVUTUTUTUTUTUTUTUTUTUTUTUTUTUTUTUTUTU
1	İ		ECKECGKSFSLRSSLTGHKRIHTGEKPFKCKDCGKAFPFUCOT C
7026) VHARIHIGEKSYECKECGKAFSCG
7020	328	1146	NPNPSIGDIKDIKKAAKSMLDPAHKSHFHPVTPSLVFLCFIFDG
1	}		DHQALLSVGVSKRSNTVVGNENEERGTPVASPEVDMENELALDE
1			SSVLKHCCDLLIGVAAGSSDKICTSSLOVODDERAMMACTODIC
1			HGESAULLISCNAESAIGWISSRPWVGELMETELEGDERGDING
1	<u> </u>		DKKSS*LPKKHR*OPINAVRMFI.DOCMDCGTAI.DATUCETDUES
1			EKKNING*KGIGEIF*VWGCTLPPHYWGAVTTNVPKLSNSGKLLC
7027	43	954	ODEOPHIFG
		234	GRRLQQQQRPEDAEDGAEGGGKRGEAGWEGGYPEIVKENKLFEH
ļ			YYQELKIVPEGEWGQFMDALREPLPATLRITGYKSHAKEILHCL
			KNKYFKELEDLEMDGQKVEVPQPLSWYPEELAWHTNLSRKILRK
1			SPHLEKFHOFLVSETESGNISRQEAVSMIPPLLLNVRPHKILD MCAAPGSKTTQLIEMLHADMNVPFPEGFVIANDVDNKRCYLLVH
1		•	QAKRLSSPCIMVVNHDASSIPRLQIDVDGRKEILFYDRILCDVP
			CSGDGTMRKNIDVWKKWTTLNSLQLHGLQLRIATRGAEQL
7028	189	608	SRPPPEPEPGTMVEKGSDSSEKGGVPGTPSTQSLGSKNFIRNS
1 1			KKMQSWYSMLSPTYKQRNEDFRKLFSKLPEAERLIVDYSCALQR
1	4		EILLOGRLYLSENWICFYSNIFRWETTISIQLKEVTCLKKEKTA
7029			KUIDNAIQ
1 /029	1343	40	VLESNTEAKQATGTSSKLRHGTGQEKGREGPRCPSGLAQLRLWG
1 1	Į.		/PCPHAGRETGPRASAPIPGS+GHGWHW+DKDGDGEDSEGDGE
1 1			SPHSPSLLNMOOAPTHVGPGMGSORPRSSIAIDEOUGUGGOVERD
1			KWKA*KSLPGAAASERTEMTKERSP/RPCOGVDSSNWPRODOKK
1 1			TREADS THE PROPERTY OF THE PRO
!			R*GRGGPRSPLTKASGTTHIPTPFFGSTD/PDTPDSCPGTDVG\
1	1		AAPGQKRGHREA*QGPEPV/WGRVTTHLQGPAG*TKPLGS\RNW
	l l		VPGPAEGEOGEGAGLEGRP*PLKGCRSTLTFSPQLSIPMVGKKP
		I	PEGTTASFFP\RSCHSE*RKPPPSCPHAPALSLPHPLPLPLPL
	l	1	PLPLPGAGT*HSARSGRPGQSETGSLCHNCHHCPPHCPKCSPGG
7030	2	521	FVCFSAPGSGQGKRRVNMELSAVGERVFAAFALLKRRIRKGRM
1		_	EYLVKWKGWSQKYSTWEPEENILDARLLAAFEEREREMELYGPK
- 1	J	Í	KRGPKPKTFLLKAQAKAKAKTYEFRSDSARGIRIPYPGRSPQDL
		ĺ	ASTSRAREGLRN\RVCPRQRAAPAPAP\PRRGPSGPGPRPG*G
7077	·		PGLHFPGPGGPSKHGFVPASEOHOHOOHI.pppgpsgpsgpsps
7031	960	29	HCSVPGAEWPRKPPAOICPOLTSRPHI.SSPPSI.SPCCCUSPGRO
1	j		/CKPS/RHCDELHEGPSRTAALPCGKPOPKHGVPFCG/PCPGCA
1	1		PREDICEPPAULVSPVGRAAPSGAL*PSGRACSACSHRIADRAAT
ł			SAAAPKPSLGSGQNASGLPAASLPPODSSOPHKTVPSDADGVDD
	!	i	LGAQARAAPPRLWCPRALVSG*EASPEAVSVAAGDDVDCDTDcm
}	j		SGSTASHSRRGC*SPR*TPAPPRRDHGRSAAFFVT.TAAAGAAG
7032	1202		ASQGGPRPTGAGRTPSPLGLPFSRGPPAASARPFCPHDet.
,,,,	1393	2104	RRPGRTEPVEPPPVPPPPRASNSKSRCR*RNI.HI.API.*OGDI DV
- 1		1 3	SRQIGTSSLPFGRSAGERPRPAATFCLSRGGSSPVFI.*DCCCt
1		1.	SPWMKKQFGRLHSLFWKSWOKMNSFLLTPKLDTSIMSGWPVDOB
1		1 -	bPKLHTFLKKSLQMASELAPPLPTPAPLAGGLDDDDCDDDT r Dy
1	i	1.	PLA*LSRSGILVPPNSGFSLSC\PLGDH+GSSGEVRGSCGSPPP
7033	689		HCWVLPPPP*LTLPPR
	303	815 I	RSRDCLSSSATSNRARRSKCSGPKRATPLDSGPGP*APPGPSSA

SEQ	Predicted	Predicted end	Amino agid gogment
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
J	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
í	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ļ			LMMPSSCPWRTGALGPSPAGSRALGRCTSSVGPGSRWLTRTSSP
l	İ		GCATRTWRTMRMEPRPLRSRMGESAPGIPAELPSAAPSGPSAPS
	ł		AAAPSAPTTPAAAGPNTL*SRRTAEWCWPPSCSCCWGWC*SWSA
	1	İ	WDWRRPPLQVSPAPSSSCRASCCWCLESIT*SSSTARSRATGAS
			SSSTCPTSRSDRGAAWTP\SPMGAPLLPCSVPLISREEALQDPR
		İ	NPSP*GVCSGSSGHAGLALGKPPVACSVP
7034	92	1942	EDTSSMPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYRERV
			KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
1			TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI
ľ			RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
	1		FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL
}	Į –		TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
1	1		IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW
ı	į į		YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
	[l	TVWKQFGGLPEFYNIFQGYTVEKREGYPLRPELIESAMYLYRAT
			GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF
1			FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI
1			FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQ
1			KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS
			QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK
		_	K K
7035	92	1942	EDTSSMPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYRERV
1			KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
] .	. ·]		TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI
1]		RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
[FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL
1 1			TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
1 . 1	ì		IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW
1 1			YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
1 1			TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT
1 1			GDFTGLELGRDAVESIEKISKVECGFATTKDI.DDUKI.DNDMBCB
i 1	ı	}	FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI
1 1			FNIEARPIDPAALHCCORLKEEOWEVEDI.MRRPVGI.KDGDGVEO
ł			KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS
] [1	İ	QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK
			K ,
7036	442	761	CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT
] [RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP
1 705			PPPPPPPPRRPPRNRRPG
7037	442	761	CLAPLESCEQIINLHLAPSGRIRWAWI.RGPGPN*T.PGFGDGTDT
] [!	RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP
			PPPPPPPPPRRPPRNRRPG
7038	155	891	GAGAASDMSSGLRAADFPRWKRHISEOLRERDRLOROAFFETTI
[i	QYNKLLEKSDLHSVLAOKLOAEKHDVPNRHETSDGHDGTMNDNO
	1	}	LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM
		1	QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA
	1	j	LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR
		ŀ	LQEAASPAAERACRSSKGTSTSRTG
7039	155	891	GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL
			QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ
}	1		LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLINIQMQRKDREM
l	İ	1.7	OMNEAKTAECLOTTEDLETEGLETEGLETEGLETEGLETEGLETEGLETEGL
!		[]	QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA
	ļ	1;	LQITFTALEGKLRKTTEENQELVTRWMABKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG
7040	34	789	KITPPREPHRESSHGSDNSSVLSGELPPAMGKTALFYHSGGSS
1	i		***FFARFAKUSSGHGSDNSSVI,SGET,DDAMGKTAT,RVUGGGGG
	1	1.0	GYESVMRDSEATGSASSAQDSTSENSSSVGGRCRSLKTPKKRSN

	SEO	Predicted	1 70- 12	
	ID	beginning	Predicted end	
	NO:	nucleotide	nucleotide location	
	1	location	corresponding	Chucamic Acid, Paphenylalaning Con
		corresponding	to first	(**************
		to first	amino acid	Debeucine, Memethionine Negaration
	}	amino acid	residue of	F=F4Q41De. O=Glibamina D_hamini
	1	residue of	amino acid	S=Serine, T=Threonine V-V-1:
	1	amino acid	sequence	Welryptophan, YeTurosine V-III
	1	sequence	ocquence	// /-possible micleatide 3-1
			 	\-Possible nucleofide incertion\
	ł	1		PGSQRRRLIPALSLDTSSPVRKPPNSTGVRWVDGPLRSSPRGLG
	ŀ			I ~~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~
	ľ	ľ		
	7041	1	567	- DESCRIPTION
			307	SGRVAMGRRAPAGGSLGRALMRHQTQRSRSHRHTDSWLHTSEL
ſ		{		1 AND ADMICKUMBUS VIEWS LIDDEL ATARICA COMPRESS
- 1		1		1 ~ 1 TO TO TO TO THE PROPERTY OF THE PROPERTY
		1		TOTAL MANUAL HONGROUD VINE ROLL TI TODDOUGHT SOME ASSESSED.
ſ	7042	7	345	/
- 1			242	PIHMAAAALRADI\ISPLFPHIQGYLLLSASHG\ATSLHTKGAL
L				I " TO TO THE TAXABLE VALUE OF THE PROPERTY OF THE PARTY
ſ	7043	2	2170	1 222 TALL AND LED KELL BEKA
		1 1	2170	ARGMAARDSDSEEDLVSYGTGLEPLEEGERPKKPIPLQDQTVRD
J]		TACKIAR TACKING AF SGGF SAGY FNTVCG CRC WTD COMPAND COMPAND
- 1		1		1 NO THE PROPERTY OF THE PROPE
		1		WARDALAPIPGATUIDINTTDAKI.CUCEDI I DIMIGUNA
- 1		1		RVKRPRRQKPDPGVKIYGCALPPGSSEGSEGEDDDYLPDNVTF
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]		TO THE TOTAL CONTROL OF THE PROPERTY AND
ĺ		ļ		KYDTVLKDEEPGDGLYGWTAPRQYKNQKESEKDLRYVGKILDGF
- 1		1 1		I
ł		;]		LSESAGKATPDPGTHSKHOLNASKRAELLGETPIQGSATSVLEF
		1		LSQKDKERIKEMKQATDLKAAQLKARSLAQNAQSSRAQPSPAAA
- 1				AGHCSWNMALGGGTATLKASNFKPFAKDPEKQKRYDEFLVHMKQ
- ([]		GQKDALERCLDPSMTEWERGRERDEFARAALLYASSHSTLSSRF THAKEEDDSDQVEVPRDQENDVGDKQSAVKMKMFGKLTRDTFEW
- 1				HPDKLLFQ/RLVGLPRVKRDKYSVFNFLTLPETASLPTTQASSE
1				KVSQHROPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK
-	7044			QQSSPLVNKEEHAPELSAN
- [,044	276	734	EVYLTDEFAKGRKVADLYELVQYAGNIIPRLYLLITVGVVYVKS
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		1		PATE TO SET TO A SUBSECTION OF THE PROPERTY OF THE PARTY
·	7045			ERERQELRILVGTNLVRLSQV
1	7045	3	513	LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP
ļ	j	1	ļ	KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK
	1	ſ	Ì	DOWN VOICE FULLIKNASISTYSTWEYDKNICUTET AVENUE - 1
\vdash	7046			
i		3		DOT MILAUSRAGOEMSI.AAI.KOHDDVITTCIADI TICOVIDE
1	- 1			ACTION DATE OF THE VYRRANG DVUC DVITATION AND AND AND AND AND AND AND AND AND AN
		· ·		~~~ VULLEF HUI KNASIS I VS TWEVDVMOOUD TA 127 118 BEFFER I
—	7047	103		
1		103		WILLERCOWS EGLTS I KGNCHNRYTA T SKOUTTVERT WALL TO SECOND
1	1			THE TO VECTOR THE YOR I PESTINION IN THE PROPERTY OF THE PERSON OF THE P
1	7048	92		
		32	V,	FECLILLSSWDYRHHATROVICEDVETMEDGOVERS
			1 '	TO THE ANGAGEM TORK I REPORTED BY DESCRIPTION OF THE PROPERTY
	- 1	1	1 -	THE PROPERTY OF THE PROPERTY O
7	7049	393		
1		3,33	938	RTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL
1	1	1	1 '	CAVORT LEUKUMULFIKIKNDGVA PUMVCUVUDA VODATO
I	1	i	{ •'	**************************************
ı	- 1		, -	TARRED AND AN
7	050	393	``	
			938 K	RTGSASYGGPPPGLGGPATXASVAGRCSSVGKI PARRCYEDEL
				THE THE PARTY OF T

SEO	75		
		Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
]	location	corresponding	
1	corresponding	Corresponding	
	to first	to first	1 DOUGLING, MEMORNIONING MARKET
ļ	co lirst	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ĺ	amino acid	residue of	S-Sering M. M R-Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	sequence	seducince	
- 1	1		VPVFEAVGRIYELRIMMDFDGKNRGYAFVMYCHKHEAKRAVREL
		i	NNVETBBCBLY CYCLOSTON OF BURNING YAF VMYCHKHEAKRAVREL
	}		The second of th
- 1	i	I	The state of the s
7051	119		
	1 119	816	KKMNLABICDNAKKGREYALLGNYDSSMVYYQGVMQQIQRHCQS VRDPAIKGKWQQWQGILLEBYDANIA
1	[ł	VRDPA TYCKWOOM ON THE THE THE THE THE THE TYPE OF THE THE TYPE OF
1	1		
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	1		ASDGEMPKFDGAGYDKDLUPAL EDDTISCHUR FORKRINDDG
7075			ASDGEMPKFDGAGYDKDLVEALERDIVSRNPSIHWDDIADLEEA KKLLREAGVLPMWM
7052	467	715	
1	1	, 13	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL
7053	467		
j	1 30,	715	SCPGRGKMSKLLNPERMTCPDVVPDCVPUC
7054	 		SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL TYRNSMYHNKHYFKDKUM DYCGGGGGYAHFGIHEEMLKDEVRTL
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	i i		CADURARE I DARRESAGAE DE DEL DEL DATA DE LA CONTRACTOR DE
1	1 1		
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j	1 1		VOOLROATEECKOUTLELDEGGEBEUHFSRPVGLFLASD
1	! !		VQQLRQAIEECKQVILELPEQSEKQKDAVVRLIHLRLKLQELKD
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7056			
	2	527	DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLLFWKTFLLYNQGP
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<u> </u>			DKHORSHLGKKPPQ+PVTKLSFPISISQPSHKNTQLHQEELCLR GYPC
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1	i		
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 		13	NAILNVKELGGADNIRKYWSRYYQGSQGVIFVLDSASSEDDLEA
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1	f	4 -	WPAFPRQPAAAAMDALLGTGPRRARGCLGAAGPTSSGRAARTPA
1	1	, -	TO AND DANDECYCY VIPIII EL COALET TOURIDED
1 1	į.	1 0	CYLSPPDSHSGCLGDTOPGERPAROGER THOUTRETDKEKSSI
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1 1	ł	, -	STATE OF STRUKLARY INCOMPANY DANGERS
1	į	G	VVVQVRIPSRVDKSESSPPKQFDQENLLPAPVVLASVHELDLF
1]	ſ	R	CFRPVI.THMOTT.WEIMITCHET IN CHERTIFIC TO THE CONTROL OF THE CONTRO
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L	ı	*	COPERFITTINUSEPKRETTROND DINTAL COMPANS
7060	90		
[-]		1670 S	VNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ
<u> </u>		l v	RFEHLUTOMKWEL OF CROPSIES OF CHARLES I EYKKLUNPSQ
			RFEHLVTQMKWRLQEGRGEAVYQIGVEDNGLLVGLAEEEMRAS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	•	\=possible nucleotide insertion)
			LKTLHRMAEKVGADITVLREREVDYDSDMPRKITEVLVRKVPDN
ļ			QQFLDLRVAVLGNVDSGKSTLLGVLTQGELDNGRGRARLNLFRH
l			LHEIQSGRTSSISFEILGFNSKGEVHGINGTQWGQTLRMGW***
1			RT*DGGRVWRLFEIV*MNALRGL*TSSAPLRKSMGNQLN*IKNG
	ĺ		VKIKRQGHPGNGLGPGNSEGVGRAGRRH*GPWALGQVVNYSDSR
			TAEEICESSKMITFIDLAGHHKYLHTTIFGLTSYCPDCALLLV
1			SANTGIAGTTREHLGLALALKVPFFIVVSKIDLCAKTTVERTVR
1			QLERVLKQPGCHKVPMLVTSEDDAVTAAQQFAQSPNVTPIFTLS
1			SVSGESLDLLKVFLNILPPLTNSKEQEELMQQLTEFQVDEIYTV
			PEVGTVVGGTLSR*IDLLATLPTQPSPIYSKTSWPKGGDPGI
7061	364	710	ARMPSPLGPPCLPVMDPETTLEEPETARLRFRGFCYQEVAGPRE
1			ALARLRELCCQWLQPEAHSKEQMLEMLVLEQFLGTLPPEIQAWV
1	Ì		RGQRPGSPEEAAALVEGLQHDP*ARMPSPLGPPCLPVMDPETTL
			EEPETARLRFRGFCYQEVAGPREALARLRELCCQWLQPEAHSKE
1			QMLEMLVLEQFLGTLPPEIQAWVRGQRPGSPEEAAALVEGLQHD
<u> </u>			PGQLLG
7062	71	744	AKAGTNLERLHWLSYFFCIPKHKLKSSQKDKVRQFMACTQAGER
			TAIYCLTQNEWRLDEATDSFFONPDSI.HRESMRNAVDVKKI.EDI.
[[YGRYKDPQDENKIGVDGIQQFCDDLSLDPASISVIVIAWKPPAA
1 1			TQCEFSRKEFLDGMTELGCDSMEKLKALLPRLEGET.KDTAKFKD
1.			FYQFTFTFAKNPGQKGLDL*MAGAYWKLVLSGRFKFLYLWNTFL
7063			MEHH
/ /003	2	562	LRTVPDLPGRRFRAMRTGQRR*PELPPDMNSLEQAEDLKAFERR
1			LTEYIHCLQPATGRWRMLLIVVSVCTATGAWNWLIDPETQKVSF
1 1			FTSLWNHPFFTISCITLIGLFFAGIHKRVVAPSIIAARCRTVLA
1 1			EYNMSCDDTGKLILKPRPHVQ*QSSLIVMGLKIAFLRISDTAKS
7064	300	884	HKGFLLRLDM .
1 1	1	004	RDTGSDPSSTRRLCSTCCTGH*PAEPIASPHPSRGTCPPASSAS
1 1	1		SRRTGCWTCPPESGHAQARRSRRASASRWGARGAVRSAVAARGC SSRAGRWLETPGRRRGPPACAAAAGRLRGPAP*AAPPTASVPAR
l 1	I		CRCPAARTGAPAAATWLRRRLSGLRAPALGRRRSPGPSPKSAAP
1 1	j		PLLTPLGAGRAGGSRANS
7065	1	555	ATTTHSARRSGRGAAAEAAASAAGGRQKGPDRKAWEGRRTTPGG
1 1			RSQSEPKAPPPQKRSEAAFASMAHSPVAVQVPGMQNNIADPEEL
l i	•		FTKLERIGKGSFGEVFKGIDNRTQQVVAIKIIDLEEAEDEIEDI
1	•		QQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMEYLGGGSALDLL
			RAGPFDEFO
7066	356	676	PGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQICDT
	1		YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND
<u></u>		1	VGVEVGGSGGCLEERTPP
7067	152	973	KENITMATEIGSPPRFFHMPRFOHOAPROLFYKRPDFAOOOAMO
	Ť	1	QLTFDGKRMRKAVNRKTIDYNPSVIKYLENRIWORDORDMRATO
	,	i	PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW
1 1	1	}	TPEGRRLVTGASSGEFTLWNGLTFNFETILOAHDSPVRAMTWSH
j		ļ	NDMWMLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNID
] [1	1	FSVVPIVMVKLPSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT
7068			HSPFCWAPF
,008	222	816	DIMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD
		1	DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
		1	VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLV
			GLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL
7069	7147		AELRIHENKVKKIQKDTFKKK
,,,,,	1147	1765	FRDHRRYFYVNEQSGESQWEFPDGEEEEEESQAQENRDETLAKQ
. 1	1	1	TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW
			TLLQSNVPVLQPPLPLEMPPPPPPPPPPESPPPPPPPPPPPAPKMPPP

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	I MATERIALIZE, LELVSTPINA DENGALEE A
	location	corresponding	I VAUVOUITO ACIO. FEDDONVISISSISSI A AN I
	corresponding	to first	1 "-" Dululue, 1=180/engine V_T
1	to first	amino acid	L-Leucine, M-Methionine N-Asparation
}	amino acid	residue of	F=FIOLINE, O=Glutamine D-Averiation
1	residue of	amino acid	Serine, TeThreonine, V-Valina
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	sequence	Doquence	1 COCOM, /=possible nucleofide deleti
		 	\=possible nucleotide insertion)
L_	į.	1	EKTKKGRKDKAKKSKTKMPSLVKKWQSIQRELDEEDNSSSSEED
7070	1	547	I NYD INGKKIEEWKOOOLVSGMAERNAMPEN
ł)	DGTMEDSEAVQRATALIEQRLAQEEENEKLRGDARQKLPMDLLV
ĺ	j	İ	1 2224 MINGAUSAALUKVKGI IKRVDKTQI DI DDDTTTDIIGG = a
- 1		1	ELRKKRKOKKRDALAASHEPPPEPEEITGPVDEETFLKAAVEGK
<u> </u>	1	ł	MKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNG ATVDFQ
7071	2	921	
1	1		ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP
ł			TOTAL DAGE ON VOTELNS VPOKS S DET. TO UDA VPD VO PARA LA
İ			FQDPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNV
			PESSI.PPASMPYADHYSTFSPRDRMNSSPYQPPPPQPYGPVPPV
1			PSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQT
	1		JUNEAU INSTITUTE OF THE PROPERTY OF THE PROPERTY AND THE PROPERTY OF THE PROPE
7072	2	921	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1			ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP
1			VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY
	1		FQDFRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNV
1	1 1		PESSLPPASMPYADHYSTFSPRDRMNSSPYQPPPPQPYGPVPPV
1]		PSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQT
			SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ
7073	50	504	IRRKPDQWAQYHTQKAPLVSSTLFVATQSPTPPSTLNRGEGS
1]		LANGSFOVSDFPAPAAAPAHTLTSFSGSLSPOFRKPLGRAPAMP
	ĺ		LVRYRKVVILGYRCVGKTSLAHQFVEGEFSEGYDPTVENTYSKI VTLGKDEFHLHLADTAGODEVSTLAHQFVEGEFSEGYDPTVENTYSKI
7074			VTLGKDEFHLHLVDTAGQDEYSILPYSFIIGVHGYVLVYSVTSL HSFQVIESLYQKLHEGHGK
7074	263	1003	VCPVLCSTRQEPGHSSLVTYFGKPTRRKEFLLGHCIAAGKMNIS
1 1			VDLETNYAELVLDVGRVTLGENSRKKMKDCKLRKKQNERVSRAM
]	!		CHARLES OF A LINE DAS A LANGUAGE DA CHARLES AND A LINE DAS A LINE
ľ			I TOTAL SUBJECT TO THE SECOND
			THE TOTAL OF DEPTIKE AND TOTAL OF THE PROPERTY
7075	598		1 TO TE DE LE DE LE LE LE LE LE LE LE LE LE LE LE LE LE
,5	398	1005	NYINFFFRKEYPPHVOKVEINPUDI.CDI.OCUPDIMU
1 1	1	ľ	THE BLAKK VOORKHOST YOUT DOT OD A COVER THE THE COLOR

7076	279		~~~
1	- 13	1049	LQSESSNAAEGNEQRHEDEQRSKRGGWSKGRKRKKPLRDSNAPK
1	}	ļ	OLDIGITARINGKKEULKAKRPEVPFPFTTPMICNERGER DDD 1
1	ł	Į.	WANT TO PUT DEVENTING RELIGIOUS AND CONTRACTOR OF THE PROPERTY
]	İ	ļ	ACCUMENCE OF THE PROPERTY AND THE PROPER
] [į	İ	NUMEROUS CONTROL OF THE PROPERTY OF THE PROPER
7077	3	1119	PARITIES TO THE PROPERTY OF THE PARITIES OF TH
1 1	-	****	SSMGSNSEINGLALRKTDKYGELGGGOVEGGY VOOTER
1 1		,	ADMINDUE SWADKAPSKREOKAKI DCDKCI DCCI DX KA MANA
1			O'COMPANDE DESCRIPTION OF THE PROPERTY OF THE
	1		AGGIGGGOULKIPKALLIABDEGACOVOV DAVA PALL A MARIA POR 1
			AT WELLVEICH ALLEGI I SAGLRATOL DORTORATT DORTOR DATA
			THE QUIDEVILLE WENCI FARTI DWAST DIM MEDGEORES 1
1	1	,	**************************************
	ļ	1.	DVMSVINDPVTEALIERENAAOLKKWRETPGELOVPDERBILLGG
7078	483	1 '	WAINEBRARQUPPLGPSSS
}		767	FQGQRMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG
i		1 '	VIVEGELLELANVQELAEGANAAYLOLLNLFAYGTVDDVIANVP
7079	2 -		DIFFUI
	-	376	VVEPKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ
			QARKKRRGIIEKRRRDRINSSLSELRRLVPTAFEKQGSSKLEK

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	
1	location		
	corresponding	corresponding	W-MARCIUIDE,
1	to first	to first	Depending, Mamethioning National
ļ	amino acid	amino acid	regionine, O=Glutamine p_hadinine
- 1	residue of	residue of	S=Serine, T=Threonine W_W_line
ŀ	amino acid	amino acid	W=Tryptophan, Y=Tyrocine v=U-lea
j		sequence	(COUCH) /=DOSSIDIE NUCLEOFIAE Actable
	sequence	<u> </u>	\=POSSIDIE nucleotide incertion\
7700			AEVLQMTVDHLKMLHATGGTGTHALLFQASFIQQIF
7080	200	595	VQLPLEAPCLSLLSCRDHSGGNRDLSRRHRDCRVYGSPQDGIPY
ł	ł		LTHPLCHODVVSVGRLQIRALATPGHTQGHLVYLLDGEPYKGPS
<u> </u>		1	CLFSGDLLFLSGCGEEDBYDERL CHRONICAL CONTROL CONT
7081	213	506	CLFSGDLLFLSGCGEFPRKREELGEEGETEVRAATVPWRALKP
	i		AVTEEMILNSLSLCYHNKLILAPMVRVGTLPMRLLALDYGADI
L	1		VYCEELIDLKMIQCKRVVNEVLSTVDFVAPDDRVVFRTCEREQN RVVFQMGTS
7082	3	1137	1 KV AL GRIGIS
İ	1	1137	APSRITMLMAWCRGPVLLCLRQGLGTNSFLHGLGQEPFEGARSL
1	}		- CONCOPRIODE MERICANOR A DENTE CONCIDE DE CONCORDA - I
l	1		DOUBLE TERESSPREI EDSSCHOODCOPTUOGCEDDON'S O
- [ſ		YOUNG VERNINSPICE TERRITOR OF THE APPROXIMENT IN
1	1		1 Product Grand Name of the Control
	1 1		ADDIVVENKKGTAITFPKDINMTISMMDINDGDTGG TAGGGG
	1		TOWNS TO DESCRIPTION OF THE PROPERTY OF THE PR
	1		VERWINDING THRUISGATEDIKSLTEDIGITEDATA TOTTOR DEL
7083	115		1 ************************************
1	1 472	541	RSNAVQLTRMEYAMKSLSLI, VPKST, SPHVSVPTSUBMOOVED
	<u> </u>		JEAMPRARPCKVSTADRSVPKCTMAVCT.PDT.T.T.VTPD.MT.L.T.
i			PFFLVLEEDGTTVETEEYFQALAGDTVFMVLQKGQKWQPPSEQG
7084			Authorities
7004	3	522	NSVSVSSQSRFLASVPGTGVQRSAAADMAASTAAGKQRIPKVAK
	i		1 VAVAGE ACTUAL OLLER CARREST, PLT DDDDOORT TO THE TOTAL OLD THE TOTAL O
			YKLRKRKTFEDNIRKNRTVISNWIKYAQWEESLKEIQRARSIYE
7085			I CODD V DI RULLI LIMLKY A EMEMKNIDO INTUNDA TEMP
/005	243	1499	RQLARLRRRGWRSPFGGAPMAHITINQYLQQVYEAIDSRDGASC
}			ABLVSFKHPHVANPRLQMASPEEKCQQVLEPPYDEMFAAHLRCT
1 1	1		YAVGNHDFIEAYKCQTVIVQSFLRAFQAHKEENWALPVMYAVAL
1 1	1		DLRVFANNADQQLVKKGKSKVGDMLEKAAELLMSCFRVCASDTR
1 1	1		AGIEDSKKWGMLFLVNQLFKIYFKINKLHLCKPLIRAIDSSNLK
1 1	- 1		DDYSTAQRVTYKYYVGRKAMFDSDFKQAEEYLSFAFEHCHRSSQ
1 1	i		KNKRMILIVILDUVMI I CUMPUTE TO THE TOTAL OF THE PROPERTY OF THE
1 (i	KNKRMILIYLLPVKMLLGHMPTVELLKKYHLMQFAEVTRAVSEG
1 1	ľ		NLLLHEALAKHEAFFIRCGIFLILEKLKIITYRNLFKKVYLLL KTHOLSLDAFIWALKEMOVENDEN
			KTHQLSLDAFLVALKFMQVEDVDIDEVQCILANLIYMGHVKGYI SHQHQKLVVSKQNPFPPLSTGC
7086	256	525	TI.A A PMCKON CKY PROPERTY OF
1 1			ILAARMGKQNSKLRPEVMQDLLESTDFTEHEIQEWYKGFLRDCP
L 1	1	ĺ	SGHLSMEEFKKIYGNFFPYGDASKFAEHVFRTFDANGDGTIDFR EF
7087	166	723	
1 1	(LSGSSAGKVAAPCVPPSNHELVPITTENAPKNVVDKGEGASRGG
1 1	J		"INCOLONGSTRVTPSVOPHLOPTPNMGUCPTMGDGGGT D
1			VIERTIAVOEPSTANEENERSNT REVIOUNT VOVUCONUT
1 1			ERREDITALHARVEEFGWPDLHTPALEKICSICKAMPTWI MALLA
7088	104	759	IIICE V LINK(*
		133	GTSAASPSSLLEMAGEITETGELYSSYVGLVYMFNLIVGTGALT
1	i		
1		1	MAINDADEEDUDSSTASUSDVI.TDDNVPDADVDDTT OUGDDGG
1	İ		**** * DI TON VONGUMASMEENKVGUNT. PVPCT TUVT UND * ****
7089	33		ANY FESTING VICSATGNDSCGVEADTKYNDTDDCWCDI DDIM
- 1	33	4,,,	SVCWEDRYLKARMEESPLSRAPSRGGVNETANARTYTENMINTER
1		1 •	TITE POINT SASDWIGIFKVEAACVDDVUTETWOOT TO COMPANY
- 1		1 .	SPIRISVQFQASYLPKPGAOLYOFRVVMPOGOVCGGGBBBG-BB-
1		1 .	FAFFIDEDVIDEBADGGSDILLVVPKATVIONOLDECORPURT
		1,	YUKUYUEGYVIBLKSKVOELERALATADORUTUI MEOUWATADA
1	}	, ,	GGLIEERDILSKOOGDHVARILEI.RDDIOTICEVAR MYDYDER D
1	ſ	1 *	WELL AND INDUKTOR OF KENDADING OF THE CASE
			NLDLKEAKSWQEEQSAQAQRLKDKVAQMKDTLGQAQQRVAELEP
•			THE THE PROPERTY OF THE PERFECT OF T

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	N=4eucine, M=Methionine N=3gmagazie;
	to first	amino acid	P=Proline, Q=Glutamine, P=Arginine
1	amino acid	residue of	S=Serine, TaThreonine V-Valine
	residue of	amino acid	W=Tryptophan, Y=Tyrosine Y-Inknown + Char
- 1	amino acid sequence	sequence	Codon, /=possible nucleatide delation
	sequence	<u> </u>	\=possible nucleotide insertion\
í			LKEQLRGAQELAASSOOKATLI.GEELASAAAADDDTTAELIDGE
1			DSVAEVNGKLAELGLHLKEEKCOWSKEPAGI.I.OSVEREVDKTI K
1			LIGHT LEADERAY QUEERTONOVERTEL APERTICAL VIOLANCE PROPERTY
1			TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN
	1		EDATTEDEEAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETQ ASLLLGLE
7090	33	1775	SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC
1			HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG
1		1	SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFRE
			PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM
			QualQueGQVTELRSRVOELERALATAPORUTELMEOVYCLORG
1			I DOELLEEKDILSKOOGDHVARILELEDDIOTCOVIC DVIII DVIII TOLD
1			RURDTVKALTREOEKLIGOLKEVOADKEOSEAETOVAGOERHIIT
1			I NADARANSWOEEUSAOAORLKDKVAOMKDATGOAOORKA BE BR
			LABQUAGAQELAASSQOKATLLGEELASAAAAAAAAAAAA
I			DEVAEVNGKLAELGLHLKEEKCOWSKERDGI.LOGURDEVDVII V
1			LEASTLIKLEKAVQEERTONOVFKTELAREKDOGIJOLOGOVDET
1			1 LUKSALKVLOKEKEOLOEEKOELI, EVMORT DADI DUTA DOUBLE
ł	1		EDATTEDERAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETO
7091	186	1076	ASLLIGLE
1	İ	2070	EGMLTREHRCGRSEEQELEPWPSPKKARSGRWLRNGFKRKMEEP
1			EEPADSGQSLVPVYIYSPEYVSMCDSLAKIPKRASMVHSLIEAY ALHKQMRIVKPKVASMEEMATFHTDAYLQHLQKVSQEGDDDHPD
			SIEYGLGYDCPATEGIFDYAAAIGGATITAAQCLIDGMCKVAIN
1			WSGGWHHAKKDEASGFCYLNDAVLGILRLRRKFERILYVDLDLH
i i			HGDGVEDAFSFTSKVMTVSLHKFSPGFFPGTGDVCDVGLCVCDV
7092			I ISVNVPIQDGIQDEKYYOICERYEPPAPNDCI.
1032	522	809	KQGINEDQEESOKPRIGEGCEPISKROMVKI I VOVOUBEODELD
1	ſ		NORKKEKKKKKLERQCQMEPNSDGHDRKRVRRDVVHSTI.PI.TT
7093	454		DESPURLM
1 1	434	655	NFGVSGVELAQQASMVRMSFVIAACQLVLGLLMTSLTESSIQNS
7094	2	508	ECPQLCVCEIRPWFTPOSTYREA
]	_	308	FVRSMHWGVGFASSRPCVVDLSWNQSISFFGWWAGSEEPFSFYG
1 1			DIIAFPLQDYGGIMAGLGSDPWWKKTLYLTGGALLAAAAYLLHE
	_		LLVIRKQQEIDSKDAIILHQFARPNNGVPSLSFFCLKMETYLRM ADLFYQNYFGGKLSAQGKMPWIEYNHEKVSGTEFII
7095	1	411	IASSLPKMASLLQSDRVLYLVQGEKKVRAPLSQLYFCRYCSELR
1 1			SLECVSHEVDSHYCPSCLENMPSAEAKLKKNRCANCFDCPGCMH
) [į		TLSTRATS ISTQLPDDPAKTTMKKAYYLACGFCRWTSRDVGMAD
7005			KSVGE:
7096	224	2067	ETRSLAVQEKPSQAGRRSSRISFAGALFLTRFLLQELLLNNFC
1			SAMSPAPDAAPAPASISLFDLSADAPVFOGI,SIJVSUADGEALAR
		•	APRISCSGSGERESPERKLLOGPMDISEKT.ECCTCDOMPONIOR
[UKEHYKLDWHRFNLKORLKDKPLLSALDFEKOSSTCDLSSTCCC
[1	EDSDSASEEDLQTLDRERATFEKLSRPPGFVPHPVI.PONAGGO
		į	LYAYRCVLGPHODPPEEAELLLONLOSKGPPDCVVII MADAGUER
		f	GAIFQGREVVTHKTFHRYTVRAKRGTAOGLEDARGGDGUGACAN
	ľ	[LRKYNEATLYKDVRDLLAGPSWAKALEEAGTIIJRADDSGDSI.B
1	[1	FGGKGAPLQRGDPRLWDIPLATRRPTFOELORVI,HKT.TTL.WIVE
1		İ	EDPREAVRIHSPOTHWKTVREERKKPTEEETRKICPDEKEALCO
1	1	1	NEES PKQGSGSEGEDGFOVELELVELTVGTT.DI.CESEVI.DVBBB
ſ	1		RKRNKKEKSRDQEAGAHRTLLQQTQEEEPSTQSSQAVAAPLGPL
	ļ		LDEAKAPGQPELWNALLAACRAGDVGVLKLQLAPSPADPRVLSL
7097	256	1228	LSAPLGSGGFTLLHAAAAAGRGSVVRLLLEAGADPTVQCQDH
· .			IRTKSAATWEAWPQCGREGSRIITEPCEANAGSRQELQTERISS
			FLAAQGDQAFHSGLETNNSNSELPLRVGLKVAQGSPLMGGQVSA

SEQ	Predicted		
ID	beginning	Predicted en	
NO:	segiming	nucleotide	
1	nucleotide	location) VANCOULC ACIO. FEDNONVIAIANIA A A.
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
{	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
į.	amino acid	residue of	S-Sering W. M R=Arginine,
ļ	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ł	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1	sequence	ocdarince	Town, / Thossible midleotide dolers.
	—	 	/-Possible nucleofide incorpion/
l			SNSFSRLHCRNANEDWMSALCDRINDWDLULLGERGE
ı			
ſ	1	i	THE PROPERTY OF THE PROPERTY O
į	1	ĺ	WLERHPREVVILACRNFEGLSEDLHEYLVACIKNIFGDMLCPRG
- 1	į.	1	EVPTLRQLWSRGQQVIVSYEDESSLRRHHELWPGVPYWWGNRVK
			TEALIRYLETMKSCGR
7098	82	956	SSFLKRCRKVLCCMCIDGROOM
1			SSFLKRCRKVLGCWGIPSEQSLFSTLEEPRDKEIDNYCVMRLQT
1			1 MAGGE MAFIRE PVN I CRM (AVIGIDAGE CERRENT CHIPTER OF THE
[}	TO THE DOUBLE OF THE PROPERTY
1	1		1 DODD VII TELWINDDLLW PRVI AVAT PRATICE CONTRACTOR CON
1	1	į	DOWN WINDGIDT MPDPSSEWI, VRUMUNTTI VECTURATA TOTAL
İ	1		TOTAL APPLICATION OF THE PROPERTY OF THE PROPE
7099	992		1 manufactor i i i i i i i i i i i i i i i i i i i
1 ,000	992	210	LFRLAPGFLRSLAROGYHOTWAFDFLDSCATATIVES
1	1 1		AND DER SEAR PUPNDALLGEHDER COCKED AD DED CORRES
			GAVLEVHVPQIGAGVSLPGILAAKCGAEVILSDSSELPHCLEVC
1	1 1		ROSCOMNNLPHLQVVGLTWGHISWDLLALPPQDIILASDVFFEP
1	i I		EDFEDILATIVE MUNICIPAL HOUSE
	L 1		EDFEDILATIYFLMHKNPKVQLWSTYQVRSADWSLEALLYKWDM KCYHIPLESFDADKEDIAESTLPGRHTVEMLVISFAKDSL
7100	205	671	ANGGEWEAN DOGOTOGOTOGOTOGOTOGOTOGOTOGOTOGOTOGOTOGO
ļ	[i		ANGGFWEAAPGSEVSLPLWVPTASHSKTTALGIGSAPPPHLSVL
1	į į		1 * DE SE SUUDE DE AFEVE KKYDRNGI MISTROPHICO - DD I
L.	i		
7101	2	503	1 COALAMEDURKEDARKCIDEALTAM
	_	303	WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRAADMKKD
1 1			VALUD VG&PKVGKTSLIMSLVSFFFPDFFUDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
J			DAVE THE VUISAAEOSUEOLHOFTSOAMUTOTUUN INDUITUUS
7102	2		VISAWIPDINEKIDKDSRLPLII.GGNKGDIJEVOD
1	2	503	WRGGPRRAKRLAGGAVGWVIJLVRGVHSVPAGGGPPPD
í í	' 1		VALUE VGEPA VGATSLIMSLVSEREDERINDED A DELTATOR DELTATOR
) (- 1		ERVPTHIVDYSEAEQSDEQLHQEISQANVICIVYAVNNKHSIDK
7103			VTSRWIPLINERTDKDSRLPLILGGNKSDLVEYSR
1103	119	438	GSOSSVAVNTPSCEEDEROVDIAGGRASDLVKYSR
1)	1.	•	GSQSSVAVNIRSGTDEESMDLMNGQASSVNIAATASEKSSSES
	ĺ		LSDKGSELKKSFDAVVFDVLKVTPBEYAGQITLMDVPVFKAIQP DELSSCGWNKKEKYSSAP
7104	1670	795	DEBSCOWNKREKISSAP
1	i	,,,,	RLWEHRSVSAGASGWGLSSPGCLLLHPSLPEEERVDILINNAGV
1	1		I MICENALLEDGE EMORGANHLIGE AWAGAN DUMONTE DODONOM
	İ		Gr. v. v. v. SULFII LNPGHFLLTNI, LI, DYI, VAQADOD T TATI CO
j	i		AVACUIDE ODDINGOTEK ANTENA VOCA OT A TUE BOXOS OF THE
	ľ	j	GOGVIVNAUHPGVARTELGRUPGIUGGPDLOUDEL TENEN STORE
	j		AGERGWPAPAOHNTLAVARELA VTGGKVPDGT VOVA DA DDA
7105			EEVARRLWAESARLVGLEAPSVREQPLPR
,105	765	143	GQMCRRPSPKSTSCLSMTCDLP/RGLQDPQCLALFRVAVDKHQA
1	j		LLKAAMSGQGVDRHLFALYIVSRFLHLQSPFLTQVHSEQWQLST
1	1	Í	SOTEVOOMULEDIEDIES SOCIETATION OF THE SOCIETATION O
1		ł	SQIPVQQMHLFDVHNYPDYVSSGGGFGPADDHGYGVSYIFMGDG
	1	ì	MITFHISSKKSSTKTDSHRLGQHIEDALLDVASLFQAGQHFKRR
7106	14	1064	**ROSGRENSRHRCGFLSROTGASKASMTSTDF
1	ł	1004	GLQAGHPHPRSASRIPEADTH\YSKLORAFOSTVNKDUKOMBOM
1		ł	IFRVGFFGSKFGDLDEOEFVYKEPATTKI.PETSUDI.PABVCCC
1	}		OME OF VEVIAUSTPVDKTKLDPNKAYTOTTFVFDVFDFVFMVDDV
1	i i	Į.	TIFERMENLIKKEMYTTPFTLEGRPRGELHEOVPPNTM TOTMUND
	1	1	PYIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLAVAINQEPPD
l		i	AKMLQMVLQGSVGATVNQGPLEVAQVFLAEIPADPKLYRHHNKL
1	į į	}	RLCFKEFIMRCGEAVEKNKRLITADQREYQQELKKNYNKLKENL
7105		[.	RPMIERKIPELYKDI EDVECOVDESHI GOSTINGELKKNYNKLKENL
7107	1145	591	RPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGS *I*WLQTGKKK
			- TANGERA

SEQ			
1 -	1	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	/A-Alanina C. Containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location		Grucamic Acid, Fapheny/alamina com
i	corresponding	corresponding	n-nistiding, leisolehoine v_t,_i_
1		to first	L=Leucine, M=Methionine, N=Asparagine,
[to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
j	amino acid	residue of	S-Sering Tumber of Rearginine,
- 1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ļ	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	COUOII, /=DOSSIDIA NICIANTIAN ANIALI-
7108			\=possible nucleotide insertion\
,100	1	942	VKVALLITNLEQPRIESEWENSFILKMFLFQFVNLNSSTFYIAF
ľ			FIGPERCUPANT DE TRANSPILIANT DE LA PROPERTIE D
i i	1	1	FLGRFTGHPGAYLRLINRWRLEECHPSGCLIDLCMQMGIIMVLK
í	1	}	AT WARE DECIPE LONG WITH TRAKEN OF DEPOSIT AND THE PROPERTY OF
		İ	QFUMAIGLEUEILEMILOFGFTTTFVAADDIADTTATTATT
1		1	RLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGILSVITNAFVI
ì	ł	1	AITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGYVNASLSVFRIS
1	}	I	DEENBERBERGERRGERREGERE
1	l .		DFENRSEPESDGSEFSGTPLKYCRYRDYRDPPHSLVPYGYTLQF WHVLAW
7109	964	 	MILL A TITAL
1	1	102	WDORKRNSLVPGPAHGPAQEEPWEKKESLGAAQEALSIQLQPKE
ı	i	i	TOPFPKSEQVYLHFLSVVTEDGPEPKDKGSLPQPPITEVESQVF
1	1	1	SEKLATOTSTERATSECTLE CONTRACTOR STATEVESQUE
1	Ì	l	SEKLATOTSTFEATSEGTLELQQRNPKAERLRWSPAQEESFRQM
- 1	1		VVIIINEIFIGRRUHECSECGKTFTVNSHIJINDADIRICADENTINA
i	1	1	BUCGRIF AQSSALGOHOR I HTGEK PERCARCAYA PRINCESSAL
1	1	İ	VALUEGEAPIECNECGKAFSOSSYLSONDDINGGEVARIATION
7110			MAIGHCERLIKHRRVHARKEPSH
1 , 110	96	697	RLDNFSGFLVEVTKEERHIVKPLYDRYRLVKOMLTRASITPVLG
1	1	1	SPSTKERCOMLODITECERALIDETERING
ſ	l	1	SPSTKRRGQMLQPIIEGETAHFFEEIKEEEEDGVNLSSELGDML
i	1	Ì	ATAVQVQSSLANSESDVEENOEKLAT.DT.DT.QQQDAAGMDDT.T.DQ
	1	1	DWARAEKKKLRKTLREFEEAFYOONGDWAOKEDDWAG
7111	 		INTINAKURULEVLISKODSSKST
1 '+++	2	414	GSGLYRGPTPGGQCIWKPNSMPPDHERNFGFTQFALELNELTAE
l	1		LERGINGTED DECEMBERS FOR TOPALELNEL TAE
i			LKRSLPSTDTRLRPDQRYLEEGNIQAAEAQKRRIEQLQRDRRKV
1	1 1		MEDINITY MOAK FERROTDSSGKEWWYTNNTYWDI.DA PDCYCNWD
7112	103		GAVLW
	103	495	PRCFPVADRGRLIGGLPDVVTIMEGKTLNLTCTVFGNPDPEVIW
1	1 !		FKNDQDIQLSEHFSVKVEQAKYVSMTIKGVTSEDSGKYSINIKN
ļ	<u> </u>		KYGGEKIDUTUONYUGEKITADA
7113	1	824	KYGGEKIDVTVSVYKHGEKIPDMAPPQQAKPKLIPASASAAGQ
{		024	ACHAQAWHEAPSSLAFTRWCSREERARGGGNLUDGTTBDDFDDG
Í	{ }		LAPSQRPMDDKKKKRSPKPCLAOPAOAPCTLDDVDVDTEURGO.
İ	1		ADGUERUESEKUKAKEKRVGKEKCPDVI.AGGGGGGAGDAGDAGGG
	1 . 1		LTEVTDVYEMEGGLLNLLNDFHSGRLQAFGKECSFEQLEHVREM
1	1 1		QEKLARLHFSLDVCGEEEDDEEEEDGVTEGLPEEQKKTMADRNL
j	! !		DOLL SNICSCICAL UDGGARGEERDG V TEGEPREQKKTMADRNL
	!		DQLLSNLGSCLGALVPGGMRGGEGTYSQSHSWALGEKVGVHGSK
7114	3	1492	SEGETHTERK
[,	1772	VWEVDEQIDHYKESQDKFLWQAAFIGKETLKDESGQECKICRKI
] .	j l	j	TIMIDIVSVKQRLPKYYSWERCSKHHINFIGONDCVGDVVDDG
	j í		CALINAVCLHINLHKAOPAERFFDPNORGKATHOKONI PROGRA
] }	1		QTGEKLYKCTECGKVFIQKANLVVHQRTHTGEKPYECCECAKAF
[1	}	SOKSTLIAHOPTUTGEVDVEGGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
I. 1	1	ļ	SQKSTLIAHQRTHTGEKPYECSECGKTFIQKSTLIKHQRTHTGE
	į į	ł	KPFVCDKCPKAPKSSYHLIRHEKTHIRQAFYKGIKCTTSSLIYQ
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l l	f	1	HIERTRKPYNNDIDYYAKRNALRAAEVWMDDFKSHVYMAWNIPM
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1	ł		IGEVRNSKASAYCLDQGAEDGDRAILYPCHGMSSOLWPVSADGI
1	ł	1.	DUCCELLGSTAFLPDSKCLVDDGTGRMPTLKKCEDVAPPTOBLED
i	i		FTQSGPIVSRATGRCLEVEMSKDANFGLRLVVQRCSGQKWMIRN
		11	WIKHARH
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			RVRMRRNAEVIEEKLSMKSWAKFRPGEPWKGYPNIDPETDPYVT
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SEQ	Predicted	Predicted en	
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7136	2	418	DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTOARAKTENDGSIDIOVANDARAKTENDGS
7136			DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET
	2	466	DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIOVPGGWGVTGGBERGVENS
		466	DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPORAGMRLEPOKKGLVARE
		466	DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPORAGMRLEPOKKGLUDER
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		466	DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKTHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCOLEPENP
7137	2	466	DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP WASGMSTVPGGSRHSLGIOVPGGRWGNTSCEERRA
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7137	2	466	DFVPSFRRPSGNTSQTVWLLRATLEKEVAGLREKTHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP
7137	2	466	DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKTHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP DLRGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPENKETGEHDGY CNINDERST
7137	2	466 466 357	DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP WASGMSTVPGGSRHSLGIOVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP ENMAGGLSDKESYKLSCQLEPENP LENNSARGLKMAASAARGAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ
7137	2	466 466 357	DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKTHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptid (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \ -possible nucleotide insertion) OAGPAEAHTRGPPRLPAATGCPPHLPGLLSGISVDIDPTGLQSG
7141	124	1073	ADFMINOCG LDSRSCWLDMEDLEEDVRFIVDETT DECCTORS - TO THE COLUMN F
7142			VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKEEDITVI BANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSPGYIWK EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM GATRSNLQPP
	658	839	LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA
7143	3	773	SLEMSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRSLARPHDFFDAOTIDALDHDALGHUS
7144	1		HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS DTTVKVWNAHKGFCMSTLRTHKDYVKALAYAKDKELVASAGLDR QIFLWDVNTLTALTASNNTVTTSSLSGNKDSIYSLAMNQLGTII VSGSTEKVLRVWDPRTCAKLMKLKGHTDNVKALLLNRDGTQCLS GSSDGTIRLWSLGQQRCIATYRVHDEGVWALQVNDAFTHVYSGG RDRKIYCTDLRNPDIRVLICE

TRADOCS:1416260.1(%CSK01!.DOC)

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, and complementary sequences thereof.

- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 6. A vector comprising the polynucleotide of claim 1.
- An expression vector comprising the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide encoded by any one of the polynucleotides of claim 1; and

- (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1786 and 3573-5358.
- 11. A composition comprising the polypeptide of claim 10 and a carrier.
- An antibody directed against the polypeptide of claim 10.
- 13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO:1-1786 and 3573-5358, under conditions sufficient to express the polypeptide in said cell; and
 - b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO:1787 -3572 and 5359-7144, the mature protein portion thereof, or the active domain thereof.

- 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO:1-1786 and 3573-5358.
- 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 26. The collection of claim 22, wherein the collection is provided in a computer-readable format.
- 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

A. CL	ASSIFICATION OF SUBJECT MATTER		1 017 03007 342	
IPC(7)	: C07H 21/04; C12N 15/11, 15/63, 15/70, 1	5/87 15/85	· C07V 14/00	
US CL	330/43.1; 433/320.1, 455, 468, 530/300 3	50		
According	to International Patent Classification (IPC) or to bot	h national c	lassification and IPC	
D. FIE	LDS SEARCHED			
Minimum d U.S. :	documentation searched (classification system follow 536/23.1; 435/320.1, 455, 468, 530/300, 350	ed by classi	fication symbols)	
Dogumente				
Documentar	tion searched other than minimum documentation to	the extent t	hat such documents are included	in the fields searched
Electronic d MEDLINE,	lata base consulted during the international search (n EAST	ame of data	base and, where practicable, se	earch terms used)
C. DOC	CUMENTS CONSIDERED TO BE RELEVANT			
Category *	Citation of document, with indication, when	e appropria	e. of the relevant passages	Relevant to claim No.
A	WAJIMA et al. The cDNA cloning and transient hydroxysteroid dehydrogenase of chickens. Gene	expression .	of an overy consider 175 and	1-11, 13-16, and 19-26
A	US 5,175,095 A (MARTINEAU et al) 29 Decem columns 3-18.	ber 1992 (2	9.12.1992), see especially	1-11, 13-16, and 19-26
A	Database PubMed, ID No. 2393392, FREUDENS inhibitor of metalloproteinase: sequence and expre Biophys. Res. Commun. August 1990. Vol.171. I	1-11, 13-16, and 19-26		
A,P	Database PubMed, ID No. 10919256, HENNEBO generation and characterization of an ovary-selecti library. Endocrinology. August 2000, Vol.141, No.	OLD et al. (Ovary-selective genes I: the	1-11, 13-16, and 19-26
A	Database PubMed, ID No. 2760883, BEIL et al. 5 the baboon (Papio anubis). J. Reprod. Fertil. July Abstract.	Synthesis of	polymontides by the control of	1-11, 13-16, and 19-26
A,P	Database PubMed, ID No. 10830289, HINSHELV upstream of the human CYP19 (aromatase) gene m transgenic mice. Endocrinology. June 2000. Vol. I	Priistes ava	ruschenifia avasansias !s	1-11, 13-16, and 19-26
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	documents are listed in the continuation of Box C.		See patent family annex.	
"A" document o	ecial categories of cited documents: defining the general state of the art which is not considered to be at relevance	"T"	later document published after the inter date and not in conflict with the applica principle or theory underlying the inve-	ation but cited to undecorate the l
	lication or patent published on or after the international filing date	"X"	document of particular relevance; the considered novel or cannot be consider	doimed investigation
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)		-Y-	document of particular relevance: the c	laimed invention control be
O" document referring to an oral disclosure, use, exhibition or other means			considered to involve an inventive step combined with one or more other such being obvious 'o a person skilled in the	when the document is
priority date		"&"	document member of the same patent fa	i i
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	ngton, D.C. 20231 (703)305-3230	ŀ	No. (703)/308-0196	/T

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/34263

This interna	servations where certain claims were found unsearchable (Continuation of Itom 1 of Superior of
	servations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)
1.	Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
2.	Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to su an extent that no meaningful international search can be carried out, specifically:
3.	Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.40
Box II Ob	oservations where unity of invention is lacking (Continuation of Item 2 of first sheet)
Γhis Internat Γhis includes	ional Searching Authority found multiple inventions in this international application, as follows: 4 invention Groups and 3572 sequence species
	As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
П.	No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional serch fees must be paid. Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group IV, claim 27, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, udner PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containg same, respectively, and methods of making as well as the first method of use of this jubject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one

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